

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2005, 02:42:13 ; Search time 7612.42 Seconds
(without alignments)
10687.319 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgtctcttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl.*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ats:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	100.0	1679	6	CQ768055 Sequence
2	1679	100.0	1679	6	AR528639 Sequence
3	1679	100.0	1679	6	AX358872 Sequence
4	1679	100.0	1679	6	AX362365 Sequence
5	1679	100.0	1679	6	AX403748 Sequence
6	1679	100.0	1679	6	AX454470 Sequence
7	1679	100.0	1679	6	AX464242 Sequence
8	1679	100.0	1679	6	AX490948 Sequence
9	1679	100.0	1679	9	AX358331 Homo sapi
10	1661.4	95.0	1693	6	AX439649 Sequence
11	1432.8	85.3	1839	6	AX665342 Sequence
12	1432.8	85.3	1839	9	AF126426 Homo sapi
13	1032	61.5	1032	6	AR439648 Sequence
14	996.8	59.4	2040	10	RNU16845
15	976.4	58.2	1615	10	BC023307
16	939	55.9	939	6	AR439650 Sequence
17	910.6	54.2	1410	10	AF282980
18	910.4	54.2	1068	6	AX665344 Sequence
19	874.4	52.1	1104	6	AX665346 Sequence

20	868	51.7	868	6	CQ729109	CQ729109 Sequence
21	856	51.0	1325	9	BC050716	BC050716 Homo sapi
22	851.8	50.7	1140	6	AX665348	AX665348 Sequence
23	643.8	38.3	1058	5	AF292935	AF292935 Gallus ga
24	641.8	38.2	1257	5	GGCEPUI	Z72497 G.gallus mr
25	638.2	38.0	1035	5	AB011810	AB011810 Gallus ga
26	623.6	37.1	1638	12	AF271233	AF271233 Synthetic
27	609.8	36.3	202505	2	AP000912	AP000912 Homo sapi
28	608.2	36.2	184716	2	AC018368	AC018368 Homo sapi
29	608.2	36.2	191071	9	AP004248	AP004248 Homo sapi
30	604.8	36.0	1013	5	AF292936	AF292936 Gallus ga
31	595.4	35.5	187203	2	AP000832	AP000832 Homo sapi
32	571.2	34.0	1533	5	PF01NH55A	Y08170 Gallus gall
33	562.6	33.5	6380	9	HS0805672	BS337377 Homo sapi
34	560.2	33.4	6005	10	BC076581	BC076581 Mus muscu
35	551.8	32.9	1556	5	AF292934	AF292934 Gallus ga
36	547.4	32.6	1108	9	BC074742	BC074742 Homo sapi
37	545.4	32.5	2593	4	BT0BCAM	X12672 Bovine mRNA
38	540.8	32.2	3069	10	RATCALMA	M88709 Rattus norv
39	539.2	32.1	1478	9	HUMOBAM	L34774 Human (clon
40	539.2	32.1	3110	6	AX665340	AX665340 Sequence
41	537.6	32.0	1111	9	BC074773	BC074773 Homo sapi
42	523	31.1	2179	10	RATCALMB	M88710 Rattus norv
43	523	31.1	2337	10	RATCALMC	M88711 Rattus norv
44	504.6	30.1	1370	5	BC074283	BC074283 Xenopus l
45	503	30.0	503	6	CQ768057	CQ768057 Sequence
46	491.2	29.3	537	6	AX593044	AX593044 Sequence
47	465.2	27.7	2935	12	AF271618	AF271618 Synthetic
48	465.2	27.7	3216	5	GGCEPUS	AJ225897 Gallus ga
49	441.2	26.3	452	6	AX079423	AX079423 Sequence
50	435.4	25.9	756	12	AF271232	AF271232 Synthetic
51	366.4	21.8	2055	5	BC081685	BC081685 Danio rer
52	362	21.6	1107	5	GGAMPFG9	Z94718 G.gallus mr
53	359.2	21.4	1158	5	GGAMPFG19	Z94720 G.gallus mr
54	357.6	21.3	2050	5	GG19SPRO	Y08171 Gallus gall
55	348.4	20.8	1194	5	GGAMPFG11	Z94719 G.gallus mr
56	347.4	20.7	1640	9	BC033803	BC033803 Homo sapi
57	343	20.4	1238	6	AR030575	AR030575 Sequence
58	343	20.4	1238	6	AR220258	AR220258 Sequence
59	343	20.4	1238	10	RNU31554	U31554 Rattus norv
60	341.6	20.3	1195	6	AR447794	AR447794 Sequence
61	340.6	20.3	924	6	AR030579	AR030579 Sequence
62	340.6	20.3	977	6	AR030574	AR030574 Sequence
63	340.6	20.3	977	6	AR220257	AR220257 Sequence
64	340.6	20.3	1014	6	AR030577	AR030577 Sequence
65	340.6	20.3	1014	6	AR220260	AR220260 Sequence
66	340.6	20.3	1017	9	HSU41901	U41901 Human limbi
67	338.6	20.2	861	6	AR030581	AR030581 Sequence
68	338.6	20.2	912	6	AR030578	AR030578 Sequence
69	337.4	20.1	945	6	AR030580	AR030580 Sequence
70	337.4	20.1	1757	6	AX704805	AX704805 Sequence
71	333.8	19.9	861	6	AR030582	AR030582 Sequence
72	331.8	19.8	1276	10	AX326256	AX326256 Rattus no
73	316.2	18.8	333	6	AX907426	AX907426 Sequence
74	316.2	18.8	333	6	BD042959	BD042959 Sequence
75	313.8	18.7	1410	5	BC074296	BC074296 Xenopus l
76	303.6	18.1	756	6	AR030589	AR030589 Sequence
77	301	17.9	309	6	AR415672	AR415672 Sequence
78	301	17.9	309	6	AX972506	AX972506 Sequence
79	301	17.9	309	6	BD111225	BD111225 EST and e
80	298.2	17.8	756	6	AR030590	AR030590 Sequence
81	282	16.8	1031	6	CQ728011	CQ728011 Sequence
82	280.4	16.7	1059	5	GGAI32999	AJ132999 Gallus Ga
83	279	16.6	1809	10	AB017139	AB017139 Rattus no
84	274.4	16.3	1179	10	MMU487032	AJ487032 Mus muscu
85	273.4	16.3	11000	2	AC110642_2	Continuation (3 of
86	273.2	16.3	1941	5	AF241638	AF241638 Danio rer
87	272.6	16.2	1165	6	AX662343	AX662343 Sequence
88	272.6	16.2	1196	6	AX662341	AX662341 Sequence
89	272.6	16.2	1327	6	AX704747	AX704747 Sequence
90	272.6	16.2	4834	6	AX358748	AX358748 Sequence
91	272.6	16.2	4834	6	AX362241	AX362241 Sequence
92	272.6	16.2	4834	6	AX403774	AX403774 Sequence

93	272.6	16.2	5582	9	HSW806161	BX538014 Homo sapi	166	108	6.4	172146	2	AC130272	AC130272 Papio anu
94	271	16.1	1119	6	AX675563	AX575563 Sequence	c 167	107.8	6.4	165205	10	AC123550	AC123550 Mus muscu
95	271	16.1	2383	6	AX747470	AX747470 Sequence	c 168	107.8	6.4	277603	2	AC079543	AC079543 Mus muscu
96	271	16.1	2383	9	AX092307	AX092307 Homo sapi	c 169	106.2	6.3	229330	2	AC137057	AC137057 Rattus no
97	269.4	16.0	2840	9	AX358132	AX358132 Homo sapi	c 170	106.2	6.3	238070	2	AC134313	AC134313 Rattus no
98	260.4	15.5	1017	6	AX644995	AX644995 Sequence	c 171	106.2	6.3	242260	2	AC094567	AC094567 Rattus no
99	258.8	15.4	1018	6	AX644993	AX644993 Sequence	c 172	106.2	6.3	255120	2	AC127219	AC127219 Rattus no
100	257.2	15.3	1136	6	AX644997	AX644997 Sequence	c 173	106	6.3	142000	9	AC078813	AC078813 Homo sapi
c 101	256	15.2	257	11	G07361	G07361 human STR W	c 174	105.6	6.3	913	6	AR542162	AR542162 Sequence
102	248.2	15.1	5605	9	BC036771	BC036771 Homo sapi	c 175	104.4	6.2	237726	2	AC124949	AC124949 Rattus no
103	248.2	14.8	186110	2	AC102204	AC102204 Mus muscu	c 176	104.4	6.2	277228	2	AC106911	AC106911 Rattus no
104	246	14.7	1169	6	AX644999	AX644999 Sequence	c 177	102.2	6.1	131490	10	AC122207	AC122207 Mus muscu
105	238.4	14.2	20731	9	AP004721	AP004721 Homo sapi	c 178	102.2	6.1	177251	10	AC124565	AC124565 Mus muscu
106	238.4	14.2	43087	9	AP005155	AP005155 Homo sapi	c 179	100	6.0	219	6	AR030583	AR030583 Sequence
c 107	235.6	14.0	203572	9	AC016769	AC016769 Homo sapi	c 180	99	5.9	219713	2	AC112456	AC112456 Rattus no
c 108	229.2	13.7	251	11	BV199013	BV199013 sqm19956	c 181	99	5.9	234283	2	AC114113	AC114113 Rattus no
109	223.2	13.3	2070	5	BC080221	BC080221 Danio rer	c 182	99	5.9	250355	2	AC127766	AC127766 Rattus no
110	223.2	13.3	2455	5	AF241637	AF241637 Danio rer	c 183	99	5.9	263661	2	AC106603	AC106603 Rattus no
111	221.8	13.2	4323	10	AK122576	AK122576 Mus muscu	c 184	99	5.9	319104	2	AC106602	AC106602 Rattus no
c 112	220.4	13.1	197553	2	AC146103	AC146103 Pan trogl	c 185	98.4	5.9	411	6	CQ731080	CQ731080 Sequence
113	217.4	12.9	36000	9	AP003166	AP003166 Homo sapi	c 186	96.8	5.8	187746	2	AC087123	AC087123 Mus muscu
c 114	209.4	12.5	152686	2	AC018913	AC018913 Homo sapi	c 187	95.2	5.7	219	6	AR030584	AR030584 Sequence
115	207.6	12.4	786	5	GGA13298	AJ13298 Gallus Ga	c 188	92.6	5.5	214942	10	AC125214	AC125214 Mus muscu
116	207.2	12.3	168745	2	AC119552	AC119552 Rattus no	c 189	89.8	5.3	114269	2	AP002341	AP002341 Homo sapi
117	207.2	12.3	248329	2	AC109989	AC109989 Rattus no	c 190	89.8	5.3	152797	2	AC012134	AC012134 Homo sapi
c 118	205.6	12.2	110000	2	AC102028 ¹	Continuation (2 of	c 191	89.8	5.3	159520	9	AC113009	AC113009 Homo sapi
119	203.8	12.1	189323	2	AC150620	AC150620 Callithri	c 192	89.8	5.3	172128	2	AP000762	AP000762 Homo sapi
120	203.8	12.1	191545	2	AC151029	AC151029 Callithri	c 193	89.8	5.3	190104	2	AP002831	AP002831 Homo sapi
121	197.4	11.8	189037	2	AC150026	AC150026 Papio anu	c 194	89.8	5.3	199079	9	AP000844	AP000844 Homo sapi
122	193.6	11.5	352	6	AX866912	AX866912 Sequence	c 195	89	5.3	987	6	CQ734933	CQ734933 Sequence
123	193.6	11.5	352	6	BD026522	BD026522 Sequence	c 196	89	5.3	170006	9	AP005122	AP005122 Homo sapi
c 124	180.4	10.7	5666	6	AX740565	AX740565 Sequence	c 197	88	5.2	882	6	CQ732721	CQ732721 Sequence
c 125	177.6	10.6	215743	2	AC148958	AC148958 Otlemur	c 198	87.2	5.2	163120	5	EX296535	EX296535 Zebrafish
126	176.6	10.5	540	6	AX665354	AX665354 Sequence	c 199	87.2	5.2	180842	2	CR536619	CR536619 Danio rer
c 127	176.6	10.5	116069	2	AP000784	AP000784 Homo sapi	c 200	87	5.2	438	6	AR416888	AR416888 Sequence
128	176.6	10.5	123320	9	AP000863	AP000863 Homo sapi	c 201	87	5.2	438	6	BD112441	BD112441 EST and e
c 129	176.6	10.5	176676	2	AC012234	AC012234 Homo sapi	c 202	87	5.2	438	6	BD112441	BD112441 EST and e
130	176.6	10.5	177102	2	AP002808	AP002808 Homo sapi	c 203	86.6	5.2	169582	2	AC102190	AC102190 Mus muscu
c 131	175	10.4	642	6	CQ732119	CQ732119 Sequence	c 204	86.2	5.1	74368	9	AL391239	AL391239 Human DNA
132	174.4	10.4	182	6	AR413330	AR413330 Sequence	c 205	86.2	5.1	131457	9	AL356600	AL356600 Human DNA
133	174.4	10.4	182	6	AX970164	AX970164 Sequence	c 206	86.2	5.1	153852	2	AC009694	AC009694 Homo sapi
134	174.4	10.4	182	6	BD108883	BD108883 EST and e	c 207	86.2	5.1	315761	2	AL158079	AL158079 Homo sapi
c 135	173.2	10.3	242565	2	AC0944728	AC0944728 Rattus no	c 208	85.8	5.1	162247	2	AC102328	AC102328 Mus muscu
136	173.2	10.3	251570	2	AC094463	AC094463 Rattus no	c 209	85.4	5.1	295	6	CQ732164	CQ732164 Sequence
c 137	172.2	10.3	133989	2	AC149777	AC149777 Bos tauru	c 210	84.2	5.0	245900	2	AC128465	AC128465 Rattus no
c 138	172.2	10.3	203732	4	AC150499	AC150499 Bos tauru	c 211	83.4	5.0	162717	10	AC127259	AC127259 Mus muscu
c 139	171.2	10.2	184012	10	AC116523	AC116523 Mus muscu	c 212	83.4	5.0	258847	2	AC112746	AC112746 Rattus no
140	166.8	9.9	504	6	CQ715694	CQ715694 Sequence	c 213	83.4	5.0	285603	2	AC104926	AC104926 Mus muscu
141	164.8	9.8	531	6	CQ719449	CQ719449 Sequence	c 214	81.8	4.9	110000	2	AC110642 ³	Continuation (4 of
c 142	163.2	9.7	585	6	AX079674	AX079674 Sequence	c 215	78.6	4.7	420	6	AX665356	AX665356 Sequence
c 143	160	9.5	408	6	AX684132	AX684132 Sequence	c 216	78.6	4.7	113063	2	AC010946	AC010946 Homo sapi
c 144	156	9.3	371	6	CQ731074	CQ731074 Sequence	c 217	78.6	4.7	191204	9	AP000843	AP000843 Homo sapi
c 145	152.4	9.1	793	5	AX932289	AX932289 Gallus ga	c 218	78.6	4.7	202505	2	AP000912	AP000912 Homo sapi
c 146	152.2	9.1	168191	2	AC151813	AC151813 Dasyypus n	c 219	77.8	4.6	177	6	AR030585	AR030585 Sequence
c 147	147.6	8.8	259743	2	AC113965	AC113965 Mus muscu	c 220	77.8	4.6	177	6	AR030586	AR030586 Sequence
148	146	8.7	200	6	AX898567	AX898567 Sequence	c 221	76.8	4.6	479	6	AX665358	AX665358 Sequence
c 149	146	8.7	200	6	BD034100	BD034100 Sequence	c 222	71.4	4.3	480	6	AX665357	AX665357 Sequence
c 150	145	8.6	150308	10	AC098294	AC098294 Rattus no	c 223	69.2	4.1	62350	9	AC067725	AC067725 Homo sapi
c 151	145	8.6	225433	2	AC106484	AC106484 Rattus no	c 224	69	4.1	146352	2	CR548641	CR548641 Danio rer
c 152	145	8.6	237199	10	AC094830	AC094830 Rattus no	c 225	69	4.1	186279	5	EX950870	EX950870 Zebrafish
c 153	140.6	8.4	152686	2	AC018913	AC018913 Homo sapi	c 226	69	4.1	191779	2	CR376789	CR376789 Danio rer
c 154	135.2	8.1	268	4	AF271584	AF271584 Bos tauru	c 227	67	4.0	176744	2	AC027631	AC027631 Homo sapi
c 155	135.2	8.1	110000	2	AC102028 ⁰	AC102028 Mus muscu	c 228	65.6	3.9	198	6	AR030587	AR030587 Sequence
c 156	135.2	8.1	186110	2	AC102204	AC102204 Mus muscu	c 229	65	3.9	195956	2	AC127626	AC127626 Rattus no
c 157	128	7.6	184716	2	AC018368	AC018368 Homo sapi	c 230	63.4	3.8	198	6	AR030588	AR030588 Sequence
c 158	113.6	6.8	195993	2	AC134953	AC134953 Pan trogl	c 231	61.6	3.7	270	6	AX665353	AX665353 Sequence
c 159	113.6	6.8	212752	9	AC063977	AC063977 Homo sapi	c 232	61.6	3.6	117951	9	AL359821	AL359821 Human DNA
c 160	112.8	6.7	157263	2	AX957285	AX957285 Danio rer	c 233	60.8	3.6	199301	2	AC119938	AC119938 Mus muscu
c 161	110.6	6.6	292	6	CQ716587	CQ716587 Sequence	c 234	60	3.6	60	6	CQ544101	CQ544101 Sequence
c 162	110.4	6.6	213331	2	AC125960	AC125960 Rattus no	c 235	58.6	3.5	2000	6	AX655393	AX655393 Sequence
c 163	109.6	6.5	175963	2	AC148913	AC148913 Sus scrof	c 236	58.6	3.5	166417	10	AC127685	AC127685 Mus muscu
c 164	109.4	6.5	134184	2	AC150028	AC150028 Canis fam	c 237	58.6	3.5	166417	10	AC127685	AC127685 Mus muscu
c 165	108	6.4	168861	2	AC130786	AC130786 Papio anu	c 238	58	3.5	143672	2	AP001806	AP001806 Homo sapi

C 385	50.2	3.0	383	6	CQ502211	Sequence	C 458	49.8	3.0	8712	6	AX344694	Sequence
C 386	50.2	3.0	383	6	CQ511079	Sequence	C 459	49.8	3.0	13758	3	SST558163	Strongylo
C 387	50.2	3.0	384	6	CQ395463	Sequence	C 460	49.8	3.0	84299	5	EX465900	Zebrafish
C 388	50.2	3.0	384	6	CQ401799	Sequence	C 461	49.8	3.0	132068	3	AC008965	Homo sapi
C 389	50.2	3.0	384	6	CQ487104	Sequence	C 462	49.8	3.0	156254	10	AC129196	AC129196 Mus muscu
C 390	50.2	3.0	448	6	CQ516969	Sequence	C 463	49.8	3.0	183762	2	AC128232	Rattus no
C 391	50.2	3.0	861	9	AK026600	Homo sapi	C 464	49.8	3.0	193796	2	AC123600	Mus muscu
C 392	50.2	3.0	1090	10	BC049543	Mus muscu	C 465	49.8	3.0	198615	10	AC123678	Mus muscu
C 393	50.2	3.0	1448	10	BC052344	Mus muscu	C 466	49.8	3.0	212604	5	AL805945	Zebrafish
C 394	50.2	3.0	1619	9	BC032001	Homo sapi	C 467	49.8	3.0	218319	2	AC107863	Mus muscu
C 395	50.2	3.0	2078	9	BC042098	Homo sapi	C 468	49.8	3.0	251721	2	AC136566	Rattus no
C 396	50.2	3.0	2104	9	BC032371	Homo sapi	C 469	49.8	3.0	263341	2	AC094581	Rattus no
C 397	50.2	3.0	2641	10	BC044860	Mus muscu	C 470	49.8	3.0	266869	2	AC123456	Rattus no
C 398	50.2	3.0	4064	10	BC072632	Mus muscu	C 471	49.8	3.0	289973	2	AC135678	Rattus no
C 399	50.2	3.0	6476	6	AX345442	Sequence	C 472	49.8	3.0	762	9	BC070287	Homo sapi
C 400	50.2	3.0	150751	9	AC092809	Homo sapi	C 473	49.6	3.0	793	9	BC018189	Homo sapi
C 401	50.2	3.0	168136	2	AC138388	Mus muscu	C 474	49.6	3.0	1003	5	BC067645	Danio rer
C 402	50.2	3.0	182871	3	AC117176	Dictyoste	C 475	49.6	3.0	1044	9	AB019565	Homo sapi
C 403	50.2	3.0	189631	2	AC009920	Homo sapi	C 476	49.6	3.0	1218	9	BC065742	Homo sapi
C 404	50.2	3.0	203114	2	AC011818	Homo sapi	C 477	49.6	3.0	1250	9	BC051908	Homo sapi
C 405	50.2	3.0	349980	6	AX344553	Sequence	C 478	49.6	3.0	1271	9	AF090934	Homo sapi
C 406	50	3.0	325	6	CQ527169	Sequence	C 479	49.6	3.0	1340	9	BC073835	Homo sapi
C 407	50	3.0	464	6	CQ519083	Sequence	C 480	49.6	3.0	1458	9	BC041443	Homo sapi
C 408	50	3.0	671	6	CQ522475	Sequence	C 481	49.6	3.0	1530	9	BC036925	Homo sapi
C 409	50	3.0	646	5	BC083988	Xenopus 1	C 482	49.6	3.0	1606	10	BC051176	Mus muscu
C 410	50	3.0	653	10	BC039566	Mus muscu	C 483	49.6	3.0	1657	8	NTACCS	X98492 Nicotiana t
C 411	50	3.0	842	9	BC051899	Homo sapi	C 484	49.6	3.0	1787	9	BC046645	Homo sapi
C 412	50	3.0	870	6	BD231669	31 human	C 485	49.6	3.0	1993	3	AK112520	Ciona int
C 413	50	3.0	2240	9	BC062587	Homo sapi	C 486	49.6	3.0	2027	9	BC063512	Homo sapi
C 414	50	3.0	2556	9	HSN805953	Dictyoste	C 487	49.6	3.0	2081	9	HSN806272	Homo sapi
C 415	50	3.0	2936	5	BC077828	Xenopus 1	C 488	49.6	3.0	2135	10	BC017640	Mus muscu
C 416	50	3.0	3203	9	BC040941	Homo sapi	C 489	49.6	3.0	2161	6	CQ414527	Sequence
C 417	50	3.0	3645	10	BC062916	Mus muscu	C 490	49.6	3.0	2350	9	BC063427	Homo sapi
C 418	50	3.0	3806	5	AJ720876	Gallus ga	C 491	49.6	3.0	2521	10	BC026021	Mus muscu
C 419	50	3.0	4942	9	HSN808887	Homo sapi	C 492	49.6	3.0	2870	9	HSN800882	Homo sapi
C 420	50	3.0	5387	6	AX344633	Sequence	C 493	49.6	3.0	3141	10	BC017634	BC017634 Mus muscu
C 421	50	3.0	9747	9	HSN806689	Homo sapi	C 494	49.6	3.0	3232	9	AF090901	AF090901 Homo sapi
C 422	50	3.0	21537	6	AX346901	Sequence	C 495	49.6	3.0	3914	9	HSN803724	AL832416 Homo sapi
C 423	50	3.0	110000	2	FWAL13_07	Continuation (8 of	C 496	49.6	3.0	3914	9	HSN806219	HSN80409 Homo sapi
C 424	50	3.0	137697	2	AC126419	Mus muscu	C 497	49.6	3.0	5134	9	BC032404	BC032404 Homo sapi
C 425	50	3.0	160706	2	AC137910	Canis fam	C 498	49.6	3.0	5355	9	HSN806819	BSX40744 Homo sapi
C 426	50	3.0	173053	10	AL844145	Mouse DNA	C 499	49.6	3.0	5520	6	AX346420	AX346420 Sequence
C 427	50	3.0	184057	10	AL928579	Mouse DNA	C 500	49.6	3.0	6015	6	AX345579	AX345579 Sequence
C 428	50	3.0	184163	2	AC120245	Rattus no	C 501	49.6	3.0	110000	2	AC102349	Mus muscu
C 429	50	3.0	189649	2	AC139641	Rattus no	C 502	49.6	3.0	142948	9	AC147025	AC147025 Pan trogl
C 430	50	3.0	212996	2	CRS48633	Danio rer	C 503	49.6	3.0	151802	3	AC114263	AC114263 Dictyoste
C 431	50	3.0	245677	10	AC129162	Rattus no	C 504	49.6	3.0	173854	2	AC073047	AC073047 Homo sapi
C 432	50	3.0	249734	2	AC097362	Rattus no	C 505	49.6	3.0	187418	10	AL672278	AL672278 Mouse DNA
C 433	49.8	3.0	263	6	CQ663258	Sequence	C 506	49.6	3.0	194398	10	AC135669	AC135669 Mus muscu
C 434	49.8	3.0	270	6	CQ655781	Sequence	C 507	49.6	3.0	214029	2	AC148335	AC148335 Mus muscu
C 435	49.8	3.0	311	6	CQ517391	Sequence	C 508	49.6	3.0	349980	6	AX344563	AX344563 Sequence
C 436	49.8	3.0	376	6	CQ526056	Sequence	C 509	49.4	2.9	408	6	CQ524818	Sequence
C 437	49.8	3.0	581	6	CQ522618	Sequence	C 510	49.4	2.9	438	6	CQ514042	Sequence
C 438	49.8	3.0	543	6	CQ524637	Sequence	C 511	49.4	2.9	481	9	BC070219	BC070219 Homo sapi
C 439	49.8	3.0	545	6	AX185705	Sequence	C 512	49.4	2.9	579	6	CQ526842	Sequence
C 440	49.8	3.0	573	11	BV060605	S209P6332	C 513	49.4	2.9	622	6	CQ427774	Sequence
C 441	49.8	3.0	726	9	HSR327951	Homo sapi	C 514	49.4	2.9	658	6	BD275413	BD275413 50 Human
C 442	49.8	3.0	815	9	BC070265	Homo sapi	C 515	49.4	2.9	781	10	BC028530	Mus muscu
C 443	49.8	3.0	854	3	AK174348	Ciona int	C 516	49.4	2.9	1081	9	BC043527	BC043527 Homo sapi
C 444	49.8	3.0	894	9	BC044257	Homo sapi	C 517	49.4	2.9	1310	9	HSN807559	BSX47414 Homo sapi
C 445	49.8	3.0	1048	6	BD223102	98 human	C 518	49.4	2.9	1589	9	BC043543	Homo sapi
C 446	49.8	3.0	1048	6	AR243800	Sequence	C 519	49.4	2.9	1603	6	CQ490224	Sequence
C 447	49.8	3.0	1073	6	BD190930	Secreted	C 520	49.4	2.9	1603	6	CQ491236	Sequence
C 448	49.8	3.0	1824	9	BC018641	Homo sapi	C 521	49.4	2.9	1603	6	CQ496086	Sequence
C 449	49.8	3.0	1837	6	AX962574	Sequence	C 522	49.4	2.9	1647	9	CQ497104	Sequence
C 450	49.8	3.0	2005	9	BC013372	Homo sapi	C 523	49.4	2.9	1647	9	HSN806060	BSX57936 Homo sapi
C 451	49.8	3.0	2012	9	AX125488	Homo sapi	C 524	49.4	2.9	2002	9	BC068030	Homo sapi
C 452	49.8	3.0	2266	9	BC047898	Homo sapi	C 525	49.4	2.9	2395	9	AF090903	AF090903 Homo sapi
C 453	49.8	3.0	2496	6	BD191411	Secreted	C 526	49.4	2.9	3475	9	HSN808741	BSX648590 Homo sapi
C 454	49.8	3.0	2539	9	BC041100	Homo sapi	C 527	49.4	2.9	4066	10	BC048824	Mus muscu
C 455	49.8	3.0	2630	9	BC038222	Homo sapi	C 528	49.4	2.9	4744	5	BC066770	BC066770 Xenopus 1
C 456	49.8	3.0	3230	9	BC063118	Homo sapi	C 529	49.4	2.9	4782	14	AY744492	AY744492 Tomato sp
C 457	49.8	3.0	7346	6	AX345247	Sequence	C 530	49.4	2.9	71532	2	AC023655	AC023655 Homo sapi

C 531	49.4	2.9	84821	10	BX276123	Mouse DNA	604	49	2.9	2700	9	BC064849	BC064849 Homo sapi
532	49.4	2.9	110000	3	AC116305	Dictyoste	605	49	2.9	2728	9	BC022218	BC022218 Homo sapi
C 533	49.4	2.9	138604	2	CR847865	Danio rer	606	49	2.9	3020	10	BC055068	BC055068 Mus muscu
C 534	49.4	2.9	169736	2	AC126225	Papio anu	607	49	2.9	3482	9	HSB800550	AL050393 Homo sapi
C 535	49.4	2.9	187024	2	CR759947	Gorilla g	608	49	2.9	3499	10	BC007476	BC007476 Mus muscu
C 536	49.4	2.9	227273	2	AC141526	Rattus no	609	49	2.9	3856	9	HSB805531	AL834437 Homo sapi
C 537	49.4	2.9	335050	3	PFA929356	Plasmodiu	610	49	2.9	3870	9	HSB806049	BX537527 Homo sapi
C 538	49.4	2.9	349980	6	AX344559	Sequence	611	49	2.9	3916	10	BC018439	BC018439 Mus muscu
C 539	49.4	2.9	349980	6	AX344566	Sequence	612	49	2.9	5703	10	BC054080	BC054080 Mus muscu
540	49.2	2.9	442	6	CQ526679	Sequence	C 613	49	2.9	5845	6	AX346564	AX346564 Sequence
541	49.2	2.9	539	6	CQ526692	Sequence	C 614	49	2.9	5930	6	CQ412529	CQ412529 Sequence
542	49.2	2.9	544	6	CQ526772	Sequence	C 615	49	2.9	6012	6	AX346960	AX346960 Sequence
543	49.2	2.9	554	6	CQ526772	Sequence	C 616	49	2.9	6161	6	AX345313	AX345313 Sequence
544	49.2	2.9	575	6	CQ526566	Sequence	C 617	49	2.9	6211	6	AX345708	AX345708 Sequence
C 545	49.2	2.9	621	6	AX187131	Sequence	C 618	49	2.9	6522	6	AX345952	AX345952 Sequence
546	49.2	2.9	650	9	BC034814	Homo sapi	C 619	49	2.9	6719	9	HSB803507	AL832200 Homo sapi
547	49.2	2.9	758	9	BC062750	Homo sapi	C 620	49	2.9	11416	6	AX251758	AX251758 Sequence
548	49.2	2.9	1191	9	BC014547	Homo sapi	C 621	49	2.9	11416	6	AX345020	AX345020 Sequence
549	49.2	2.9	1381	5	BC063358	Xenopus t	C 622	49	2.9	11416	6	AX348567	AX348567 Sequence
550	49.2	2.9	1537	9	HSB803079	Sequence	C 623	49	2.9	40862	6	AX346974	AX346974 Sequence
551	49.2	2.9	1629	10	BC033451	Sequence	C 624	49	2.9	125020	9	AF429315	AF429315 Homo sapi
552	49.2	2.9	1702	9	BC052293	Homo sapi	C 625	49	2.9	135050	2	AC118536	AC118536 Canis fam
553	49.2	2.9	2270	9	HSB805047	Homo sapi	C 626	49	2.9	160230	10	BX072552	BX072552 Mouse DNA
554	49.2	2.9	2451	9	BC050636	Homo sapi	C 627	49	2.9	180352	2	AC120550	AC120550 Mus muscu
C 555	49.2	2.9	2501	6	AX599024	Sequence	C 628	49	2.9	198792	2	AC117825	AC117825 Mus muscu
556	49.2	2.9	2628	9	BC032691	Homo sapi	C 629	49	2.9	203422	2	AC107857	AC107857 Mus muscu
557	49.2	2.9	2661	10	BC026137	Homo sapi	C 630	49	2.9	248353	2	AC106139	AC106139 Rattus no
558	49.2	2.9	3030	3	AK116919	Ciona int	C 631	49	2.9	349980	6	AX344561	AX344561 Sequence
559	49.2	2.9	3300	9	BC011656	Homo sapi	C 632	49	2.9	349980	6	AX344565	AX344565 Sequence
560	49.2	2.9	3341	9	BC032308	Homo sapi	C 633	48.8	2.9	299	6	CQ397773	CQ397773 Sequence
561	49.2	2.9	3392	3	AF300334	Dictyoste	C 634	48.8	2.9	299	6	CQ404070	CQ404070 Sequence
562	49.2	2.9	3686	10	BC023773	Mus muscu	C 635	48.8	2.9	308	6	CQ517578	CQ517578 Sequence
563	49.2	2.9	3836	9	BC063854	Homo sapi	C 636	48.8	2.9	313	6	CQ523441	CQ523441 Sequence
564	49.2	2.9	4265	9	HSB807603	Homo sapi	C 637	48.8	2.9	326	6	CQ472519	CQ472519 Sequence
565	49.2	2.9	6644	6	E23356	Virus vecto	C 638	48.8	2.9	446	6	CQ487730	CQ487730 Sequence
C 566	49.2	2.9	7058	6	AX348438	Sequence	C 639	48.8	2.9	489	6	CQ491815	CQ491815 Sequence
567	49.2	2.9	7372	6	E23357	Sequence	C 640	48.8	2.9	489	6	CQ497713	CQ497713 Sequence
568	49.2	2.9	7797	6	E23355	Virus vecto	C 641	48.8	2.9	510	6	CQ526266	CQ526266 Sequence
569	49.2	2.9	7996	6	E23359	Virus vecto	C 642	48.8	2.9	836	6	AX704815	AX704815 Sequence
C 570	49.2	2.9	11394	6	AX323608	Sequence	C 643	48.8	2.9	844	9	BC009571	BC009571 Homo sapi
C 571	49.2	2.9	35962	6	AX598904	Sequence	C 644	48.8	2.9	1007	10	BC049682	BC049682 Mus muscu
572	49.2	2.9	153064	9	AC011492	Homo sapi	C 645	48.8	2.9	1345	10	BC048718	BC048718 Mus muscu
C 573	49.2	2.9	162473	9	AC005803	Homo sapi	C 646	48.8	2.9	1362	9	BC065292	BC065292 Homo sapi
574	49.2	2.9	226142	2	AC126422	Mus muscu	C 647	48.8	2.9	1462	10	BC006018	BC006018 Mus muscu
575	49.2	2.9	245117	2	AC111284	Rattus no	C 648	48.8	2.9	1570	10	BC049624	BC049624 Mus muscu
576	49.2	2.9	302156	3	AC116977	Dictyoste	C 649	48.8	2.9	1770	9	BC025717	BC025717 Homo sapi
C 577	49.2	2.9	349980	6	AX344573	Sequence	C 650	48.8	2.9	1813	6	AR164089	AR164089 Sequence
C 578	49	2.9	256	6	AX182154	Sequence	C 651	48.8	2.9	1990	10	BC042668	BC042668 Mus muscu
579	49	2.9	347	6	CQ526680	Sequence	C 652	48.8	2.9	2064	10	BC053424	BC053424 Mus muscu
580	49	2.9	429	6	CQ525532	Sequence	C 653	48.8	2.9	2394	5	BC063911	BC063911 Xenopus t
581	49	2.9	469	6	CQ524790	Sequence	C 654	48.8	2.9	2500	9	BC065207	BC065207 Homo sapi
582	49	2.9	472	6	CQ525172	Sequence	C 655	48.8	2.9	2735	9	BC046366	BC046366 Homo sapi
583	49	2.9	541	6	CQ522898	Sequence	C 656	48.8	2.9	2823	9	BC018694	BC018694 Homo sapi
584	49	2.9	608	10	BC061544	Rattus no	C 657	48.8	2.9	2968	9	BC060758	BC060758 Homo sapi
585	49	2.9	757	9	HSB802777	Homo sapi	C 658	48.8	2.9	3134	9	HSB805794	BS537718 Homo sapi
586	49	2.9	967	9	BC060554	Rattus no	C 659	48.8	2.9	3380	9	HSB807223	BX547079 Homo sapi
587	49	2.9	1232	10	BC060554	Rattus no	C 660	48.8	2.9	4436	10	BC058961	BC058961 Mus muscu
588	49	2.9	1414	3	AK112149	Ciona int	C 661	48.8	2.9	4454	9	HSB806344	BX538143 Homo sapi
589	49	2.9	1755	9	BC031825	Homo sapi	C 662	48.8	2.9	5378	6	AX346781	AX346781 Sequence
590	49	2.9	1763	5	AY079192	Xenopus t	C 663	48.8	2.9	6386	9	HSB803518	AL832211 Sequence
591	49	2.9	1850	9	BC040123	Homo sapi	C 664	48.8	2.9	83391	6	AX458578	AX458578 Sequence
592	49	2.9	1853	10	BC052346	Mus muscu	C 665	48.8	2.9	110000	2	AC101802	Continuation (3 of
593	49	2.9	1869	5	BC076804	Xenopus l	C 666	48.8	2.9	141914	2	AC108177	AC108177 Fellea cat
594	49	2.9	1891	9	HSB807589	Homo sapi	C 667	48.8	2.9	174495	2	AC101795	AC101795 Mus muscu
595	49	2.9	1912	10	BC027060	Mus muscu	C 668	48.8	2.9	175202	9	AC134684	AC134684 Homo sapi
596	49	2.9	1935	5	BC065678	Danio rer	C 669	48.8	2.9	188884	9	AC130367	AC130367 Homo sapi
597	49	2.9	1954	6	BD270057	Secreted	C 670	48.8	2.9	214132	2	AC124975	AC124975 Mus muscu
598	49	2.9	1960	9	BC038806	Homo sapi	C 671	48.8	2.9	228842	10	AC116130	AC116130 Mus muscu
599	49	2.9	2045	9	BC047761	Homo sapi	C 672	48.8	2.9	273978	2	AC130001	AC130001 Rattus no
600	49	2.9	2116	9	BC034379	Homo sapi	C 673	48.8	2.9	274097	2	AC111767	AC111767 Rattus no
601	49	2.9	2197	9	BC045177	Homo sapi	C 674	48.8	2.9	349980	6	AX344564	AX344564 Sequence
602	49	2.9	2347	9	BC027875	Homo sapi	C 675	48.6	2.9	291	6	CQ398062	CQ398062 Sequence
603	49	2.9	2553	10	BC061558	Rattus no	C 676	48.6	2.9	291	6	CQ404353	CQ404353 Sequence

677	48.6	2.9	320	6	CQ517221	Sequence	750	48.4	2.9	3942	10	BC063741	Mus muscu
c 678	48.6	2.9	425	6	CQ506214	Sequence	751	48.4	2.9	4073	6	AX269342	Sequence
679	48.6	2.9	471	6	CQ515907	Sequence	c 752	48.4	2.9	4316	6	CQ806814	Sequence
680	48.6	2.9	547	9	BC070202	Homo sapi	c 753	48.4	2.9	4316	6	CQ807088	Sequence
681	48.6	2.9	816	6	CQ486089	Sequence	c 754	48.4	2.9	4316	6	AX795752	Sequence
682	48.6	2.9	835	9	HSM801514	Sequence	c 755	48.4	2.9	4316	6	AX795868	Sequence
683	48.6	2.9	843	10	BC026460	Sequence	c 756	48.4	2.9	4316	6	AX822260	Sequence
684	48.6	2.9	932	9	BC043537	Sequence	c 757	48.4	2.9	4316	6	AX822388	Sequence
685	48.6	2.9	1486	9	BC042084	Homo sapi	c 758	48.4	2.9	4316	6	AX825900	Sequence
686	48.6	2.9	1569	10	BC083659	Sequence	c 759	48.4	2.9	4316	6	AX826028	Sequence
687	48.6	2.9	1642	5	BC064224	Xenopus t	c 760	48.4	2.9	5195	6	AX345823	Sequence
688	48.6	2.9	1781	9	BC043529	Homo sapi	c 761	48.4	2.9	6070	6	AX281468	Sequence
689	48.6	2.9	1808	6	AX535019	Sequence	c 762	48.4	2.9	6070	6	AX346581	Sequence
690	48.6	2.9	1959	9	BC043548	Homo sapi	c 763	48.4	2.9	6070	6	AX348804	Sequence
691	48.6	2.9	1994	3	AK116078	Homo sapi	c 764	48.4	2.9	6070	6	AX458614	Sequence
692	48.6	2.9	2009	9	BC050391	Sequence	c 765	48.4	2.9	6577	6	AX251920	Sequence
693	48.6	2.9	2034	6	AX127529	Sequence	c 766	48.4	2.9	6577	6	AX346258	Sequence
694	48.6	2.9	2034	6	AX675184	Sequence	c 767	48.4	2.9	6577	6	AX348993	Sequence
695	48.6	2.9	2390	9	AF090900	Homo sapi	c 768	48.4	2.9	6690	9	HSM803755	Sequence
696	48.6	2.9	3000	9	BC036812	Homo sapi	c 769	48.4	2.9	6849	10	AX324169	Mouse DNA
c 697	48.6	2.9	5532	6	AX345680	Sequence	c 770	48.4	2.9	6944	6	AX347467	Sequence
c 698	48.6	2.9	5946	6	AX345813	Sequence	c 771	48.4	2.9	6944	6	AX349188	Sequence
c 699	48.6	2.9	14615	6	AX251461	Sequence	c 772	48.4	2.9	6944	6	AX657867	Sequence
700	48.6	2.9	68222	9	AL391904	Human DNA	c 773	48.4	2.9	6944	6	AX659141	Sequence
c 701	48.6	2.9	111865	2	AL355883	Homo sapi	c 774	48.4	2.9	7467	6	CQ807272	Sequence
c 702	48.6	2.9	139772	2	AC068270	Homo sapi	c 775	48.4	2.9	8546	6	AX828406	Sequence
c 703	48.6	2.9	151736	2	AC138596	Mus muscu	776	48.4	2.9	8546	6	HSA306906	Sequence
c 704	48.6	2.9	157311	10	AC132236	Mus muscu	c 777	48.4	2.9	9117	6	AX345970	Sequence
705	48.6	2.9	167489	5	BX664600	Sequence	c 778	48.4	2.9	11097	6	AX826972	Sequence
c 706	48.6	2.9	167728	9	AC115889	Mus muscu	c 779	48.4	2.9	11097	6	AX826972	Sequence
707	48.6	2.9	177083	10	AC126805	Mus muscu	780	48.4	2.9	18207	9	AF156100	Homo sapi
708	48.6	2.9	181226	10	AC147111	Mus muscu	781	48.4	2.9	18207	9	AF156100	Homo sapi
709	48.6	2.9	182229	2	AC145600	Mus muscu	782	48.4	2.9	26459	2	AL3390854	Human DNA
710	48.6	2.9	184736	10	AL808128	Mouse DNA	783	48.4	2.9	42839	2	AC027282	Homo sapi
c 711	48.6	2.9	185291	2	AC123147	Rattus no	c 784	48.4	2.9	73778	6	AX344575	Sequence
c 712	48.6	2.9	206324	10	AL807786	Mouse DNA	c 785	48.4	2.9	145275	9	AF189745	Homo sapi
713	48.6	2.9	210233	2	AC128584	Rattus no	c 786	48.4	2.9	149813	2	EX942840	Danio rer
714	48.6	2.9	210269	2	BX927280	Danio rer	c 787	48.4	2.9	165146	2	AP002415	Homo sapi
c 715	48.6	2.9	212557	2	AC120134	Mus muscu	c 788	48.4	2.9	167671	2	AC142166	Mus sapi
c 716	48.6	2.9	212908	2	CR847533	Danio rer	c 789	48.4	2.9	176929	9	AC004887	Homo sapi
c 717	48.6	2.9	221023	10	AL844487	Mouse DNA	c 790	48.4	2.9	182871	3	AC117176	Diclyostere
718	48.6	2.9	231447	2	AC121422	Rattus no	c 791	48.4	2.9	183648	3	AC117081	Diclyostere
c 719	48.6	2.9	269576	2	AC073684	Mus muscu	c 792	48.4	2.9	188555	10	AC122417	Mus muscu
720	48.4	2.9	147	6	AR418886	Sequence	c 793	48.4	2.9	198377	2	CR792437	Danio rer
721	48.4	2.9	147	6	AX979580	Sequence	794	48.4	2.9	199472	9	AC022267	Homo sapi
722	48.4	2.9	147	6	BD114439	EST and e	c 795	48.4	2.9	204278	10	AC124507	Mus muscu
723	48.4	2.9	186	6	CQ677473	Sequence	c 796	48.4	2.9	208921	2	AP001911	Homo sapi
c 724	48.4	2.9	388	6	CQ410454	Sequence	c 797	48.4	2.9	215676	2	AC131299	Mus muscu
725	48.4	2.9	432	6	CQ524989	Sequence	798	48.4	2.9	221944	2	AC119914	Mus muscu
726	48.4	2.9	451	6	CQ524930	Sequence	799	48.4	2.9	228178	2	AC101866	Mus muscu
727	48.4	2.9	661	10	BC051629	Sequence	c 800	48.4	2.9	232304	2	AC103201	Rattus no
728	48.4	2.9	1078	9	BC035314	Homo sapi	c 801	48.4	2.9	258658	3	AE014832	Plasmodiu
729	48.4	2.9	1117	5	AR123145	Sequence	c 802	48.4	2.9	349980	6	AX344558	Sequence
730	48.4	2.9	1175	5	BC049447	Danio rer	c 803	48.4	2.9	349980	6	AX344570	Sequence
731	48.4	2.9	1445	9	BC063545	Homo sapi	c 804	48.2	2.9	153	6	AX340795	Sequence
732	48.4	2.9	1550	9	BC063432	Homo sapi	c 805	48.2	2.9	268	6	AX185659	Sequence
733	48.4	2.9	1586	9	BC027882	Homo sapi	c 806	48.2	2.9	317	6	CQ526915	Sequence
734	48.4	2.9	1727	10	BC050800	Sequence	c 807	48.2	2.9	359	6	CQ431130	Sequence
735	48.4	2.9	1872	9	BC038952	Homo sapi	c 808	48.2	2.9	385	6	CQ398297	Sequence
736	48.4	2.9	1978	9	BC012750	Homo sapi	c 809	48.2	2.9	385	6	CQ404584	Sequence
737	48.4	2.9	2065	5	BC066376	Danio rer	c 810	48.2	2.9	430	9	BC062435	Homo sapi
738	48.4	2.9	2184	9	AB060903	Macaca fa	811	48.2	2.9	453	6	CQ517526	Sequence
739	48.4	2.9	2238	5	BC063964	Danio rer	812	48.2	2.9	504	6	CQ525672	Sequence
740	48.4	2.9	2265	9	BC063477	Homo sapi	813	48.2	2.9	527	10	BC049658	Mus muscu
741	48.4	2.9	2402	5	BC077592	Xenopus l	814	48.2	2.9	633	10	BC059147	Rattus no
742	48.4	2.9	2652	3	AK174388	Ciona int	815	48.2	2.9	724	10	BC049721	Mus muscu
743	48.4	2.9	2679	10	BC006021	Mus muscu	816	48.2	2.9	745	10	BC049606	Mus muscu
744	48.4	2.9	3270	9	BC050552	Homo sapi	817	48.2	2.9	1119	10	BC021629	Mus muscu
745	48.4	2.9	3422	9	HSM805920	Sequence	818	48.2	2.9	1561	9	BC040443	Homo sapi
746	48.4	2.9	3454	9	HSM802993	Sequence	819	48.2	2.9	1608	10	BC057455	Homo sapi
747	48.4	2.9	3498	5	BC065688	Danio rer	820	48.2	2.9	1725	5	BC080409	Xenopus l
748	48.4	2.9	3521	9	BC027712	Homo sapi	821	48.2	2.9	1770	10	BC060519	Rattus no
749	48.4	2.9	3810	9	HSM803390	Homo sapi	822	48.2	2.9	1942	10	BC062081	Rattus no

823	48.2	2.9	2038	6	AX573129	Sequence	896	48	2.9	1985	9	AY358500	AY358500 Homo sapi
824	48.2	2.9	2096	10	BC034131	BC034131 Mus muscu	897	48	2.9	2003	9	BC051760	BC051760 Homo sapi
825	48.2	2.9	2137	9	AB062938	Macaca fa	898	48	2.9	2081	10	BC043712	BC043712 Mus muscu
826	48.2	2.9	2406	5	BC017107	Homo sapi	899	48	2.9	2155	9	BC075814	BC075814 Homo sapi
827	48.2	2.9	4765	5	BC068982	Danio rer	900	48	2.9	2155	9	BC075814	BC075814 Homo sapi
C 828	48.2	2.9	7037	6	AX346653	Sequence	901	48	2.9	2202	10	BC052362	BC052362 Mus muscu
C 829	48.2	2.9	7238	6	AX345350	Sequence	902	48	2.9	2209	9	BC063878	BC063878 Homo sapi
C 830	48.2	2.9	8895	6	AX345234	Sequence	903	48	2.9	2248	5	BC068963	BC068963 Xenopus l
C 831	48.2	2.9	11996	6	AX281381	Sequence	904	48	2.9	2250	9	BC064421	BC064421 Homo sapi
832	48.2	2.9	110000	2	AL954350 ⁴	Continuation (5 of	905	48	2.9	2632	5	BC030698	BC030698 Homo sapi
833	48.2	2.9	157996	10	AL772203	Mouse DNA	906	48	2.9	2777	5	BC063344	BC063344 Xenopus t
834	48.2	2.9	161297	10	AC139135	AC139135 Mus muscu	907	48	2.9	2905	3	AK174395	AK174395 Ciona int
835	48.2	2.9	167418	10	AC133944	AC133944 Mus muscu	C 908	48	2.9	2915	10	BC061479	BC061479 Mus muscu
C 836	48.2	2.9	171298	10	AC123735	AC123735 Mus muscu	C 909	48	2.9	3223	6	CQ806938	CQ806938 Sequence
837	48.2	2.9	179206	2	AC113199	AC113199 Mus muscu	C 910	48	2.9	3223	6	CQ807212	CQ807212 Sequence
C 838	48.2	2.9	195634	2	AC119930	AC119930 Mus muscu	911	48	2.9	3723	9	HSM808835	HSM808835 Homo sapi
C 839	48.2	2.9	195888	10	AC114604	AC114604 Mus muscu	C 912	48	2.9	3880	10	BC048229	BC048229 Mus muscu
C 840	48.2	2.9	218297	2	AC126035	AC126035 Mus muscu	C 913	48	2.9	3973	6	AX345073	AX345073 Sequence
841	48.2	2.9	219106	10	AC123640	AC123640 Mus muscu	914	48	2.9	3983	9	HSM803572	HSM803572 Homo sapi
842	48.2	2.9	222725	2	AC110732	AC110732 Mus muscu	915	48	2.9	4306	10	BC059824	BC059824 Mus muscu
C 843	48.2	2.9	257700	2	AC147391	Pan trogl	C 916	48	2.9	4389	10	BC058345	BC058345 Mus muscu
844	48	2.9	312	6	CQ699683	CQ699683 Sequence	C 917	48	2.9	5070	6	AX345703	AX345703 Sequence
845	48	2.9	323	6	CQ524910	CQ524910 Sequence	C 918	48	2.9	5338	9	HSM808825	HSM808825 Homo sapi
846	48	2.9	452	6	CQ527434	CQ527434 Sequence	C 919	48	2.9	5774	10	BC060122	BC060122 Mus muscu
847	48	2.9	515	6	CQ526571	CQ526571 Sequence	C 920	48	2.9	6145	6	AX345875	AX345875 Sequence
848	48	2.9	533	6	CQ525634	CQ525634 Sequence	C 921	48	2.9	6192	6	AX251440	AX251440 Sequence
849	48	2.9	540	6	CQ526524	CQ526524 Sequence	C 922	48	2.9	12669	6	AX252150	AX252150 Sequence
850	48	2.9	580	10	BC006049	BC006049 Mus muscu	C 923	48	2.9	12669	6	AX344518	AX344518 Sequence
851	48	2.9	583	11	HUMU75097	L17690 Human STS U	C 924	48	2.9	12669	6	AX348921	AX348921 Sequence
852	48	2.9	585	6	CQ526237	CQ526237 Sequence	C 925	48	2.9	18281	6	AX345864	AX345864 Sequence
C 853	48	2.9	602	6	BC008488	BC008488 Homo sapi	C 926	48	2.9	109342	5	BX465846	BX465846 Zebrafish
C 854	48	2.9	606	6	CQ503321	CQ503321 Sequence	C 927	48	2.9	170496	2	AC140472	AC140472 Mus muscu
C 855	48	2.9	606	6	CQ512068	CQ512068 Sequence	928	48	2.9	184039	10	AC139376	AC139376 Mus muscu
856	48	2.9	721	9	AK026526	AK026526 Homo sapi	C 929	48	2.9	184365	2	AC079639	AC079639 Mus muscu
857	48	2.9	760	9	BC032326	BC032326 Homo sapi	C 930	48	2.9	187028	10	BX111956	Mouse DNA
858	48	2.9	836	10	BC049716	BC049716 Mus muscu	C 931	48	2.9	194180	2	AC069140	AC069140 Homo sapi
859	48	2.9	869	10	BC054421	BC054421 Mus muscu	C 932	48	2.9	200510	2	AC097048	AC097048 Rattus no
860	48	2.9	927	10	BC047927	BC047927 Mus muscu	C 933	48	2.9	213401	2	AC124940	AC124940 Rattus no
861	48	2.9	988	5	BC055636	BC055636 Danio rer	C 934	48	2.9	224630	2	AC101853	AC101853 Mus muscu
862	48	2.9	1248	5	BC071085	BC071085 Xenopus l	C 935	48	2.9	232080	2	AC145374	AC145374 Mus muscu
863	48	2.9	1277	5	BC084489	BC084489 Xenopus t	C 936	48	2.9	232324	2	AC108634	AC108634 Rattus no
864	48	2.9	1352	3	AK115954	AK115954 Ciona int	C 937	48	2.9	235189	10	AC133208	AC133208 Mus muscu
865	48	2.9	1391	5	BC074604	BC074604 Xenopus t	C 938	48	2.9	247650	2	AC094213	AC094213 Rattus no
866	48	2.9	1409	5	BC064261	BC064261 Xenopus t	C 939	48	2.9	257109	3	AC116963	AC116963 Dictyoste
867	48	2.9	1409	10	BC040771	BC040771 Mus muscu	C 940	48	2.9	309805	2	AC026340	AC026340 Homo sapi
868	48	2.9	1415	10	BC020016	BC020016 Mus muscu	C 941	48	2.9	321708	2	AC087142	AC087142 Mus muscu
869	48	2.9	1426	5	BC054250	BC054250 Xenopus l	C 942	48	2.9	349980	6	AX344554	AX344554 Sequence
870	48	2.9	1483	9	AK026528	AK026528 Homo sapi	C 943	48	2.9	349980	6	AX344554	AX344554 Sequence
871	48	2.9	1526	5	BC084459	BC084459 Xenopus t	C 944	48	2.9	349980	6	AX344554	AX344554 Sequence
872	48	2.9	1608	9	AY358187	AY358187 Homo sapi	C 945	48	2.9	349980	6	AX344554	AX344554 Sequence
873	48	2.9	1622	9	BC043524	BC043524 Homo sapi	946	48	2.9	349980	6	AX344554	AX344554 Sequence
874	48	2.9	1632	5	BC068370	BC068370 Danio rer	C 947	48	2.9	349980	6	AX344554	AX344554 Sequence
875	48	2.9	1637	6	AX460089	AX460089 Sequence	C 948	48	2.9	349980	6	AX344554	AX344554 Sequence
876	48	2.9	1643	10	BC024405	BC024405 Mus muscu	949	48	2.9	349980	6	AX344554	AX344554 Sequence
877	48	2.9	1646	6	BC051812	BC051812 Homo sapi	950	48	2.9	349980	6	AX344554	AX344554 Sequence
878	48	2.9	1690	6	E32442	E32442 Mammal-deri	951	48	2.9	349980	6	AX344554	AX344554 Sequence
879	48	2.9	1720	10	BC046603	BC046603 Mus muscu	C 952	48	2.9	349980	6	AX344554	AX344554 Sequence
880	48	2.9	1727	5	BC071446	BC071446 Homo sapi	953	48	2.9	349980	6	AX344554	AX344554 Sequence
881	48	2.9	1860	9	BC058897	BC058897 Homo sapi	954	48	2.9	349980	6	AX344554	AX344554 Sequence
882	48	2.9	1985	6	BD172402	BD172402 Secreted	955	48	2.9	349980	6	AX344554	AX344554 Sequence
883	48	2.9	1985	6	BD172721	BD172721 Secreted	C 956	48	2.9	349980	6	AX344554	AX344554 Sequence
884	48	2.9	1985	6	BD173040	BD173040 Secreted	957	48	2.9	349980	6	AX344554	AX344554 Sequence
885	48	2.9	1985	6	BD173359	BD173359 Secreted	958	48	2.9	349980	6	AX344554	AX344554 Sequence
886	48	2.9	1985	6	BD175393	BD175393 Secretory	959	48	2.9	349980	6	AX344554	AX344554 Sequence
887	48	2.9	1985	6	CQ881212	CQ881212 Sequence	C 960	48	2.9	349980	6	AX344554	AX344554 Sequence
888	48	2.9	1985	6	AR410771	AR410771 Sequence	C 961	48	2.9	349980	6	AX344554	AX344554 Sequence
889	48	2.9	1985	6	AR439135	AR439135 Sequence	C 962	48	2.9	349980	6	AX344554	AX344554 Sequence
890	48	2.9	1985	6	AR473155	AR473155 Sequence	963	48	2.9	349980	6	AX344554	AX344554 Sequence
891	48	2.9	1985	6	AR527141	AR527141 Sequence	964	48	2.9	349980	6	AX344554	AX344554 Sequence
892	48	2.9	1985	6	AR566174	AR566174 Sequence	965	48	2.9	349980	6	AX344554	AX344554 Sequence
893	48	2.9	1985	6	AX375960	AX375960 Sequence	966	48	2.9	349980	6	AX344554	AX344554 Sequence
894	48	2.9	1985	6	AX697621	AX697621 Sequence	967	48	2.9	349980	6	AX344554	AX344554 Sequence
895	48	2.9	1985	6	BD075542	BD075542 Secretary	968	48	2.9	349980	6	AX344554	AX344554 Sequence

969	47.8	2.8	990	9	BC070127	BC070127 Homo sapi	c1042	47.8	2.8	113515	6	AX347077	AX347077 Sequence
970	47.8	2.8	995	9	BC043534	BC043534 Homo sapi	1043	47.8	2.8	114897	2	AP003624	AP003624 Oryza sat
971	47.8	2.8	1004	9	BC043536	BC043536 Homo sapi	1044	47.8	2.8	124048	10	AC134526	AC134526 Mus muscu
972	47.8	2.8	1035	10	BC055104	BC055104 Mus muscu	1045	47.8	2.8	133276	2	AC087147	AC087147 Mus muscu
c 973	47.8	2.8	1052	8	AJ840524	AJ840524 Arabidops	1046	47.8	2.8	143226	9	AL3353802	AL3353802 Human DNA
974	47.8	2.8	1080	9	HS0805509	AL834421 Homo sapi	c1047	47.8	2.8	167181	2	AC131701	AC131701 Mus muscu
975	47.8	2.8	1110	9	BC040953	BC040953 Homo sapi	c1048	47.8	2.8	168025	10	AC117778	AC117778 Mus muscu
976	47.8	2.8	1115	10	BC049575	BC049575 Mus muscu	c1049	47.8	2.8	175107	10	AC119911	AC119911 Mus muscu
977	47.8	2.8	1264	6	BD227246	BD227246 Secreted	c1050	47.8	2.8	189865	10	AC145606	AC145606 Mus muscu
978	47.8	2.8	1279	9	BC062634	BC062634 Homo sapi	1051	47.8	2.8	199101	10	MM05000665	AE000665 Mus muscu
979	47.8	2.8	1345	9	BC073861	BC073861 Homo sapi	c1052	47.8	2.8	201293	2	AC118780	AC118780 Rattus no
980	47.8	2.8	1368	10	BC083654	BC083654 Rattus no	1053	47.8	2.8	204437	10	AC117678	AC117678 Mus muscu
981	47.8	2.8	1375	9	BC043554	BC043554 Homo sapi	c1054	47.8	2.8	205939	10	AC145469	AC145469 Mus muscu
982	47.8	2.8	1488	10	BC055456	BC055456 Mus muscu	c1055	47.8	2.8	209947	2	AC121454	AC121454 Rattus no
983	47.8	2.8	1500	5	BC065586	BC065586 Danio rer	1056	47.8	2.8	214331	2	AC141645	AC141645 Mus muscu
984	47.8	2.8	1580	8	BC067146	BC067146 Danio rer	c1057	47.8	2.8	216799	10	AC125382	AC125382 Mus muscu
985	47.8	2.8	1728	9	AB070110	AB070110 Macaca fa	1058	47.8	2.8	225000	2	AC129674	AC129674 Rattus no
986	47.8	2.8	1743	10	BC051150	BC051150 Mus muscu	1059	47.8	2.8	228302	2	AC109973	AC109973 Rattus no
987	47.8	2.8	1767	9	HS0800099	AL049314 Homo sapi	c1060	47.8	2.8	233887	2	AC133687	AC133687 Rattus no
988	47.8	2.8	1788	5	BC084147	BC084147 Xenopus t	1061	47.8	2.8	247796	2	AC094539	AC094539 Rattus no
989	47.8	2.8	1819	9	BC073865	BC073865 Homo sapi	c1062	47.8	2.8	252504	2	AC073815	AC073815 Mus muscu
990	47.8	2.8	1963	10	BC083817	BC083817 Rattus no	1063	47.8	2.8	252508	2	AC129658	AC129658 Rattus no
991	47.8	2.8	2076	5	BC053185	BC053185 Danio rer	c1064	47.8	2.8	256391	2	AC107557	AC107557 Rattus no
992	47.8	2.8	2158	9	AB070046	AB070046 Macaca fa	c1065	47.8	2.8	257501	2	AC097734	AC097734 Rattus no
993	47.8	2.8	2172	9	AB096591	AB096591 Macaca fa	1066	47.8	2.8	258819	2	AC118292	AC118292 Rattus no
994	47.8	2.8	2173	10	BC048927	BC048927 Mus muscu	1067	47.8	2.8	333321	3	AC116986	AC116986 Dictyoste
995	47.8	2.8	2208	10	BC052921	BC052921 Mus muscu	1068	47.6	2.8	347	6	AR418757	AR418757 Sequence
996	47.8	2.8	2407	10	BC058192	BC058192 Mus muscu	1069	47.6	2.8	147	6	AX979451	AX979451 Sequence
997	47.8	2.8	2478	9	AF125948	AF125948 Homo sapi	1070	47.6	2.8	147	6	BD114310	BD114310 EST and e
998	47.8	2.8	2556	9	CO491158	CO491158 Sequence	1071	47.6	2.8	291	6	CQ517629	CQ517629 Sequence
999	47.8	2.8	3020	6	CO497023	CO497023 Sequence	c1072	47.6	2.8	345	6	CQ475827	CQ475827 Sequence
1000	47.8	2.8	3178	9	HS0803719	AL832411 Homo sapi	1073	47.6	2.8	358	6	CQ671266	CQ671266 Sequence
1001	47.8	2.8	3310	9	BC054816	BC054816 Homo sapi	1074	47.6	2.8	368	10	BC049735	BC049735 Mus muscu
1002	47.8	2.8	3430	9	BC065220	BC065220 Homo sapi	1075	47.6	2.8	376	6	CQ521729	CQ521729 Sequence
1003	47.8	2.8	3574	6	CO412010	CO412010 Sequence	1076	47.6	2.8	391	6	CQ524976	CQ524976 Sequence
1004	47.8	2.8	4057	10	BC067005	BC067005 Mus muscu	1077	47.6	2.8	394	6	CQ527287	CQ527287 Sequence
1005	47.8	2.8	4121	6	AR344255	AR344255 Sequence	1078	47.6	2.8	410	6	CQ522484	CQ522484 Sequence
1006	47.8	2.8	4121	6	AX019229	AX019229 Sequence	c1079	47.6	2.8	465	11	BV155767	BV155767 RPAMSEQ0
1007	47.8	2.8	4121	6	BD130455	BD130455 Expressio	1080	47.6	2.8	470	6	CQ516232	CQ516232 Sequence
1008	47.8	2.8	4213	5	BC084298	BC084298 Xenopus l	1081	47.6	2.8	479	6	CQ522457	CQ522457 Sequence
1009	47.8	2.8	4298	6	AX780085	AX780085 Sequence	1082	47.6	2.8	480	10	BC028543	BC028543 Mus muscu
1010	47.8	2.8	4562	9	HS0805779	BS537704 Homo sapi	1083	47.6	2.8	514	6	CQ522634	CQ522634 Sequence
1011	47.8	2.8	4636	10	BC057352	BC057352 Mus muscu	1084	47.6	2.8	520	6	CQ523964	CQ523964 Sequence
1012	47.8	2.8	4818	9	HS0807492	BS647348 Homo sapi	1085	47.6	2.8	529	5	BC053827	BC053827 Xenopus l
c1013	47.8	2.8	6486	6	AX458534	AX458534 Sequence	1086	47.6	2.8	631	10	MMU296942	AJ296942 Mus muscu
c1014	47.8	2.8	8079	6	AX356488	AX356488 Sequence	1087	47.6	2.8	732	5	AY522586	AY522586 Oreochrom
c1015	47.8	2.8	8298	6	AX344783	AX344783 Sequence	1088	47.6	2.8	873	6	AX780227	AX780227 Sequence
c1016	47.8	2.8	8913	6	AX599017	AX599017 Sequence	1089	47.6	2.8	889	10	BC049685	BC049685 Mus muscu
c1017	47.8	2.8	9021	6	AX347134	AX347134 Sequence	1090	47.6	2.8	959	9	BC031674	BC031674 Homo sapi
c1018	47.8	2.8	9021	6	AX347426	AX347426 Sequence	1091	47.6	2.8	1000	9	HS0806624	BS571748 Homo sapi
c1019	47.8	2.8	9021	6	AX348462	AX348462 Sequence	1092	47.6	2.8	1001	10	BC049605	BC049605 Mus muscu
c1020	47.8	2.8	9021	6	AX349147	AX349147 Sequence	1093	47.6	2.8	1130	10	BC043698	BC043698 Mus muscu
c1021	47.8	2.8	9021	6	AX657808	AX657808 Sequence	1094	47.6	2.8	1157	9	BC013883	BC013883 Homo sapi
c1022	47.8	2.8	9021	6	AX659082	AX659082 Sequence	1095	47.6	2.8	1314	5	BC054577	BC054577 Danio rer
c1023	47.8	2.8	11913	6	CO787442	CO787442 Sequence	1096	47.6	2.8	1343	10	BC061103	BC061103 Mus muscu
c1024	47.8	2.8	11913	6	CS0807085	CO807085 Sequence	1097	47.6	2.8	1383	9	BC032432	BC032432 Homo sapi
c1025	47.8	2.8	11913	6	AX795865	AX795865 Sequence	1098	47.6	2.8	1408	10	BC048693	BC048693 Mus muscu
c1026	47.8	2.8	11913	6	AX822385	AX822385 Sequence	1099	47.6	2.8	1411	10	BC049571	BC049571 Mus muscu
c1027	47.8	2.8	11913	6	AX826025	AX826025 Sequence	1100	47.6	2.8	1412	3	AF083228	AF083228 Caenorhab
c1028	47.8	2.8	13606	6	AX251315	AX251315 Sequence	1101	47.6	2.8	1457	6	BD231695	BD231695 31 human
c1029	47.8	2.8	13606	6	AX278002	AX278002 Sequence	1102	47.6	2.8	1694	9	BC012597	BC012597 Homo sapi
c1030	47.8	2.8	13606	6	AX323599	AX323599 Sequence	1103	47.6	2.8	1744	8	BT009253	BT009253 Triticum
c1031	47.8	2.8	13606	6	AX346712	AX346712 Sequence	1104	47.6	2.8	1805	9	AB070053	AB070053 Macaca fa
c1032	47.8	2.8	15832	6	AX327943	AX327943 Sequence	1105	47.6	2.8	1820	5	BC066434	BC066434 Danio rer
c1033	47.8	2.8	15832	6	AX323630	AX323630 Sequence	1106	47.6	2.8	1836	10	BC034256	BC034256 Mus muscu
c1034	47.8	2.8	15832	6	AX346245	AX346245 Sequence	1107	47.6	2.8	1880	9	AB060863	AB060863 Macaca fa
1035	47.8	2.8	16156	2	AC149363	AC149363 Phakopsor	1108	47.6	2.8	2019	10	BC063758	BC063758 Mus muscu
c1036	47.8	2.8	5153	3	AX251552	AX251552 Sequence	1109	47.6	2.8	2085	5	BC077186	BC077186 Xenopus l
c1037	47.8	2.8	57538	3	AC115682	AC115682 Dictyoste	1110	47.6	2.8	2165	5	BC054602	BC054602 Danio rer
c1038	47.8	2.8	71021	2	AC101648	AC101648 Mus muscu	1111	47.6	2.8	2198	6	BD270040	BD270040 Secreted
c1039	47.8	2.8	9930	9	AC068640	AC068640 Homo sapi	1112	47.6	2.8	2284	9	AB055303	AB055303 Macaca fa
1040	47.8	2.8	104992	2	AC005504	AC005504 Plasmodiu	1113	47.6	2.8	2369	9	AK074384	AK074384 Homo sapi
c1041	47.8	2.8	110000	3	PF001122_0	AL0311745 Plasmodiu	1114	47.6	2.8	2420	5	BC066695	BC066695 Danio rer

c1115	47.6	2.8	2447	6	AR079032	Sequence	AR079032	Sequence	c1188	47.6	2.8	187545	10	AC127550	Mus muscu
c1116	47.6	2.8	2447	6	BD190886	Secreted	BD190886	Secreted	c1189	47.6	2.8	188823	2	AC016990	Homo sapi
c1117	47.6	2.8	2447	9	BC027927	Homo sapi	BC027927	Homo sapi	c1190	47.6	2.8	194760	9	CNS01RG7	AL837510 Mouse DNA
c1118	47.6	2.8	2607	6	AX598878	Sequence	AX598878	Sequence	c1191	47.6	2.8	199537	10	AL837510	AL837510 Mouse DNA
c1119	47.6	2.8	2607	5	BC054610	Sequence	BC054610	Sequence	c1192	47.6	2.8	202640	2	AC113851	AC113851 Rattus no
c1120	47.6	2.8	2610	10	BC063267	Sequence	BC063267	Sequence	c1193	47.6	2.8	211371	2	CR450764	CR450764 Danio rer
c1121	47.6	2.8	2621	10	MUSBRED	Sequence	L31396	Mus musculu	c1194	47.6	2.8	213397	2	AC125027	AC125027 Mus muscu
c1122	47.6	2.8	2674	6	AR183261	Sequence	AR183261	Sequence	c1195	47.6	2.8	213558	2	AC149587	AC149587 Mus muscu
c1123	47.6	2.8	2674	6	AR456323	Sequence	AR456323	Sequence	c1196	47.6	2.8	217740	2	AC139949	AC139949 Rattus no
c1124	47.6	2.8	2752	9	HSN806735	Sequence	BSX641046	Homo sapi	c1197	47.6	2.8	226256	2	AC130087	AC130087 Rattus no
c1125	47.6	2.8	2770	9	HSN807752	Sequence	BSX647606	Homo sapi	c1198	47.6	2.8	226734	2	AC103431	AC103431 Rattus no
c1126	47.6	2.8	2782	9	HSN803706	Sequence	BSX647606	Homo sapi	c1199	47.6	2.8	233219	2	AC113253	AC113253 Rattus no
c1127	47.6	2.8	2804	9	HSN807489	Sequence	BSX647745	Homo sapi	c1200	47.6	2.8	233660	2	AC128377	AC128377 Rattus no
c1128	47.6	2.8	2840	10	BC0532769	Sequence	BC052769	Mus muscu	c1201	47.6	2.8	241394	2	AC131549	AC131549 Rattus no
c1129	47.6	2.8	3448	10	BC034679	Sequence	BC034679	Mus muscu	c1202	47.6	2.8	248214	2	AL138811	AL138811 Homo sapi
c1130	47.6	2.8	3582	10	BC053927	Sequence	BC053927	Mus muscu	c1203	47.6	2.8	257700	2	AC147391	AC147391 Pan trogl
c1131	47.6	2.8	3924	10	MUSBRED	Sequence	L31397	Mus musculu	c1204	47.6	2.8	258818	2	AC135265	AC135265 Rattus no
c1132	47.6	2.8	4001	6	AX347363	Sequence	AX347363	Sequence	c1205	47.6	2.8	264350	2	AC127094	AC127094 Rattus no
c1133	47.6	2.8	4001	6	AX349084	Sequence	AX349084	Sequence	c1206	47.6	2.8	301536	2	AC134158	AC134158 Rattus no
c1134	47.6	2.8	4001	6	AX657851	Sequence	AX657851	Sequence	c1207	47.6	2.8	315790	3	AB003484	AB003484 Drosophil
c1135	47.6	2.8	4001	6	AX659125	Sequence	AX659125	Sequence	c1208	47.6	2.8	334028	2	AC116537	AC116537 Drosophil
c1136	47.6	2.8	4004	9	BC041086	Sequence	BC041086	Homo sapi	c1209	47.6	2.8	349980	6	AX344552	AX344552 Sequence
c1137	47.6	2.8	4418	9	BC006195	Sequence	BC006195	Homo sapi	c1210	47.6	2.8	349980	6	AX344572	AX344572 Sequence
c1138	47.6	2.8	4421	10	BC042512	Sequence	BC042512	Homo sapi	c1211	47.6	2.8	267	6	CQ525163	CQ525163 Sequence
c1139	47.6	2.8	4447	9	HSN808517	Sequence	BSX648369	Homo sapi	c1212	47.4	2.8	268	6	CQ526263	CQ526263 Sequence
c1140	47.6	2.8	4675	9	HSN803445	Sequence	AL832138	Homo sapi	c1213	47.4	2.8	291	6	CQ399019	CQ399019 Sequence
c1141	47.6	2.8	5306	6	AX345413	Sequence	AX345413	Sequence	c1214	47.4	2.8	291	6	CQ405298	CQ405298 Sequence
c1142	47.6	2.8	6134	6	AX458624	Sequence	AX458624	Sequence	c1215	47.4	2.8	301	6	CQ516510	CQ516510 Sequence
c1143	47.6	2.8	6436	6	AX345583	Sequence	AX345583	Sequence	c1216	47.4	2.8	376	6	CQ517117	CQ517117 Sequence
c1144	47.6	2.8	6458	9	HSN806837	Sequence	BSX641067	Homo sapi	c1217	47.4	2.8	406	6	CQ517355	CQ517355 Sequence
c1145	47.6	2.8	6775	6	AX458643	Sequence	AX458643	Sequence	c1218	47.4	2.8	407	6	CQ522526	CQ522526 Sequence
c1146	47.6	2.8	6802	6	AX346133	Sequence	AX346133	Sequence	c1219	47.4	2.8	439	6	CQ518358	CQ518358 Sequence
c1147	47.6	2.8	7416	6	CQ574115	Sequence	CQ574115	Sequence	c1220	47.4	2.8	453	6	CQ477688	CQ477688 Sequence
c1148	47.6	2.8	7967	3	AF22717	Plasmodi	AF22717	Plasmodi	c1221	47.4	2.8	467	3	AF156168	AF156168 Butus ma
c1149	47.6	2.8	8900	6	CQ806977	Sequence	CQ806977	Sequence	c1222	47.4	2.8	472	6	CQ518059	CQ518059 Sequence
c1150	47.6	2.8	8900	6	CQ807251	Sequence	CQ807251	Sequence	c1223	47.4	2.8	484	6	CQ526160	CQ526160 Sequence
c1151	47.6	2.8	8910	6	AX344725	Sequence	AX344725	Sequence	c1224	47.4	2.8	506	6	CQ518031	CQ518031 Sequence
c1152	47.6	2.8	9483	6	AX251786	Sequence	AX251786	Sequence	c1225	47.4	2.8	516	6	CQ524041	CQ524041 Sequence
c1153	47.6	2.8	9483	6	AX345278	Sequence	AX345278	Sequence	c1226	47.4	2.8	546	6	AX186746	AX186746 Sequence
c1154	47.6	2.8	9483	6	AX348947	Sequence	AX348947	Sequence	c1227	47.4	2.8	589	10	BC049706	BC049706 Mus muscu
c1155	47.6	2.8	9666	6	AX281420	Sequence	AX281420	Sequence	c1228	47.4	2.8	631	10	BC049570	BC049570 Mus muscu
c1156	47.6	2.8	9666	6	AX345987	Sequence	AX345987	Sequence	c1229	47.4	2.8	643	6	CQ423476	CQ423476 Sequence
c1157	47.6	2.8	9666	6	AX348688	Sequence	AX348688	Sequence	c1230	47.4	2.8	671	5	BC082915	BC082915 Xenopus l
c1158	47.6	2.8	11700	2	AC013911	Drosophil	AC013911	Drosophil	c1231	47.4	2.8	682	10	BC049545	BC049545 Mus muscu
c1159	47.6	2.8	17848	6	AX277865	Sequence	AX277865	Sequence	c1232	47.4	2.8	685	10	BC049720	BC049720 Mus muscu
c1160	47.6	2.8	17848	6	AX323550	Sequence	AX323550	Sequence	c1233	47.4	2.8	685	11	CNS06EJ4	AL395174 T3 end of
c1161	47.6	2.8	17848	6	AX348363	Sequence	AX348363	Sequence	c1234	47.4	2.8	685	10	BC060302	BC060302 Mus muscu
c1162	47.6	2.8	35962	6	AX598758	Sequence	AX598758	Sequence	c1235	47.4	2.8	688	6	CQ423987	CQ423987 Sequence
c1163	47.6	2.8	63585	2	AC026983	Sequence	AC026983	Sequence	c1236	47.4	2.8	690	9	BC040927	BC040927 Homo sapi
c1164	47.6	2.8	77322	2	AC021334	Homo sapi	AC021334	Homo sapi	c1237	47.4	2.8	705	9	HSN800237	HSN800237 Homo sapi
c1165	47.6	2.8	84492	2	AC021676	Homo sapi	AC021676	Homo sapi	c1238	47.4	2.8	805	10	BC063183	BC063183 Rattus no
c1166	47.6	2.8	95026	3	AC125292	Drosophil	AC125292	Drosophil	c1239	47.4	2.8	811	11	BV073335	BV073335 S212P6813
c1167	47.6	2.8	110000	2	PFMAL13_1	Continuation (12 o	Continuation (12 o	Continuation (12 o	c1240	47.4	2.8	824	9	BC070291	BC070291 Homo sapi
c1168	47.6	2.8	110000	2	PFMAL13_1	Continuation (3 of	Continuation (3 of	Continuation (3 of	c1241	47.4	2.8	843	10	BC038641	BC038641 Mus muscu
c1169	47.6	2.8	110000	2	PFMAL13_2	Continuation (3 of	Continuation (3 of	Continuation (3 of	c1242	47.4	2.8	887	9	AB125184	AB125184 Macaca fa
c1170	47.6	2.8	110000	2	PFMAL13_2	Continuation (3 of	Continuation (3 of	Continuation (3 of	c1243	47.4	2.8	887	9	AB125184	AB125184 Macaca fa
c1171	47.6	2.8	113027	9	AC090669	Homo sapi	AC090669	Homo sapi	c1244	47.4	2.8	905	10	BC048724	BC048724 Mus muscu
c1172	47.6	2.8	120211	10	AL773515	Mouse DNA	AL773515	Mouse DNA	c1245	47.4	2.8	935	10	BC049693	BC049693 Mus muscu
c1173	47.6	2.8	127580	9	HSN747J1	Sequence	AL049692	Human DNA	c1246	47.4	2.8	942	5	BC049498	BC049498 Danio rer
c1174	47.6	2.8	151501	9	BS000215	Sequence	BS000215	Sequence	c1247	47.4	2.8	971	10	BC030946	BC030946 Mus muscu
c1175	47.6	2.8	153320	2	AC135762	Rattus no	AC135762	Rattus no	c1248	47.4	2.8	989	10	BC051033	BC051033 Mus muscu
c1176	47.6	2.8	155646	9	AC146044	Pan trogl	AC146044	Pan trogl	c1249	47.4	2.8	997	9	BC071943	BC071943 Homo sapi
c1177	47.6	2.8	156459	10	AC147155	Mus muscu	AC147155	Mus muscu	c1250	47.4	2.8	1068	9	BC071641	BC071641 Homo sapi
c1178	47.6	2.8	159803	2	AC117771	Mus muscu	AC117771	Mus muscu	c1251	47.4	2.8	1071	9	BC073941	BC073941 Homo sapi
c1179	47.6	2.8	165025	10	AL844493	Mouse DNA	AL844493	Mouse DNA	c1252	47.4	2.8	1107	3	AK173973	AK173973 Ciona int
c1180	47.6	2.8	168292	10	AC123049	Mus muscu	AC123049	Mus muscu	c1253	47.4	2.8	1113	9	BC030277	BC030277 Homo sapi
c1181	47.6	2.8	168439	10	AC131803	Mus muscu	AC131803	Mus muscu	c1254	47.4	2.8	1222	9	BC035237	BC035237 Homo sapi
c1182	47.6	2.8	173585	2	AC021113	Homo sapi	AC021113	Homo sapi	c1255	47.4	2.8	1240	5	BC055418	BC055418 Homo sapi
c1183	47.6	2.8	174893	5	BX0004876	Zebrafish	BX0004876	Zebrafish	c1256	47.4	2.8	1281	5	BC083538	BC083538 Danio rer
c1184	47.6	2.8	175106	2	AC148984	Mus muscu	AC148984	Mus muscu	c1257	47.4	2.8	1299	10	BC021404	BC021404 Mus muscu
c1185	47.6	2.8	175261	5	BSX27252	Zebrafish	BSX27252	Zebrafish	c1258	47.4	2.8	1332	10	BC060992	BC060992 Mus muscu
c1186	47.6	2.8	176312	3	AC023745	Drosophil	AC023745	Drosophil	c1259	47.4	2.8	1348	9	BC070154	BC070154 Homo sapi
c1187	47.6	2.8	185195	10	AC134565	Mus muscu	AC134565	Mus muscu	c1260	47.4	2.8	1425	9	BC036851	BC036851 Homo sapi

1261	47.4	2.8	1433	5	BC082836	BC082836 Xenopus 1	c1334	47.4	2.8	14006	6	AX346860	Sequence
1262	47.4	2.8	1445	10	BC071177	BC071177 Rattus no	c1335	47.4	2.8	14798	6	AX345934	Sequence
1263	47.4	2.8	1463	6	CQ494467	CQ494467 Sequence	c1336	47.4	2.8	17721	6	AX346631	Sequence
1264	47.4	2.8	1463	6	CQ497350	CQ497350 Sequence	c1337	47.4	2.8	19289	2	AC090926	Homo sapi
1265	47.4	2.8	1490	9	HS0805897	BX538346 Homo sapi	c1338	47.4	2.8	40324	3	AX458633	Sequence
1266	47.4	2.8	1453	3	AK174058	AK174058 Ciona int	c1339	47.4	2.8	57538	6	AX458632	Dictyoste
1267	47.4	2.8	1591	9	HS0807298	BX647154 Homo sapi	c1340	47.4	2.8	67374	2	AC118933	Mus muscu
1268	47.4	2.8	1653	9	BC083548	BC083548 Rattus no	c1341	47.4	2.8	72981	10	BX511117	Mouse DNA
1269	47.4	2.8	1661	9	BC025753	BC025753 Homo sapi	c1342	47.4	2.8	73778	6	AX344562	Sequence
1270	47.4	2.8	1696	6	AR256293	AR256293 Sequence	c1343	47.4	2.8	82771	2	AC011953	Homo sapi
1271	47.4	2.8	1719	10	BC045148	BC045148 Mus muscu	c1344	47.4	2.8	85916	3	AC117080	Dictyoste
1272	47.4	2.8	1738	6	AR560934	AR560934 Sequence	c1345	47.4	2.8	110000	2	AC113129	Continuation (3 of
1273	47.4	2.8	1738	8	BT009079	BT009079 Trificum	c1346	47.4	2.8	110000	2	AC114623	Continuation (2 of
1274	47.4	2.8	1744	9	BC019265	BC019265 Homo sapi	c1347	47.4	2.8	110000	10	AE014180	Continuation (2 of
1275	47.4	2.8	1750	9	BC048294	BC048294 Homo sapi	c1348	47.4	2.8	120653	5	BX645950	Zebrafish
1276	47.4	2.8	1925	9	BC050524	BC050524 Homo sapi	c1349	47.4	2.8	121554	2	AC142244	Mus muscu
1277	47.4	2.8	1939	5	BC079974	BC079974 Xenopus 1	c1350	47.4	2.8	142324	5	BX005420	Zebrafish
1278	47.4	2.8	1980	10	BC027199	BC027199 Mus muscu	c1351	47.4	2.8	148053	2	CR352222	Danio rer
1279	47.4	2.8	1999	9	BC020684	BC020684 Homo sapi	c1352	47.4	2.8	152506	10	AC145589	Mus muscu
1280	47.4	2.8	2161	9	AB063084	AB063084 Macaca fa	c1353	47.4	2.8	156060	2	AC004153	Plasmodiu
1281	47.4	2.8	2224	6	BD189940	BD189940 Tumor ant	c1354	47.4	2.8	162646	2	AC112977	Mus muscu
1282	47.4	2.8	2224	9	AB062292	AB062292 Homo sapi	c1355	47.4	2.8	163035	2	AC142822	Macaca mu
1283	47.4	2.8	2237	3	AK112710	AK112710 Ciona int	c1356	47.4	2.8	164520	2	AC020738	Homo sapi
1284	47.4	2.8	2245	9	BC037547	BC037547 Homo sapi	c1357	47.4	2.8	166529	10	AC147621	Mus muscu
1285	47.4	2.8	2307	5	BC081197	BC081197 Xenopus 1	c1358	47.4	2.8	179253	5	AL928870	Zebrafish
1286	47.4	2.8	2320	10	BC046962	BC046962 Mus muscu	c1359	47.4	2.8	181571	2	AC108949	Mus muscu
1287	47.4	2.8	2335	5	BC068409	BC068409 Danio rer	c1360	47.4	2.8	191119	2	CR749163	Danio rer
1288	47.4	2.8	2372	9	BC042652	BC042652 Homo sapi	c1361	47.4	2.8	194362	10	AC124716	Mus muscu
1289	47.4	2.8	2403	9	HS0808752	BX648601 Homo sapi	c1362	47.4	2.8	195972	10	AC117567	Mus muscu
1290	47.4	2.8	2477	9	BC034692	BC034692 Homo sapi	c1363	47.4	2.8	198590	10	AC113983	Mus muscu
1291	47.4	2.8	2539	10	BC046284	BC046284 Mus muscu	c1364	47.4	2.8	199274	2	AC123626	Mus muscu
1292	47.4	2.8	2593	9	HS0807470	BX647326 Homo sapi	c1365	47.4	2.8	200934	10	AC123850	Mus muscu
1293	47.4	2.8	2601	5	BC072034	BC072034 Xenopus 1	c1366	47.4	2.8	205878	2	CR392366	Danio rer
1294	47.4	2.8	2765	3	AK115430	AK115430 Ciona int	c1367	47.4	2.8	212144	2	AC140356	Mus muscu
1295	47.4	2.8	2783	10	BC058527	BC058527 Mus muscu	c1368	47.4	2.8	215427	2	AC130980	Rattus no
1296	47.4	2.8	2789	9	AK114441	AK114441 Ciona int	c1369	47.4	2.8	219491	2	AC092256	Mus muscu
1297	47.4	2.8	2824	9	BC042665	BC042665 Homo sapi	c1370	47.4	2.8	221068	2	AC102378	Mus muscu
1298	47.4	2.8	2980	6	BD270060	BD270060 Secreted	c1371	47.4	2.8	222932	2	AC137869	Mus muscu
1299	47.4	2.8	3186	5	BC068331	BC068331 Danio rer	c1372	47.4	2.8	223869	2	AC119834	Mus muscu
1300	47.4	2.8	3446	9	HS0802955	AL713742 Homo sapi	c1373	47.4	2.8	227395	10	AL512346	Mouse DNA
1301	47.4	2.8	3492	5	BC078645	BC078645 Danio rer	c1374	47.4	2.8	230184	10	AC138679	Mus muscu
1302	47.4	2.8	3502	9	HS0807726	BX647580 Homo sapi	c1375	47.4	2.8	235664	2	AC126522	Rattus no
1303	47.4	2.8	3664	6	AX598782	AX598782 Sequence	c1376	47.4	2.8	238781	10	AC127351	Mus muscu
1304	47.4	2.8	3664	6	AX598928	AX598928 Sequence	c1377	47.4	2.8	240185	2	AC115132	Rattus no
1305	47.4	2.8	3664	6	AX598928	AX598928 Sequence	c1378	47.4	2.8	240931	2	AC107097	Rattus no
1306	47.4	2.8	3664	6	AX705378	AX705378 Sequence	c1379	47.4	2.8	240931	2	AC107097	Rattus no
1307	47.4	2.8	3664	6	AX705400	AX705400 Sequence	c1380	47.4	2.8	244656	10	AC091278	Mus muscu
1308	47.4	2.8	3930	9	BC027963	BC027963 Homo sapi	c1381	47.4	2.8	245859	2	AC099418	Rattus no
1309	47.4	2.8	3964	5	BC077739	BC077739 Xenopus 1	c1382	47.4	2.8	252632	3	AE014818	Plasmodiu
1310	47.4	2.8	3997	6	AX086658	AX086658 Sequence	c1383	47.4	2.8	253441	2	AC135668	Mus muscu
1311	47.4	2.8	4154	9	HS0803629	AL832322 Homo sapi	c1384	47.4	2.8	255189	2	AC106391	Rattus no
1312	47.4	2.8	4180	10	BC08042645	BC08042645 Mus muscu	c1385	47.4	2.8	258938	2	AC099416	Mus muscu
1313	47.4	2.8	4237	6	BD057918	BD057918 Secreted	c1386	47.4	2.8	262640	2	AC139057	Mus muscu
1314	47.4	2.8	4550	10	AB015672	AB015672 Mus muscu	c1387	47.4	2.8	267140	2	AC097568	Rattus no
1315	47.4	2.8	4679	9	HS0808418	BX648370 Homo sapi	c1388	47.4	2.8	275156	2	AC105868	Rattus no
1316	47.4	2.8	5182	6	AX252007	AX252007 Sequence	c1389	47.4	2.8	302489	2	AC100742	Sequence
1317	47.4	2.8	5182	6	AX348780	AX348780 Sequence	c1390	47.2	2.8	203	6	CQ524826	Sequence
1318	47.4	2.8	5349	6	AX345242	AX345242 Sequence	c1391	47.2	2.8	240	6	CQ663206	Sequence
1319	47.4	2.8	5437	6	AX346644	AX346644 Sequence	c1392	47.2	2.8	281	6	CQ410312	Sequence
1320	47.4	2.8	5893	6	AX345761	AX345761 Sequence	c1393	47.2	2.8	348	6	CQ524785	Sequence
1321	47.4	2.8	6664	6	AX252071	AX252071 Sequence	c1394	47.2	2.8	396	6	CQ525748	Sequence
1322	47.4	2.8	6664	6	AX822358	AX822358 Sequence	c1395	47.2	2.8	504	6	CQ526419	Sequence
1323	47.4	2.8	6664	6	AX822486	AX822486 Sequence	c1396	47.2	2.8	539	10	BC031454	Mus muscu
1324	47.4	2.8	6664	6	AX825998	AX825998 Sequence	c1397	47.2	2.8	623	9	BC043516	Homo sapi
1325	47.4	2.8	6664	6	AX826126	AX826126 Sequence	c1398	47.2	2.8	625	10	BC059134	Rattus no
1326	47.4	2.8	6898	6	AX344814	AX344814 Sequence	c1399	47.2	2.8	656	6	CQ487057	Sequence
1327	47.4	2.8	8059	5	BC076779	BC076779 Xenopus 1	c1400	47.2	2.8	675	10	BC059112	Rattus no
1328	47.4	2.8	8305	6	AX346470	AX346470 Sequence	c1401	47.2	2.8	720	3	AK174023	Ciona int
1329	47.4	2.8	8607	6	AR453095	AR453095 Sequence	c1402	47.2	2.8	749	9	BC008417	Homo sapi
1330	47.4	2.8	8607	6	AX281207	AX281207 Sequence	c1403	47.2	2.8	756	6	CQ399155	Sequence
1331	47.4	2.8	8607	6	AX356478	AX356478 Sequence	c1404	47.2	2.8	756	6	CQ405433	Sequence
1332	47.4	2.8	12138	6	AX346530	AX346530 Sequence	c1405	47.2	2.8	760	9	BC040885	Homo sapi
1333	47.4	2.8	12138	6	AX348420	AX348420 Sequence	c1406	47.2	2.8	780	8	CNS019TW	Botrytis

1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611	1612	1613	1614	1615	1616	1617	1618	1619	1620	1621	1622	1623	1624	1625	1626	1627	1628	1629	1630	1631	1632	1633	1634	1635	1636	1637	1638	1639	1640	1641	1642	1643	1644	1645	1646	1647	1648	1649	1650	1651	1652	1653	1654	1655	1656	1657	1658	1659	1660	1661	1662	1663	1664	1665	1666	1667	1668	1669	1670	1671	1672	1673	1674	1675	1676	1677	1678	1679	1680	1681	1682	1683	1684	1685	1686	1687	1688	1689	1690	1691	1692	1693	1694	1695	1696	1697	1698	1699	1700	1701	1702	1703	1704	1705	1706	1707	1708	1709	1710	1711	1712	1713	1714	1715	1716	1717	1718	1719	1720	1721	1722	1723	1724	1725	1726	1727	1728	1729	1730	1731	1732	1733	1734	1735	1736	1737	1738	1739	1740	1741	1742	1743	1744	1745	1746	1747	1748	1749	1750	1751	1752	1753	1754	1755	1756	1757	1758	1759	1760	1761	1762	1763	1764	1765	1766	1767	1768	1769	1770	1771	1772	1773	1774	1775	1776	1777	1778	1779	1780	1781	1782	1783	1784	1785	1786	1787	1788	1789	1790	1791	1792	1793	1794	1795	1796	1797	1798	1799	1800	1801	1802	1803	1804	1805	1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825	1826	1827	1828	1829	1830	1831	1832	1833	1834	1835	1836	1837	1838	1839	1840	1841	1842	1843	1844	1845	1846	1847	1848	1849	1850	1851	1852	1853	1854	1855	1856	1857	1858	1859	1860	1861	1862	1863	1864	1865	1866	1867	1868	1869	1870	1871	1872	1873	1874	1875	1876	1877	1878	1879	1880	1881	1882	1883	1884	1885	1886	1887	1888	1889	1890	1891	1892	1893	1894	1895	1896	1897	1898	1899	1900	1901	1902	1903	1904	1905	1906	1907	1908	1909	1910	1911	1912	1913	1914	1915	1916	1917	1918	1919	1920	1921	1922	1923	1924	1925	1926	1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	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RESULT 2
AR528639 1679 bp DNA linear PAT 08-OCT-2004
LOCUS
DEFINITION Sequence 375 from patent US 6725730.
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Bollinger, C.L., Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 375 27-APR-2004;
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Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 4
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LOCUS Sequence 125 from Patent WO0208288.
DEFINITION AX362365
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.B., Smith,V., Stephan,J.P.,
Watanabe,C.K., and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1 .1679
/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE
AUTHORS
Ashkenazi, A., Baker, K., Botstein, D., Desnovers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
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 REFERENCE 1
 AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
 Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
 and Ye,W.
 TITLE Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
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 Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
 Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
 Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
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Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
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LOCUS Sequence 55 from Patent WO0200690.
DEFINITION AX490948
ACCESSION AX490948
VERSION AX490948.1 GI:22323811
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.P., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 55 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR439649 Sequence 2 from patent US 6664383.

DEFINITION AR439649

ACCESSION AR439649

VERSION AR439649.1 GI:42665573

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1693)

AUTHORS Fukushima,D., Shibayama,S. and Tada,H.

TITLE Polypeptides, cDNA encoding the same and utilization thereof

JOURNAL Patent: US 6664383-A 2 16-DEC-2003;

FEATURES Location/Qualifiers

source

1..1693

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 99.0%; Score 1661.4; DB 6; Length 1693;

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Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db	765	TACTTGGAGACACAT	CTCTCCCAAGCGGT	TGGCTTTGTGAGTGAACGAATACTTTGGA	824	
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ACCESSION	AR439648		
VERSION	AR439648.1	GI:42665572	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1032)		
TITLE	Fukushima,D., Shibayama,S. and Tada,H.		
JOURNAL	Polypeptides, cDNA encoding the same and utilization thereof		
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QY	674	AGTGAAGACGAATACTTTGGAATTTCAAGGCGCATCACCCGGGAGCAGTCAGGGGACTACG	733
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Db 1021 CTTCTCAAAATTT 1032

RESULT 14
RNU16845 2040 bp mRNA linear ROD 26-MAY-1995
LOCUS RNU16845
DEFINITION Rattus norvegicus neurotrophin mRNA, complete cds.
ACCESSION U16845
VERSION U16845.1 GI:755184
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Struyk A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
and Salzer,J.L.
TITLE Cloning of neurotrophin defines a new subfamily of differentially
expressed neural cell adhesion molecules
J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
JOURNAL 95198094
MEDLINE
PUBMED 7891157
REFERENCE 2 (bases 1 to 2040)
AUTHORS Salzer,J.L.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
Center, 550 First Avenue, New York, NY 10016, USA
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1.2040
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Db 624 CAGGCGGGGAGAGCGCCACCTCAGGTGCACTATTGACAACCGGGTCAACCCGGGTGGC 683
QY 334 CTGGCTAAACCGCAGCACCATCTCTATGTCTGGGAATGAAGAATGGTGTGCTGATCTCG 393
Db 684 CTGGCTAAACCGCAGTACCATCTCTATGTCTGGAAATGACAAGTGGTGTGCTGATCTCG 743
QY 394 CGTGGTCTTCTGAGCAACCCAAACGAGTACAGATCGAGATCCAGAACGTGGATGT 453
Db 744 TGTGGTCTCTGAGTAAACCCAGACCCAGATTCAGATTCAGAAATGTAGATTTCTTCA 803
QY 454 GTATGACGAGGGCCCTTTACACCTGCTCGGTGCAGACAGCAACCAACCAAGACCTCTAG 513
Db 804 GTATGATGAGGGCCCTTTATACCTGCTCGGTGCAGACAGCAACCAACCAAGACCTCAG 863
QY 514 GGTCCACCTCATTTGTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCAATATCTCCAT 573
Db 864 GGTCCACCTCATTTGTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCAATATCTCCAT 923
QY 574 TAATGAAGGGAACAATATTAGCCTCAGTGCATAGCAACTCGTAGACAGAGCCTTACCGT 633
Db 924 TAATGAAGGGAACAATATTAGCCTCAGTGCATAGCAACTCGTAGAGAGCCTTACAGT 983
QY 634 TACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGTAGTGAAGACGAATACTTGA 693
Db 984 AACCTGGAGACATATTTCTCCAAAGCTGTCCGCTTTGTGAGTGGAGTGTAGTACCTGGA 1043
QY 694 AATTGAGGACATACCCGGGAGCAGTACGGGACTACGAGTGCAGTGCCTCCAATGAGT 753
Db 1044 GATCCAGGGACATCACTCGGAGCAGTACGGGAGTATGAGTGCAGCGCCTCCAAGCAGT 1103
QY 754 GGCCGCGCCGTGTGTACGAGAGTAAAGTCAACCGTGAACCTATCCACCATACATTTTACA 813
Db 1104 GGAGAGCAGCAGTGTGTAAGAGAGTGAAGTCAACCGTGAACCTATCCACCATACATCTCA 1163
QY 814 AGCCAAGGATACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAAGTGTGAAGCCTCAGC 873
Db 1164 AGCTAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACTCTGCAAGTGTGAAGCCTCGGC 1223
QY 874 AGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAAAGAGTGTGTAAGGAAAGAA 933
Db 1224 AGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAAAGAGTGTGTAAGGAAAGAA 1283
QY 934 AGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTCATTTCTTCAATGTCTCTGA 993
Db 1284 GGGAGTCAAGTGGAAACAGACCTTCTCTCAAGACTCACTTTTCAAGTCTCTGA 1343
QY 994 ACATGACTATGGGAACTACACTTGGTGGCCTCCAAAGCTGGGCCACCAATGTCAG 1053
Db 1344 ACACGACTATGGGAACTACACATGTGTGGCATCCAAACAAAGTTGGGCCACCAATGTCAG 1403
QY 1054 CATCATGCTATTTGGTCCAGGCGCGTCCAGGAGTGAACACGCACTCGAGAGGGC 1113
Db 1404 CATCATGCTATTTGGCCAGGTGTGTGAGGAGTCAACATGGGAGTCAAGGAGGC 1463
QY 1114 AGGTGCTCTGCGTGTGCTCTTCTGCTTGTGCACTGCTTCTCAATTTTGTGTA 1173
Db 1464 AGGTGCTATTTGGCTCTCTCTTCTGCTTGTGCACTGCTCTCTCAATTTTGTGTA 1523
QY 1174 GTGCCATTTCCCAACCGGGGAAAGGCTGCCGCCACCAACCAACACACAGCAATG 1233
Db 1524 GTGCCCTTCTTCCCGGGGAGA-GCTGCTGCCACCGCATC--TCAATTCACAGCACTG 1580
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Db 124 AGGAGTCCGGTGGTAGCGGAGATGCCACCTTTCCAAAGCTATGACAAACGCTGACGGT 183
 Qy 274 CCGCAGGGGAGAGCGCCACCTTCAGGTGACACTATTGACAAACGGGTTCACCCGGGTGGC 333
 Db 184 CAGGCAGGGGAGAGCGCCACCTTCAGGTGACAAATTGACAAACGGGTTCACCCGGGTGGC 243
 Qy 334 CTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGGTCCCTGGATCCTCG 393
 Db 244 CTGGCTAAACCGCAGTACCATCTCTATGCTGGGAATGACAAAGTGGTCCCTGGATCCTCG 303
 Qy 394 CGTGGTCTCTCTGAGCAACACCCAAACGACGATACAGATCCAGATCCAGAAACGCTGGATGT 453
 Db 304 TGTGGTCTCTCTGAGTAAACCCAGACCCAGTACAGATTCAGATCCAGAAATGCTGGATGT 363
 Qy 454 GTATGACGAGGGCCCTTACACCTGCTGGTGCAGACAGACCAACCAACCAAGACCTCTAG 513
 Db 364 GTACGATGAGGGCCCTTATACCTGCTGGTGCAGACAGACCAACCAACCAAGACCTCTAG 423
 Qy 514 GGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT 573
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 Db 1193 TGAGACAGAAATTCGAGGAGGGGACAAAGCATACTGTGTGTAAGGGGGAAGAAAGGTT 1252

Qy 1349 TAAAAA---GAAATTGAAATTCCTTTGAGATATTTAGGTACAAATGGAGTTTCTTT- 1404
 Db 1253 TAAGAAAGGAAATTTGGAAATTCCTTTGAGATATTTGCGTACGCTGAGTTTCTTTTC 1312
 Qy 1405 TCCCAACGGGAAGAACACAGCACACCCGGGTTGGACCCACTG-CAAGCTGATCGTGCA 1463
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 Qy 1464 ACCTCTTTGGTGGCCAGTGTGGGCAAGGCTCAGCCTCTCTGCCAC-AGAGTGGCCCCAC 1522
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 Qy 1523 GTGGAACATTTCTGAGGCTGGCCATCCCAAAATTCATCAGTCCATAGAGACGAACAGATG 1582
 Db 1433 ATGAAACATTTCTGGAGTTGGCCATCCCAAAATTTTCATCGGTCCATAGACACAGCAG 1492
 Qy 1583 ---AGACCTTCCGCGCCCAAGCGTGGCGTGGCGGACCTTTGGTAGACTGTGCCACCGG 1639
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 Qy 1640 CGTCTGTGTGAACGCTGAATTAAGAGCAAAAAA 1679
 Db 1553 CGTGTGTATGAAGTGTGAATCTGGAGGAAGAAAAA 1592

Search completed: June 16, 2005, 10:20:35
 Job time : 7742.42 secs


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Run on: June 15, 2005, 23:29:46 ; Search time 982.407 Seconds
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Title: US-10-017-084A-522
Perfect score: 1679
Sequencing: 1 gttgtgctcttcagcaaac.....ataaaagagcaaaaaaaa 1679
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
                4390206 seqs, 2959870667 residues
                Total number of hits satisfying chosen parameters: 8780412
                Minimum DB seq length: 0
                Maximum DB seq length: 2000000000
                Post-processing: Minimum Match 0%
                                Maximum Match 100%
                                Listing first 1500 summaries
Database : N_Geneseq_16Dec04.*
1: Geneseqn1980s.*
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4: Geneseqn2001as.*
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9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
No. Score Match Length DB ID Description
RESULT 1
ID AAC78590 standard; cDNA; 1679 BP.
DE Human PRO337 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 2; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID AAC78590 standard; cDNA; 1679 BP.
DE Human PRO337 nucleotide sequence SEQ ID NO:522.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 3; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAC7037 standard; cDNA; 1679 BP.
DE Nucleotide sequence of human polypeptide PRO337.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 4; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4
ID AAC21431 standard; cDNA; 1679 BP.
DE Human cDNA sequence encoding for PRO337 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 4; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 5
ID ABK33598 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO protein, Seq ID No 125.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 4; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ABL88099 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA sequence SEQ ID NO:55.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ABL95588 standard; cDNA; 1679 BP.
DE Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID ACA63892 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID ACA03790 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID ACA04996 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACA72056 standard; cDNA; 1679 BP.
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN US200217553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ABX89328 standard; cDNA; 1679 BP.
DE DNA encoding novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 13
ID ABX92696 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073212-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACD41982 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #188.
FN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACA60526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ACA04516 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 DNA.
FN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACA66437 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA04211 standard; cDNA; 1679 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
FN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACA65657 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ADA67548 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ABY44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADA61598 standard; cDNA; 1679 BP.
DE Homo sapiens.
FN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADB19383 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADB27924 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADA86403 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADB15967 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADA47753 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADA67548 standard; cDNA; 1679 BP.

DE Human PRO polynucleotide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADB30555 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADAB5851 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADA97063 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADA79367 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ADA87506 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADB16708 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADA91800 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADB14863 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADA25061 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADA47275 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADB18824 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADA94039 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ADB19935 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADB13247 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ACD98611 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ACD30038 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADA12722 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADA74501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068798-A1.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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ID ADB24734 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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RESULT 51
ID ADA82258 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADA75221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADA85299 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADA84747 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB30003 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADA80531 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ADA75773 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ADA46998 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADB25294 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADA93470 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADB26820 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADB31107 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 9; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 68
ID ADA95959 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 69
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 70
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 71
ID ACD82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 72
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 73
ID ADA77532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 74
ID ADB18272 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 75
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 76
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 77
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 78
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 79
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 80
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 81
ID ADA88610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 82
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 83
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 84
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 85
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 86
ID ABA43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.

Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 77
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 78
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 79
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 80
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 81
ID ADA88610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 82
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 83
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 84
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 85
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
RESULT 86
ID ABA43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.

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PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADA66996 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADB22857 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADB23630 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADA92352 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADB15415 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADB83615 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADB80721 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADB73262 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ADB38667 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082766-A1.

PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADB78344 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADB38115 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADB66587 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADB84992 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADB89667 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADB90399 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADB39500 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADB78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADB74028 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003045462-A1.
PD 06-MAR-2003.
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PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADB87164 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADB84746 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADB47123 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADB83861 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADB86730 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADB73016 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092897-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADB76744 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADB77335 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADB35596 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADB33940 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADB35044 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADB36148 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADB46543 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADC44170 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADC61930 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ADC63894 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ADC66994 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADC69118 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US20030364407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ADC63178 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US20030368648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADC68243 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US20030369178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ADC41563 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADC67618 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADC62554 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADC36854 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US20030808065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADC42187 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADC21844 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADC50416 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADC71963 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADC59942 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADC49875 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US20030808064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADC49074 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US20030808070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADC49591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US20030808071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADC47452 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US20030808072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US20030807365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US20030807366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141

ID ADC60494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ADC34594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ADC55956 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADD03200 standard; cDNA; 1679 BP.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ADC78072 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADD10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADD11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADD37097 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADD51777 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADD02576 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADD50516 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADD02010 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADD54192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADE16724 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADD73339 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ADE42008 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADE17825 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADD91957 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADE33420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADE33972 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ADD80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADD79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADD51281 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ADE49556 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADD92509 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ADD91405 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADE04019 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADE32316 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADE22248 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADD79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADP93061 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ADD72697 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADE19481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADE18929 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ADE43125 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ADP95914 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ADE22800 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ADD78918 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214

ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ADP97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ADG3119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ADG80013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ADI61199 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADH81386 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ACA66903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

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PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID AC68655 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID AC67181 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADM82555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADN15954 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ADN16583 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ADN15402 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ADN14850 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ADC48828 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ADC81112 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092115-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADE20999 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ADE05843 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ADD76560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ADD75072 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ADD75818 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ADD85050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ADD86876 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ADE20753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ADE39050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ADE87924 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ADE86328 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ADE05597 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ADE73582 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ADE75776 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ADE48856 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ADE78422 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ADE41305 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ADE23352 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ADE21245 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ADE77360 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ADE20507 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADE75572 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100664-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ADE74088 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ADE74334 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADE76064 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ADE85556 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ADE23904 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 269		
ID ADE24547 standard; cDNA; 1679 BP.		
DE DE cDNA encoding human PRO polypeptide #188.		
PN US2003092111-A1.		
PD 15-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 270		
ID ADD87372 standard; cDNA; 1679 BP.		
DE DE Human PRO polynucleotide #188.		
PN US2003203439-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 271		
ID ADE05105 standard; cDNA; 1679 BP.		
DE DE Human PRO polynucleotide #63.		
PN US2003100726-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 272		
ID ADD75318 standard; cDNA; 1679 BP.		
DE DE Human PRO polynucleotide #63.		
PN US2003100714-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 273		
ID ADD76862 standard; cDNA; 1679 BP.		
DE DE Novel human secreted and transmembrane protein PRO337 cDNA.		
PN US2003100715-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 274		
ID ADD86630 standard; cDNA; 1679 BP.		
DE DE Novel human secreted and transmembrane protein PRO337 cDNA.		
PN US2003100719-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 275		
ID ADE89238 standard; cDNA; 1679 BP.		
DE DE Human PRO polynucleotide #188.		
PN US2003199062-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 276		
ID ADE41198 standard; cDNA; 1679 BP.		
DE DE Human secreted/transmembrane polypeptide PRO337 cDNA.		
PN US2003104558-A1.		
PD 05-JUN-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;
RESULT 277		
ID ADD78098 standard; cDNA; 1679 BP.		
DE DE Novel human secreted and transmembrane protein PRO337 cDNA.		
PN US2003100731-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1679; DB 12; Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;


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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ADD73842 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ADD74580 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ADD77108 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ADD8502 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ADE05351 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ADD74826 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ADF61597 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ADF40289 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADF46085 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ADE94706 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ADE91117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ADF24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 303
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 304
ID ADE92264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 305
ID ADE90565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 306
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 307
ID ADF33216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 308
ID ADF25592 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 309
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 310
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 311
ID ADF46709 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 312
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 313
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 314
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 315
ID ADG02291 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 316
ID ADG22077 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 317
ID ADG20147 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 318
ID ADF98053 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 319
ID ADG24270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 320
ID ADF98624 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
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PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ADG16761 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ADG05220 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ADG19487 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ADG11255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ADG13324 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ADG08381 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ADG15551 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003219885-A1.

PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ADG12034 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ADF96949 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ADG06134 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ADG23718 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ADG04007 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ADG24908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ADF94591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ADG07205 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ADG07757 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ADG06687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ADG55252 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ADG60916 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ADG62020 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ADG82221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ADG57460 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ADG56908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ADG55804 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADG58564 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ADG70930 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ADH39031 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ADG58012 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ADG53596 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ADG71482 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ADG50695 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ADG81669 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ADH30631 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ADG63633 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 357
ID ADH11998 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ADG50071 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ADG51943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ADG52420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADG54148 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ADG49447 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ADG81117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366

ID ADG48823 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ADG54700 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ADG62719 standard; cDNA; 1679 BP.

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DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID AD181164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID AD133591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
ID ADG09907 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID AD115378 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ADG09255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 383
ID AD114710 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID AD129846 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID AD118305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ADM27243 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ADJ77481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ADK82833 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ADK66601 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ADJ65603 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ADM27739 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1679; DB 12; Length 1679;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ADM17521 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
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PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ADL07355 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ADM2463 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ADM28325 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID AD195807 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID AD196359 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200307354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 399
ID AA247893 standard; cDNA; 1693 BP.
DE Human protein encoding cDNA SEQ ID NO:3.
PN WO9958668-A1.
PD 18-NOV-1999.
PA (ONOH) ONO PHARM CO LTD.
Query Match 99.0%; Score 1661.4; DB 3; Length 1693;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 400
ID AA88791 standard; cDNA; 2012 BP.
DE Human SECX cDNA Clone 11753149.0.37.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 97.9%; Score 1643.4; DB 3; Length 2012;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 401
ID ADD18290 standard; DNA; 2012 BP.
DE Human molecule (MOL) protein MOL11 DNA sequence.
PN WO200303984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.9%; Score 1643.4; DB 10; Length 2012;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 402
ID AA88790 standard; cDNA; 1603 BP.
DE Human SECX cDNA Clone 11753149.0.6.
PN WO200061754-A2.
PD 19-OCT-2000.

PA (CURA-) CURAGEN CORP.
Query Match 95.4%; Score 1601.4; DB 3; Length 1603;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 403
ID ADD18288 standard; DNA; 1603 BP.
DE Human molecule (MOL) protein MOL10 DNA sequence.
PN WO200303984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 95.4%; Score 1601.4; DB 10; Length 1603;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 404
ID ABK49272 standard; cDNA; 1873 BP.
DE Human Kruppel associated DNA binding protein 42 cDNA.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 89.9%; Score 1509.8; DB 6; Length 1873;
Best Local Similarity 93.1%; Pred. No. 0;
RESULT 405
ID AAI57869 standard; cDNA; 1678 BP.
DE Human polynucleotide SEQ ID NO 72.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 86.8%; Score 1457; DB 4; Length 1678;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ADQ22984 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;
Best Local Similarity 98.9%; Pred. No. 0;
RESULT 407
ID ADQ24601 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;
Best Local Similarity 98.9%; Pred. No. 0;
RESULT 408
ID ABT17390 standard; DNA; 1839 BP.
DE Human IG gene related nucleic acid SEQ ID NO 16.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 409
ID ABX76448 standard; DNA; 1839 BP.
DE Lung cancer-associated polynucleotide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 410
ID ADG63208 standard; DNA; 1839 BP.
DE Human neurotrophin DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 85.3%; Score 1432.8; DB 10; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 411
ID ADN39137 standard; cDNA; 1839 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 85.3%; Score 1432.8; DB 11; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 412
ID ADI21817 standard; cDNA; 2884 BP.
DE Novel human protein cDNA #76.
FN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 85.3%; Score 1432.8; DB 10; Length 2884;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 413
ID ADI35771 standard; DNA; 2129 BP.
DE Human neurotrophin DNA.
FN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 84.5%; Score 1418.2; DB 10; Length 2129;
Best Local Similarity 97.6%; Pred. No. 0;
RESULT 414
ID AA159655 standard; cDNA; 1690 BP.
DE Human polynucleotide SEQ ID NO 3644.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 78.3%; Score 1315; DB 4; Length 1690;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 415
ID ADI21360 standard; cDNA; 1690 BP.
DE Novel human expressed sequence tag, EST #59.
FN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 78.3%; Score 1315; DB 10; Length 1690;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 416
ID AA247892 standard; cDNA; 1032 BP.
DE Human protein encoding cDNA SEQ ID NO:2.
FN WO9958668-A1.
PD 18-NOV-1999.
PA (ONVOY) ONO PHARM CO LTD.
Query Match 61.5%; Score 1032; DB 3; Length 1032;
Best Local Similarity 100.0%; Pred. No. 2.2e-262;
RESULT 417
ID ABT17393 standard; DNA; 1061 BP.
DE Human IG gene related nucleic acid SEQ ID No 19.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 58.0%; Score 974; DB 8; Length 1061;
Best Local Similarity 100.0%; Pred. No. 5e-247;
RESULT 418
ID AA247894 standard; cDNA; 939 BP.
DE Human protein encoding cDNA SEQ ID NO:5.
FN WO9958668-A1.
PD 18-NOV-1999.
PA (ONVOY) ONO PHARM CO LTD.
Query Match 55.9%; Score 939; DB 3; Length 939;
Best Local Similarity 100.0%; Pred. No. 8.6e-238;
RESULT 419
ID ABT17391 standard; DNA; 1094 BP.
DE Human IG gene related nucleic acid SEQ ID No 17.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 55.4%; Score 931; DB 8; Length 1094;
Best Local Similarity 96.7%; Pred. No. 1.2e-235;
RESULT 420
ID ADG63210 standard; DNA; 1068 BP.
DE Human neurotrophin DNA +33bp isoform.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 54.2%; Score 910.4; DB 10; Length 1068;

Best Local Similarity 96.6%; Pred. No. 3.4e-230;
RESULT 421
ID ABT17392 standard; DNA; 1130 BP.
DE Human IG gene related nucleic acid SEQ ID No 18.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 53.1%; Score 891.8; DB 8; Length 1130;
Best Local Similarity 93.2%; Pred. No. 2.9e-225;
RESULT 422
ID ADG63212 standard; DNA; 1104 BP.
DE Human neurotrophin DNA +69bp isoform.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 52.1%; Score 874.4; DB 10; Length 1104;
Best Local Similarity 93.2%; Pred. No. 1.2e-220;
RESULT 423
ID ADG63214 standard; DNA; 1140 BP.
DE Human neurotrophin DNA +108bp isoform.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 50.7%; Score 851.8; DB 10; Length 1140;
Best Local Similarity 99.8%; Pred. No. 1.1e-214;
RESULT 424
ID AAA44536 standard; cDNA; 832 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1111.
FN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 47.9%; Score 803.8; DB 3; Length 832;
Best Local Similarity 99.8%; Pred. No. 5e-202;
RESULT 425
ID ADE07017 standard; DNA; 3298 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #83.
FN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 33.6%; Score 564.2; DB 10; Length 3298;
Best Local Similarity 69.6%; Pred. No. 2.7e-138;
RESULT 426
ID AAQ51015 standard; cDNA; 3069 BP.
DE Rat opioid receptor gene.
FN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN) LEE N M.
PA (LOHH) LOH H H.
PA (LIPP) LIPPMAN D.
Query Match 32.2%; Score 540.8; DB 2; Length 3069;
Best Local Similarity 71.2%; Pred. No. 4e-132;
RESULT 427
ID ABT17409 standard; DNA; 1478 BP.
DE Human IG gene related nucleic acid SEQ ID No 35.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.1%; Score 539.2; DB 8; Length 1478;
Best Local Similarity 73.0%; Pred. No. 7.4e-132;
RESULT 428
ID ABT17406 standard; DNA; 3110 BP.
DE Human IG gene related nucleic acid SEQ ID No 32.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.1%; Score 539.2; DB 8; Length 3110;
Best Local Similarity 73.0%; Pred. No. 1.1e-131;
RESULT 429
ID ADG63206 standard; DNA; 3110 BP.
DE Opioid-binding protein/cell adhesion molecule-like DNA.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

Query Match 32.1%; Score 539.2; DB 10; Length 3110;
Best Local Similarity 73.0%; Pred. No. 1.1e-131;
RESULT 430
ID ABT17408 standard; DNA; 1071 BP.
DE Human IG gene related nucleic acid SEQ ID NO 34.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.0%; Score 537.6; DB 8; Length 1071;
Best Local Similarity 72.9%; Pred. No. 1.7e-131;
RESULT 431
ID ABT17407 standard; DNA; 1080 BP.
DE Human IG gene related nucleic acid SEQ ID NO 33.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.0%; Score 537.6; DB 8; Length 1080;
Best Local Similarity 72.9%; Pred. No. 1.7e-131;
RESULT 432
ID AAQ51017 standard; cDNA; 2179 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match 31.1%; Score 523; DB 2; Length 2179;
Best Local Similarity 72.2%; Pred. No. 1.7e-127;
RESULT 433
ID AAQ51016 standard; cDNA; 2337 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match 31.1%; Score 523; DB 2; Length 2337;
Best Local Similarity 72.2%; Pred. No. 1.8e-127;
RESULT 434
ID AA234325 standard; DNA; 503 BP.
DE Human EST DNA42301.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 435
ID AAC78591 standard; cDNA; 503 BP.
DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN WO200053755-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 436
ID ACA63893 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein DNA42301.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 437
ID ACA72057 standard; DNA; 503 BP.
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 438
ID ABX92697 standard; cDNA; 503 BP.
DE Human PRO337 EST polynucleotide sequence.

PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 439
ID ACA66438 standard; cDNA; 503 BP.
DE Human secreted/transmembrane protein EST DNA42301.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 440
ID ADA25063 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 441
ID ACD30039 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 442
ID ADA12724 standard; cDNA; 503 BP.
DE Human secreted/transmembrane polypeptide PRO337 EST.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 443
ID ACD29454 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #134.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 444
ID ADB74030 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 445
ID ADB76746 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 446
ID ADC44172 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 447
ID ADC61932 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 448
ID ADC63896 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 449
ID ADC66996 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 450
ID ADC69120 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 451
ID ADC63180 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 452
ID ADC68245 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 453
ID ADC41565 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 454
ID ADC67620 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 455
ID ADC62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 456
ID ADC42189 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 457
ID ADE49558 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 458
ID ADE35612 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 459
ID ADE16726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 460
ID ADD73341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 461
ID ADD72699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 462
ID ADE17350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 463
ID ADF47364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 464
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 465
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;

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Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 466
ID ADI61201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 467
ID ACD42858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 468
ID ADE4858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 469
ID ADE8959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 470
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 471
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 472
ID ADF46087 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 473
ID ADF24483 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 474
ID ADF40915 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 475
ID ADP23859 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 476
ID ADF33842 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 477
ID ADF27309 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 478
ID ADF27945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 479
ID ADF41539 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 480
ID ADF33218 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
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Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 481
ID ADF25584 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 482
ID ADF26685 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 483
ID ADF34474 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 484
ID ADF46711 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 485
ID ADF50697 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 486
ID ADF50073 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 487
ID ADF51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 488
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 489
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;

RESULT 490
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 491
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 492
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 493
ID ADH25746 standard; cDNA; 503 BP.
DE Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
FN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 494
ID ADM17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 495
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 496
ID AAC91321 standard; cDNA; 537 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
FN WO200073509-A2.
PD 07-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 29.3%; Score 491.2; DB 4; Length 537;
Best Local Similarity 98.6%; Pred. No. 2.2e-119;
RESULT 497
ID ADM47274 standard; DNA; 617 BP.
DE Oestrogen regulated protein like NOVX 25b gene.
FN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 26.8%; Score 449.4; DB 11; Length 617;
Best Local Similarity 97.6%; Pred. No. 2.8e-108;
RESULT 498
ID AAF93346 standard; cDNA; 452 BP.
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
FN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 441.2; DB 5; Length 452;
Best Local Similarity 99.1%; Pred. No. 3.5e-106;
RESULT 499

ID ACH15238 standard; cDNA; 437 BP.
DE Human adult brain cDNA #2450.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 24.1%; Score 404; DB 9; Length 437;
Best Local Similarity 97.4%; Pred. No. 2.4e-96;
RESULT 500
ID AAS78035 standard; cDNA; 484 BP.
DE DNA encoding novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.6%; Score 396; DB 5; Length 484;
Best Local Similarity 92.3%; Pred. No. 3.4e-94;
RESULT 501
ID ACH46276 standard; cDNA; 409 BP.
DE Human infant brain cDNA #339.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 21.1%; Score 353.8; DB 9; Length 409;
Best Local Similarity 98.1%; Pred. No. 4.6e-83;
RESULT 502
ID AAL50356 standard; cDNA; 1411 BP.
DE Human limbic system associated membrane protein 36-85 coding sequence.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 20.5%; Score 343.8; DB 6; Length 1411;
Best Local Similarity 62.1%; Pred. No. 3.8e-80;
RESULT 503
ID AAT42080 standard; cDNA to mRNA; 1238 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.4%; Score 343; DB 2; Length 1238;
Best Local Similarity 62.0%; Pred. No. 5.8e-80;
RESULT 504
ID ABX63560 standard; cDNA; 1195 BP.
DE Human cDNA #560 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 20.3%; Score 341.6; DB 8; Length 1195;
Best Local Similarity 60.1%; Pred. No. 1.3e-79;
RESULT 505
ID ADL12674 standard; cDNA; 1195 BP.
DE Human steroid-induced C3A liver cell cDNA #403.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.3%; Score 341.6; DB 12; Length 1195;
Best Local Similarity 60.1%; Pred. No. 1.3e-79;
RESULT 506
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 2.2e-79;
RESULT 507
ID AAT42079 standard; cDNA to mRNA; 977 BP.
DE Human LAMP residues 8-332 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 977;
Best Local Similarity 63.3%; Pred. No. 2.2e-79;
RESULT 508
ID AAT42081 standard; cDNA to mRNA; 1014 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 2.3e-79;
RESULT 509
ID ABT17402 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 28.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 20.3%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2.3e-79;
RESULT 510
ID ABT17404 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 30.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 20.3%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2.3e-79;
RESULT 511
ID AAT42086 standard; cDNA to mRNA; 861 BP.
DE Human LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.2%; Score 338.6; DB 2; Length 861;
Best Local Similarity 63.7%; Pred. No. 7.1e-79;
RESULT 512
ID AAT42082 standard; cDNA to mRNA; 912 BP.
DE Human mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.2%; Score 338.6; DB 2; Length 912;
Best Local Similarity 63.7%; Pred. No. 7.3e-79;
RESULT 513
ID AAT42085 standard; cDNA to mRNA; 945 BP.
DE Rat LAMP residues 1-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.1%; Score 337.4; DB 2; Length 945;
Best Local Similarity 63.1%; Pred. No. 1.5e-78;
RESULT 514
ID ABZ76264 standard; cDNA; 1757 BP.
DE Human GENSET cDNA clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GENS-) GENSET SA.
Query Match 20.1%; Score 337.4; DB 8; Length 1757;
Best Local Similarity 63.8%; Pred. No. 2.1e-78;
RESULT 515
ID AAT42083 standard; cDNA to mRNA; 930 BP.
DE Rat mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.1%; Score 337; DB 2; Length 930;
Best Local Similarity 62.1%; Pred. No. 2e-78;
RESULT 516
ID ABT17403 standard; DNA; 1075 BP.
DE Human IG gene related nucleic acid SEQ ID No 29.

PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC. 20.0%; Score 335; DB 8; Length 1075;
Query Match Best Local Similarity 63.5%; Pred. No. 7.1e-78;
RESULT 517
ID AAT42087 standard; cDNA to mRNA; 861 BP.
DE Rat LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match Best Local Similarity 63.4%; Pred. No. 1.3e-77;
RESULT 518
ID AAT42116 standard; cDNA to mRNA; 1307 BP.
DE Rat LAMP clone 6c coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match Best Local Similarity 63.3%; Pred. No. 5.5e-77;
RESULT 519
ID AAT42425 standard; cDNA; 1153 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 19.4%; Score 325.2; DB 4; Length 1153;
RESULT 520
ID AAC19214 standard; cDNA; 333 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23289.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSEST) GENSET.
Query Match Best Local Similarity 18.8%; Score 316.2; DB 3; Length 333;
RESULT 521
ID ABT17405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID No 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match Best Local Similarity 18.7%; Score 314.6; DB 8; Length 898;
RESULT 522
ID AAT42094 standard; cDNA to mRNA; 756 BP.
DE Human LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match Best Local Similarity 18.1%; Score 303.6; DB 2; Length 756;
RESULT 523
ID AAT42095 standard; cDNA to mRNA; 756 BP.
DE Rat LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match Best Local Similarity 17.8%; Score 298.2; DB 2; Length 756;
RESULT 524
ID AAT878034 standard; cDNA; 443 BP.
DE DNA encoding novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSEQ) HYSEQ INC.
Query Match Best Local Similarity 17.7%; Score 296.8; DB 5; Length 443;
RESULT 525
ID ABT17401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID No 27.
PN WO200299040-A2.

PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC. 16.6%; Score 279; DB 8; Length 1809;
Query Match Best Local Similarity 57.8%; Pred. No. 6.2e-63;
RESULT 526
ID ADS82049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) IG LIFE SCI LTD.
Query Match Best Local Similarity 16.3%; Score 274.2; DB 13; Length 4891;
RESULT 527
ID ABO82338 standard; cDNA; 1165 BP.
DE Human NOV12b encoding cDNA SEQ ID NO:25.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 6; Length 1165;
RESULT 528
ID AD128059 standard; cDNA; 1327 BP.
DE ECMCAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 6; Length 1327;
RESULT 529
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 4; Length 4834;
RESULT 530
ID ABK33536 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 6; Length 4834;
RESULT 531
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 8; Length 4834;
RESULT 532
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 8; Length 4834;
RESULT 533
ID ACA04534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 16.2%; Score 272.6; DB 8; Length 4834;
RESULT 534
ID ACA68497 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308063-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 535
ID ACA65675 standard; cDNA; 4834 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO6004.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 536
ID ABT44226 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 537
ID ADA47301 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
FN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 538
ID ABT44509 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
FN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 539
ID ACB82176 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO 6004 cDNA.
FN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 540
ID ACD30291 standard; cDNA; 4834 BP.
DE Human cDNA encoding Pro6004.
FN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 541
ID ABT43882 standard; cDNA; 4834 BP.
DE Human membrane bound receptor/protein PRO6004 cDNA sequence.
FN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 542
ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 543
ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003080658-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 544
ID ADB73138 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096568-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 545
ID ADB78220 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 546
ID ADB84868 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 547
ID ADB77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 548
ID ADB87040 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US200308067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 549
ID ADB84622 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 550
ID ADB83737 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 551
ID ADB72892 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 552
ID ADC36730 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US200308065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;

Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 553
ID ADC21720 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 554
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 555
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 556
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 557
ID ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 558
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 559
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 560
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 561
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 562
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 563
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 564
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 565
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 566
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 567
ID ADG63810 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 568
ID ACA66841 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO polypeptide #1.
FN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 569
ID ACD42405 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 570
ID ACD68593 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 571

ID ADC48704 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 572
ID ADE20875 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 573
ID ADE05719 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 574
ID ADD74948 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 575
ID ADD75694 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 576
ID ADD84926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 577
ID ADD86752 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 578
ID ADE20629 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 579
ID ADE38926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 580
ID ADE05473 standard; cDNA; 4834 BP.

DE Human PRO polynucleotide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 581
ID ADD73458 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 582
ID ADD78298 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 583
ID ADE21121 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 584
ID ADD77236 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 585
ID ADE20383 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 586
ID ADD75448 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 587
ID ADD73964 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 588
ID ADD74210 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 589
ID ADD75940 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 590
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 591
ID ADS04981 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 592
ID ADD75194 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 593
ID ADD76738 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 594
ID ADD86506 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 595
ID ADS41224 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 596
ID ADD77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 597
ID ADD77482 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 598
ID ADD77728 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100730-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 599
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 600
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 601
ID ADD74456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 602
ID ADD76984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 603
ID ADD85678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 604
ID ADS05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 605
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 606
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 607
ID ADG27068 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096962-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 608
ID ADG11131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 609
ID ADG11910 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 610
ID ADF94467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 611
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 612
ID ADH38907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 613
ID ADG63658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 614
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 615
ID ADI33467 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 616
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 617
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 618
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200404179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 619
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US200404180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 620
ID ABO82337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.2%; Score 272.2; DB 6; Length 1196;
Best Local Similarity 58.3%; Pred. No. 3.2e-61;
RESULT 621
ID ABN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 271; DB 6; Length 1119;
Best Local Similarity 58.3%; Pred. No. 6.3e-61;
RESULT 622
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBBF20110210.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 16.1%; Score 271; DB 10; Length 2383;
Best Local Similarity 58.3%; Pred. No. 9.3e-61;
RESULT 623
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 3; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 624
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 625
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.

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Query Match      16.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 626
ID ABX92783 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PA (GETH ) GENENTECH INC.
PD 13-MAR-2003.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 627
ID ACA66524 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 628
ID ADA25149 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050241-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 629
ID ACD30125 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050240-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 630
ID ADA12811 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane polypeptide PRO4993.
PN US2003055216-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 631
ID ACD29540 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #139.
PN US2003049633-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 632
ID ADB74117 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003045462-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 633
ID ADB76833 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003083248-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 634
ID ADC44259 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 635
ID ADC62019 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 636
ID ADC63983 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 637
ID ADC67083 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 638
ID ADC69207 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 639
ID ADC63267 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 640
ID ADC68332 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 641
ID ADC41652 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 642
ID ADC67707 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 643
ID ADC62643 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PA (GETH ) GENENTECH INC.
Query Match      16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 644
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ID ADC42276 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 645
ID ADE49645 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 646
ID ADE35699 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 647
ID ADE16813 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 648
ID ADD73428 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 649
ID ADP72786 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 650
ID ADE17437 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 651
ID ADF47451 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 652
ID ADG53208 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 653
ID ADG60528 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 654
ID ADI61288 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 655
ID ACD42944 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 656
ID ADE48945 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 657
ID ADE90046 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PRON/) PRONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 658
ID ADF61686 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 659
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ID ADF40378 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US200319894-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 660
ID ADF46174 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 661
ID ADF24570 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 662
ID ADF41002 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 663
ID ADF23946 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 664
ID ADF33929 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 665
ID ADF27396 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 666
ID ADF28032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 667
ID ADF41626 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 668
ID ADF33305 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 669
ID ADF25671 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 670
ID ADF26772 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 671
ID ADF34561 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 672
ID ADF46798 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 673
ID ADF50784 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 674
ID ADF50160 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 675
ID ADF52032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 676
ID ADF49536 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 677
ID ADF48912 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.

DE Human gene of the invention NOV11q SEQ ID NO:313.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1030;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 695
ID ADH71411 standard; DNA; 1033 BP.
DE Human gene of the invention NOV1ln SEQ ID NO:307.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 696
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV1lb SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 697
ID ADH71413 standard; DNA; 1035 BP.
DE Human gene of the invention NOV1lo SEQ ID NO:309.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1035;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 698
ID ABS76364 standard; DNA; 1427 BP.
DE DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.5%; Score 260.4; DB 6; Length 1427;
Best Local Similarity 59.5%; Pred. No. 4.6e-58;
RESULT 699
ID AAD47371 standard; DNA; 2653 BP.
DE Human LP289 DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 15.5%; Score 260.4; DB 8; Length 2653;
Best Local Similarity 59.5%; Pred. No. 6.3e-58;
RESULT 700
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.4%; Score 258.8; DB 6; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;
RESULT 701
ID ADL35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATV/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 15.4%; Score 258.8; DB 11; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;

RESULT 702
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV1lh SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.4%; Score 258.8; DB 12; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;
RESULT 703
ID ABS71700 standard; DNA; 1136 BP.
DE DNA encoding human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 6; Length 1136;
Best Local Similarity 59.3%; Pred. No. 2.9e-57;
RESULT 704
ID ADH71403 standard; DNA; 1171 BP.
DE Human gene of the invention NOV1lj SEQ ID NO:299.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1171;
Best Local Similarity 59.3%; Pred. No. 2.9e-57;
RESULT 705
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV1la SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 3e-57;
RESULT 706
ID ADH71421 standard; DNA; 1271 BP.
DE Human gene of the invention NOV1ls SEQ ID NO:317.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 3e-57;
RESULT 707
ID ADH71419 standard; DNA; 1271 BP.
DE Human gene of the invention NOV1lr SEQ ID NO:315.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.2%; Score 255.6; DB 12; Length 1271;
Best Local Similarity 59.1%; Pred. No. 8.1e-57;
RESULT 708
ID AAH87585 standard; DNA; 255 BP.
DE Human single nucleotide polymorphism containing DNA sequence #2442.
PN WO9553095-A2.
PD 21-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 15.2%; Score 255; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.2e-57;
RESULT 709
ID AAX10694 standard; DNA; 251 BP.
DE Human biallelic polymorphic DNA fragment WI-9617.
PN WO9820165-A2.
PD 14-MAY-1998.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 14.9%; Score 250.6; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 7.5e-56;
RESULT 710
ID ABK35606 standard; DNA; 1011 BP.
DE Gene encoding novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 14.7%; Score 246; DB 6; Length 1011;

Best Local Similarity 58.4%; Pred. No. 2.5e-54;
RESULT 711
ID ABS71701 standard; DNA; 1169 BP.
DE DNA encoding human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.7%; Score 246; DB 6; Length 1169;
Best Local Similarity 58.4%; Pred. No. 2.7e-54;
RESULT 712
ID ADH71407 standard; DNA; 1169 BP.
DE Human gene of the invention NOV111 SEQ ID NO:303.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.7%; Score 246; DB 12; Length 1169;
Best Local Similarity 58.4%; Pred. No. 2.7e-54;
RESULT 713
ID ABA06475 standard; cDNA; 2813 BP.
DE Human cDNA SEQ ID NO: 141.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.3%; Score 240.8; DB 4; Length 2813;
Best Local Similarity 58.3%; Pred. No. 1e-52;
RESULT 714
ID ABV83812 standard; cDNA; 2813 BP.
DE Human polynucleotide SEQ ID NO 141.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA-) BARASH S C.
Query Match 14.3%; Score 240.8; DB 6; Length 2813;
Best Local Similarity 58.3%; Pred. No. 1e-52;
RESULT 715
ID ADH71391 standard; DNA; 760 BP.
DE Human gene of the invention NOV11d SEQ ID NO:287.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.1%; Score 236.6; DB 12; Length 760;
Best Local Similarity 59.9%; Pred. No. 6.7e-52;
RESULT 716
ID AAD47374 standard; DNA; 2601 BP.
DE Human LP319b DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 13.9%; Score 234; DB 8; Length 2601;
Best Local Similarity 58.3%; Pred. No. 6.1e-51;
RESULT 717
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 13.8%; Score 232; DB 6; Length 1056;
Best Local Similarity 58.1%; Pred. No. 1.3e-50;
RESULT 718
ID ADL35982 standard; cDNA; 1168 BP.
DE Human NOVX cDNA #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.

PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 13.8%; Score 231.2; DB 11; Length 1168;
Best Local Similarity 58.1%; Pred. No. 2.2e-50;
RESULT 719
ID ADL35980 standard; cDNA; 1133 BP.
DE Human NOVX cDNA #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 13.4%; Score 224.8; DB 11; Length 1133;
Best Local Similarity 59.3%; Pred. No. 1.1e-48;
RESULT 720
ID AAS28811 standard; cDNA; 4656 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 220.6; DB 4; Length 4656;
Best Local Similarity 57.5%; Pred. No. 2.9e-47;
RESULT 721
ID ADB31536 standard; cDNA; 4656 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 57.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 220.6; DB 10; Length 4656;
Best Local Similarity 57.5%; Pred. No. 2.9e-47;
RESULT 722
ID AAS78003 standard; cDNA; 2883 BP.
DE DNA encoding novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 217.8; DB 5; Length 2883;
Best Local Similarity 71.1%; Pred. No. 1.2e-46;
RESULT 723
ID ADE08816 standard; DNA; 2883 BP.
DE Novel DNA-related contig nucleotide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 217.8; DB 10; Length 2883;
Best Local Similarity 71.1%; Pred. No. 1.2e-46;
RESULT 724
ID AAD47372 standard; DNA; 754 BP.
DE Human LP289 splice variant (LP343) DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 12.6%; Score 211.4; DB 8; Length 754;
Best Local Similarity 61.1%; Pred. No. 3.1e-45;
RESULT 725
ID ADP28686 standard; DNA; 666 BP.
DE Human secreted protein encoding sequence SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.5%; Score 210; DB 12; Length 666;

Best Local Similarity 60.2%; Pred. No. 6.9e-45;
RESULT 726
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
FN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 12.4%; Score 208.6; DB 8; Length 2597;
RESULT 727
ID AAC02777 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2775.
FN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match
Best Local Similarity 11.5%; Score 193.6; DB 3; Length 352;
RESULT 728
ID AB499899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
FN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.7%; Score 180.4; DB 6; Length 5666;
RESULT 729
ID ADG63283 standard; DNA; 540 BP.
DE Human OBCAM gene exon 2.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 10.5%; Score 176.6; DB 10; Length 540;
RESULT 730
ID ADQ83739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
FN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match
Best Local Similarity 10.4%; Score 175; DB 12; Length 919;
RESULT 731
ID AAS78037 standard; cDNA; 767 BP.
DE DNA encoding novel human diagnostic protein #13841.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 10.1%; Score 170.2; DB 5; Length 767;
RESULT 732
ID AAF93597 standard; cDNA; 585 BP.
DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
FN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 163.2; DB 5; Length 585;
RESULT 733
ID ABS52769 standard; cDNA; 408 BP.
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
FN WO200246475-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.5%; Score 160; DB 6; Length 408;
RESULT 734
ID AAC10355 standard; cDNA; 200 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14430.
FN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.

Query Match
Best Local Similarity 8.7%; Score 146; DB 3; Length 200;
RESULT 735
ID AAS78038 standard; cDNA; 693 BP.
DE DNA encoding novel human diagnostic protein #13842.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.2%; Score 137.2; DB 5; Length 693;
RESULT 736
ID ADQ21981 standard; DNA; 125 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 6.6%; Score 110.8; DB 12; Length 125;
RESULT 737
ID AAS78592 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #14396.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.4%; Score 107; DB 5; Length 1275;
RESULT 738
ID AAS71904 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #7708.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.4%; Score 107; DB 5; Length 1275;
RESULT 739
ID AAS78036 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #13840.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.4%; Score 107; DB 5; Length 1275;
RESULT 740
ID ABX71182 standard; cDNA; 913 BP.
DE Novel human cDNA sequence #407.
FN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match
Best Local Similarity 6.3%; Score 105.6; DB 8; Length 913;
RESULT 741
ID ADQ54463 standard; DNA; 351 BP.
DE Novel canine microarray-related DNA sequence SeqID5765.
FN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match
Best Local Similarity 6.2%; Score 104.6; DB 13; Length 351;
RESULT 742
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match
Best Local Similarity 6.0%; Score 100; DB 2; Length 219;
RESULT 743
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.

PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 5.7%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 9.6e-15;
RESULT 744
ID AAS67246 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 5.5e-14;
RESULT 745
ID AAS71723 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 5.5e-14;
RESULT 746
ID AAS64445 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 6e-14;
RESULT 747
ID AAS64798 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #602.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 6e-14;
RESULT 748
ID ADM18382 standard; DNA; 2026 BP.
DE Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.
PN WO2004029283-A2.
PD 08-APR-2004.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 5.3%; Score 89; DB 12; Length 2026;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 749
ID ADG63285 standard; DNA; 420 BP.
DE Human OBCAM gene exon 4.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 4.7%; Score 78.6; DB 10; Length 420;
Best Local Similarity 70.5%; Pred. No. 3.3e-10;
RESULT 750
ID AAT42090 standard; cDNA to mRNA; 177 BP.
DE Human LAMP residues 156-204 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 4.6%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 3.5e-10;
RESULT 751
ID AAT42091 standard; cDNA to mRNA; 177 BP.
DE Rat LAMP residues 156-204 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 4.6%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 3.5e-10;
RESULT 752
ID ADG63287 standard; DNA; 480 BP.
DE Human OBCAM gene exon 6.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

Query Match 4.6%; Score 76.8; DB 10; Length 480;
Best Local Similarity 70.8%; Pred. No. 1.1e-09;
RESULT 753
ID AAS28866 standard; cDNA; 293 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 112.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 754
ID ABA06681 standard; cDNA; 293 BP.
DE Human cDNA SEQ ID NO: 347.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 755
ID ABV84018 standard; cDNA; 293 BP.
DE Human polynucleotide SEQ ID NO 347.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.3%; Score 73; DB 6; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 756
ID ADB31591 standard; cDNA; 293 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 112.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 10; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 757
ID ADG63286 standard; DNA; 480 BP.
DE Human OBCAM gene exon 5.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 4.3%; Score 71.4; DB 10; Length 480;
Best Local Similarity 74.4%; Pred. No. 2.8e-08;
RESULT 758
ID AAT42092 standard; cDNA to mRNA; 198 BP.
DE Human LAMP residues 232-297 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 3.8%; Score 64.6; DB 2; Length 198;
Best Local Similarity 61.3%; Pred. No. 1.1e-06;
RESULT 759
ID AAT42093 standard; cDNA to mRNA; 198 BP.
DE Rat LAMP residues 232-297 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 3.8%; Score 63.4; DB 2; Length 198;
Best Local Similarity 60.7%; Pred. No. 2.4e-06;
RESULT 760
ID ADG63282 standard; DNA; 270 BP.
DE Human OBCAM gene exon 1.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 3.7%; Score 61.6; DB 10; Length 270;
Best Local Similarity 88.6%; Pred. No. 8.3e-06;
RESULT 761
ID ABN40988 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13736.
PN WO200210449-A2.
PD 07-FEB-2002.

PA (COMP-) COMPUGEN INC. 3.6%; Score 60; DB 6; Length 60;
Query Match Similarity 100.0%; Pred. No. 1e-05;
RESULT 762
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.5%; Score 58.6; DB 8; Length 2000;
Best Local Similarity 9.5%; Pred. No. 0.00014;
RESULT 763
ID ADG63284 standard; DNA; 420 BP.
DE Human OECAM gene exon 3.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 3.4%; Score 57.6; DB 10; Length 420;
Best Local Similarity 65.6%; Pred. No. 0.00012;
RESULT 764
ID ACN55172 standard; cDNA; 248 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-K6-C8, SEQ:9953.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.4%; Score 57.2; DB 13; Length 248;
Best Local Similarity 58.0%; Pred. No. 0.00012;
RESULT 765
ID ABX47608 standard; cDNA; 399 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12773.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.4%; Score 56.6; DB 8; Length 399;
Best Local Similarity 57.7%; Pred. No. 0.00021;
RESULT 766
ID ABV56779 standard; cDNA; 247 BP.
DE Human prostate expression marker cDNA 56770.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 55.6; DB 5; Length 247;
Best Local Similarity 54.4%; Pred. No. 0.00031;
RESULT 767
ID ABK39945 standard; DNA; 6359 BP.
DE Human chemically pretreated gene sequence #13 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 55; DB 6; Length 6359;
Best Local Similarity 66.4%; Pred. No. 0.00023;
RESULT 768
ID ACH15235 standard; cDNA; 514 BP.
DE Human adult brain cDNA #2447.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.2%; Score 54.4; DB 9; Length 514;
Best Local Similarity 62.3%; Pred. No. 0.00093;
RESULT 769
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match Similarity 61.1%; Score 54.4; DB 6; Length 6171;
Best Local Similarity 61.1%; Pred. No. 0.00033;
RESULT 770
ID AAI86998 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 7058.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 53.2; DB 4; Length 390;
Best Local Similarity 58.0%; Pred. No. 0.0017;
RESULT 771
ID AAD05318 standard; cDNA; 671 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLF064, SEQ ID NO:29.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 53.2; DB 4; Length 671;
Best Local Similarity 60.3%; Pred. No. 0.0022;
RESULT 772
ID ABV58693 standard; cDNA; 607 BP.
DE Human prostate expression marker cDNA 58684.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 53; DB 5; Length 607;
Best Local Similarity 56.6%; Pred. No. 0.0024;
RESULT 773
ID ABV48356 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 48347.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 52.8; DB 5; Length 392;
Best Local Similarity 57.1%; Pred. No. 0.0022;
RESULT 774
ID ADH23363 standard; cDNA; 3351 BP.
DE Fruit fly PAK4 serine/threonine kinase cDNA.
PN US2003186254-A1.
PD 02-OCT-2003.
PA (CELL-) CELL SIGNALING TECHNOLOGY INC.
Query Match 3.1%; Score 52.8; DB 12; Length 3351;
Best Local Similarity 58.1%; Pred. No. 0.0064;
RESULT 775
ID ABL33589 standard; DNA; 5567 BP.
DE Human immune system associated gene SEQ ID NO: 1562.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.8; DB 6; Length 5567;
Best Local Similarity 63.3%; Pred. No. 0.0082;
RESULT 776
ID ABL92273 standard; DNA; 5567 BP.
DE Chemically treated DNA repair gene fragment complementary to#41.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.8; DB 6; Length 5567;
Best Local Similarity 63.3%; Pred. No. 0.0082;
RESULT 777
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.1%; Score 52.6; DB 8; Length 2000;
Best Local Similarity 8.4%; Pred. No. 0.0055;
RESULT 778
ID ABQ25430 standard; DNA; 579 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12021.
PN WO200218632-A2.
PD 07-MAR-2002.

PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 52.4; DB 6; Length 579;
 Best Local Similarity 60.6%; Pred. No. 0.0033;
 RESULT 779
 ID ABQ25431 standard; DNA; 579 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12022.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 52.4; DB 6; Length 579;
 Best Local Similarity 60.6%; Pred. No. 0.0033;
 RESULT 780
 ID ACN81600 standard; DNA; 679 BP.
 DE Breast cancer related marker, seq id 2750.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 52.4; DB 11; Length 679;
 Best Local Similarity 55.2%; Pred. No. 0.0036;
 RESULT 781
 ID ABK40004 standard; DNA; 5586 BP.
 DE Human chemically pretreated gene sequence #43 strand 2.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 52.4; DB 6; Length 5586;
 Best Local Similarity 59.3%; Pred. No. 0.011;
 RESULT 782
 ID ACN52334 standard; cDNA; 571 BP.
 DE Cotton androecium tissue EST Clone ID: L1B3828-014-Q1-N6-B11, SEQ: 7115.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 3.1%; Score 52.2; DB 13; Length 571;
 Best Local Similarity 57.8%; Pred. No. 0.0038;
 RESULT 783
 ID AAL11399 standard; cDNA; 666 BP.
 DE Human breast cancer expressed polynucleotide 3856.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.1%; Score 52.2; DB 4; Length 666;
 Best Local Similarity 56.8%; Pred. No. 0.0041;
 RESULT 784
 ID ABL1515 standard; cDNA; 2010 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.1%; Score 52.2; DB 4; Length 2010;
 Best Local Similarity 45.6%; Pred. No. 0.0071;
 RESULT 785
 ID AAF72803 standard; DNA; 2057 BP.
 DE Secreted protein gene #5.
 PN WO200107459-A1.
 PD 01-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.1%; Score 52.2; DB 4; Length 2057;
 Best Local Similarity 57.8%; Pred. No. 0.0072;
 RESULT 786
 ID ABS67818 standard; DNA; 3063 BP.
 DE Human receptors and membrane associated protein REMAP-40 gene.
 PN WO200263008-A2.
 PD 15-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 3.1%; Score 52.2; DB 6; Length 3063;
 Best Local Similarity 64.5%; Pred. No. 0.0088;
 RESULT 787
 ID ABL33948 standard; DNA; 18218 BP.
 DE Human immune system associated gene SEQ ID NO: 1921.

PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 52.2; DB 6; Length 18218;
 Best Local Similarity 60.0%; Pred. No. 0.022;
 RESULT 788
 ID ADS73024 standard; cDNA; 183 BP.
 DE Human kidney tumour specific cDNA, SEQ ID 1621.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.1%; Score 52; DB 7; Length 183;
 Best Local Similarity 60.7%; Pred. No. 0.0024;
 RESULT 789
 ID ABV58708 standard; cDNA; 484 BP.
 DE Human prostate expression marker cDNA 58699.
 PN WO200150860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.1%; Score 52; DB 5; Length 484;
 Best Local Similarity 58.3%; Pred. No. 0.0039;
 RESULT 790
 ID ABT08076 standard; cDNA; 791 BP.
 DE Human breast specific coding sequence SEQ ID NO: 22.
 PN WO200266607-A2.
 PD 29-AUG-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 3.1%; Score 52; DB 6; Length 791;
 Best Local Similarity 60.7%; Pred. No. 0.005;
 RESULT 791
 ID ABL32719 standard; DNA; 5739 BP.
 DE Human immune system associated gene SEQ ID NO: 692.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 52; DB 6; Length 5739;
 Best Local Similarity 59.5%; Pred. No. 0.014;
 RESULT 792
 ID ABQ54403 standard; cDNA; 2911 BP.
 DE Human ovarian antigen HAPOE30 cDNA, SEQ ID NO: 283.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.1%; Score 51.6; DB 6; Length 2911;
 Best Local Similarity 59.6%; Pred. No. 0.012;
 RESULT 793
 ID AAA16619 standard; cDNA; 3508 BP.
 DE Human secreted protein clone 10311_8 nucleotide sequence SEQ ID NO: 3.
 PN WO200009552-A1.
 PD 24-FEB-2000.
 PA (GENY) GENETICS INST INC.
 Query Match 3.1%; Score 51.6; DB 3; Length 3508;
 Best Local Similarity 62.3%; Pred. No. 0.014;
 RESULT 794
 ID ADS89723 standard; DNA; 5759 BP.
 DE Oligonucleotide of the invention SEQ ID NO: 739.
 PN WO2004035803-A2.
 PD 29-APR-2004.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 51.6; DB 13; Length 5759;
 Best Local Similarity 56.5%; Pred. No. 0.017;
 RESULT 795
 ID AB210109 standard; DNA; 8759 BP.
 DE Haematopoietic cell proliferation disorder related DNA sequence #249.
 PN WO20027272-A2.
 PD 03-OCT-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 3.1%; Score 51.6; DB 8; Length 8759;
 Best Local Similarity 56.5%; Pred. No. 0.022;
 RESULT 796
 ID AB210237 standard; DNA; 8759 BP.
 DE Haematopoietic cell proliferation disorder related DNA sequence #377.
 PN WO20027272-A2.

PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 8; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 797
ID ADB54213 standard; DNA; 8759 BP.
DE Pretreated genomic DNA region 137.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 10; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 798
ID ADB84147 standard; DNA; 8759 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #83.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 10; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 799
ID ADB89513 standard; DNA; 8759 BP.
DE Oligonucleotide of the invention SEQ ID NO:529.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 13; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 800
ID ABL32784 standard; DNA; 8979 BP.
DE Human immune system associated gene SEQ ID NO: 757.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 801
ID ABK31270 standard; DNA; 8979 BP.
DE Signal transduction associated Gene modified DNA #57.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 802
ID ABL70231 standard; DNA; 8979 BP.
DE Chemically treated cell signalling DNA sequence#61.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 803
ID AAS61178 standard; DNA; 8979 BP.
DE Human gene regulation-associated gene oligonucleotide #133.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 804
ID AAT87807 standard; cDNA; 419 BP.
DE Human polynucleotide SEQ ID NO 7867.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 51.4; DB 4; Length 419;
Best Local Similarity 60.3%; Pred. No. 0.0052;
RESULT 805
ID ACN52877 standard; cDNA; 421 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.1%; Score 51.4; DB 13; Length 421;
Best Local Similarity 58.0%; Pred. No. 0.0052;
RESULT 806
ID ACN50120 standard; cDNA; 585 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-D8, SEQ:4901.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.1%; Score 51.4; DB 13; Length 585;
Best Local Similarity 58.0%; Pred. No. 0.0062;
RESULT 807
ID ABV58626 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 58617.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 51.2; DB 5; Length 504;
Best Local Similarity 57.5%; Pred. No. 0.0065;
RESULT 808
ID ABK43454 standard; cDNA; 894 BP.
DE DNA encoding novel central nervous system protein #34.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 51.2; DB 4; Length 894;
Best Local Similarity 66.1%; Pred. No. 0.0087;
RESULT 809
ID ADI53841 standard; cDNA; 894 BP.
DE cDNA encoding novel human protein seq id 44.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.0%; Score 51.2; DB 12; Length 894;
Best Local Similarity 66.1%; Pred. No. 0.0087;
RESULT 810
ID AAI83204 standard; cDNA; 386 BP.
DE Human polynucleotide SEQ ID NO 3264.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 51; DB 4; Length 386;
Best Local Similarity 59.2%; Pred. No. 0.0064;
RESULT 811
ID ACN56273 standard; cDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.0%; Score 51; DB 13; Length 517;
Best Local Similarity 59.2%; Pred. No. 0.0074;
RESULT 812
ID ADJ81646 standard; DNA; 10428 BP.
DE Human tyrosine phosphatase SHP1 disulphited genomic DNA SeqID 6.
PN JP2004000128-A.
PD 08-JAN-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 3.0%; Score 51; DB 12; Length 10428;
Best Local Similarity 59.2%; Pred. No. 0.034;
RESULT 813
ID ACN87837 standard; DNA; 643 BP.
DE Breast cancer related marker, seq id 8987.

PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.0%; Score 50.8; DB 11; Length 643;
 Best Local Similarity 57.8%; Pred. No. 0.0094;
 RESULT 814
 ID ADL41364 standard; DNA; 393 BP.
 DE Human ovarian cancer DNA marker #15254.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.0%; Score 50.6; DB 5; Length 393;
 Best Local Similarity 57.1%; Pred. No. 0.0082;
 RESULT 815
 ID ABN98845 standard; DNA; 856 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match 3.0%; Score 50.6; DB 6; Length 856;
 Best Local Similarity 54.8%; Pred. No. 0.012;
 RESULT 816
 ID AAC63439 standard; cDNA; 876 BP.
 DE Human secreted protein coding sequence SEQ ID NO: 40.
 PN WO200061779-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.0%; Score 50.6; DB 3; Length 876;
 Best Local Similarity 63.6%; Pred. No. 0.012;
 RESULT 817
 ID AB273647 standard; cDNA; 876 BP.
 DE Secreted protein-encoding gene 367 cDNA clone HUSIR18, SEQ ID NO:377.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.0%; Score 50.6; DB 8; Length 876;
 Best Local Similarity 63.6%; Pred. No. 0.012;
 RESULT 818
 ID ADA98139 standard; cDNA; 876 BP.
 DE Human secreted protein cDNA sequence #233.
 PN WO2003004623-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.0%; Score 50.6; DB 8; Length 876;
 Best Local Similarity 63.6%; Pred. No. 0.012;
 RESULT 819
 ID AB267241 standard; cDNA; 876 BP.
 DE Human secreted protein encoding cDNA SEQ ID NO 361.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.0%; Score 50.6; DB 10; Length 876;
 Best Local Similarity 63.6%; Pred. No. 0.012;
 RESULT 820
 ID ADD71195 standard; cDNA; 2200 BP.

DE Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.
 PN WO2003039348-A2.
 PD 15-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 3.0%; Score 50.6; DB 10; Length 2200;
 Best Local Similarity 70.1%; Pred. No. 0.02;
 RESULT 821
 ID ADB79863 standard; DNA; 2924 BP.
 DE Rat myosin heavy chain coding sequence, SEQ ID 103.
 PN EP127974-A2.
 PD 29-JAN-2003.
 PA (WARN-) WARNER LAMBERT CO.
 Query Match 3.0%; Score 50.6; DB 10; Length 2924;
 Best Local Similarity 63.6%; Pred. No. 0.023;
 RESULT 822
 ID ABV25005 standard; cDNA; 4990 BP.
 DE Human prostate expression marker cDNA 24996.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.0%; Score 50.6; DB 5; Length 4990;
 Best Local Similarity 58.2%; Pred. No. 0.03;
 RESULT 823
 ID ABV25400 standard; cDNA; 4990 BP.
 DE Human prostate expression marker cDNA 25391.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.0%; Score 50.6; DB 5; Length 4990;
 Best Local Similarity 58.2%; Pred. No. 0.03;
 RESULT 824
 ID ACN89861 standard; DNA; 5001 BP.
 DE Breast cancer related marker, seq id 11011.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.0%; Score 50.6; DB 11; Length 5001;
 Best Local Similarity 58.2%; Pred. No. 0.03;
 RESULT 825
 ID ABL92257 standard; DNA; 6029 BP.
 DE Chemically treated DNA repair gene fragment complementary to#33.
 PN WO200181622-A2.
 PD 01-NOV-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.0%; Score 50.6; DB 6; Length 6029;
 Best Local Similarity 57.1%; Pred. No. 0.033;
 RESULT 826
 ID AAD22326 standard; DNA; 6029 BP.
 DE Chemically treated human genomic DNA #16 associated with DNA adducts.
 PN WO200177378-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.0%; Score 50.6; DB 6; Length 6029;
 Best Local Similarity 57.1%; Pred. No. 0.033;
 RESULT 827
 ID ABX41821 standard; cDNA; 272 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #6986.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 3.0%; Score 50.4; DB 8; Length 272;
 Best Local Similarity 60.0%; Pred. No. 0.0077;
 RESULT 828
 ID AAH71505 standard; cDNA; 310 BP.
 DE Human cervical cancer marker nucleic acid 2779.
 PN WO200142467-A2.
 PD 14-JUN-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.0%; Score 50.4; DB 4; Length 310;
 Best Local Similarity 56.7%; Pred. No. 0.0082;

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RESULT 829
ID ABL33696 standard; DNA; 6668 BP.
DE Human immune system associated gene SEQ ID NO: 1669.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.4; DB 6; Length 6668;
Best Local Similarity 58.8%; Pred. No. 0.039;
RESULT 830
ID ABV19038 standard; cDNA; 201 BP.
DE Human prostate expression marker cDNA 19029.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 201;
Best Local Similarity 59.8%; Pred. No. 0.0075;
RESULT 831
ID AAT76782 standard; DNA; 240 BP.
DE Staphylococcus aureus exfoliative toxin A gene capture probe.
PN US5627054-A.
PD 06-MAY-1997.
PA (USSA-) US SEC OF ARMY.
Query Match 3.0%; Score 50.2; DB 2; Length 240;
Best Local Similarity 58.3%; Pred. No. 0.0082;
RESULT 832
ID ABV42927 standard; cDNA; 382 BP.
DE Human prostate expression marker cDNA 42918.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 382;
Best Local Similarity 55.4%; Pred. No. 0.01;
RESULT 833
ID ABV34060 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 34051.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 383;
Best Local Similarity 55.4%; Pred. No. 0.01;
RESULT 834
ID ABV18980 standard; cDNA; 384 BP.
DE Human prostate expression marker cDNA 18971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 48.1%; Pred. No. 0.01;
RESULT 835
ID AD169792 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #2534.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 52.6%; Pred. No. 0.01;
RESULT 836
ID AD176128 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #8870.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 52.6%; Pred. No. 0.01;
RESULT 837
ID ABV48817 standard; cDNA; 448 BP.
DE Human prostate expression marker cDNA 48808.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 448;
Best Local Similarity 59.8%; Pred. No. 0.011;
RESULT 838
ID ABL32540 standard; DNA; 6476 BP.
DE Human immune system associated gene SEQ ID NO: 513.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.2; DB 6; Length 6476;
Best Local Similarity 62.2%; Pred. No. 0.043;
RESULT 839
ID ABV59017 standard; cDNA; 325 BP.
DE Human prostate expression marker cDNA 59008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 325;
Best Local Similarity 61.5%; Pred. No. 0.011;
RESULT 840
ID ABV50931 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 50922.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 464;
Best Local Similarity 63.1%; Pred. No. 0.013;
RESULT 841
ID ABV54323 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 54314.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 471;
Best Local Similarity 52.4%; Pred. No. 0.013;
RESULT 842
ID ACH45627 standard; cDNA; 520 BP.
DE Human foetal brain cDNA #352.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 50; DB 9; Length 520;
Best Local Similarity 53.8%; Pred. No. 0.014;
RESULT 843
ID AAC79893 standard; cDNA; 680 BP.
DE Human secreted protein encoding cDNA for gene 45.
PN WO200055176-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 3; Length 680;
Best Local Similarity 58.9%; Pred. No. 0.016;
RESULT 844
ID AAA61261 standard; DNA; 870 BP.
DE Human secreted protein gene 2 clone HHFBY53.
PN WO20029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 3; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 845
ID ADA39860 standard; cDNA; 870 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 8; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 846
ID ACC50464 standard; cDNA; 870 BP.
DE Human secreted protein coding sequence, SEQ ID 131.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
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Query Match 3.0%; Score 50; DB 8; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 847
ID ADO62706 standard; DNA; 1971 BP.
DE Transcription factor G2550 orthologous sequence, SEQ ID 1173.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 3.0%; Score 50; DB 12; Length 1971;
Best Local Similarity 67.0%; Pred. No. 0.027;
RESULT 848
ID ADO24914 standard; DNA; 3469 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7734.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.0%; Score 50; DB 12; Length 3469;
Best Local Similarity 56.8%; Pred. No. 0.036;
RESULT 849
ID ABN80041 standard; DNA; 5387 BP.
DE Human chemically modified disease associated gene SEQ ID NO 58.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 3.0%; Score 50; DB 6; Length 5387;
Best Local Similarity 57.8%; Pred. No. 0.045;
RESULT 850
ID ABX56303 standard; DNA; 8243 BP.
DE Human NOV25b CG93858-02 DNA SEQ ID 85.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.0%; Score 50; DB 8; Length 8243;
Best Local Similarity 49.7%; Pred. No. 0.055;
RESULT 851
ID ABL33999 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1972.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 3.0%; Score 50; DB 6; Length 21537;
Best Local Similarity 60.1%; Pred. No. 0.09;
RESULT 852
ID ABV49239 standard; cDNA; 311 BP.
DE Human prostate expression marker cDNA 49230.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 311;
Best Local Similarity 58.4%; Pred. No. 0.012;
RESULT 853
ID ABV57904 standard; cDNA; 376 BP.
DE Human prostate expression marker cDNA 57895.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 376;
Best Local Similarity 58.4%; Pred. No. 0.013;
RESULT 854
ID ABV54466 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 54457.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 381;
Best Local Similarity 62.4%; Pred. No. 0.013;
RESULT 855
ID ACH39052 standard; cDNA; 465 BP.
DE Human foetal brain cDNA #419.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 49.8; DB 9; Length 465;
Best Local Similarity 55.9%; Pred. No. 0.015;
RESULT 856
ID ACH22893 standard; cDNA; 506 BP.
DE Human adult ovary cDNA #1273.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 49.8; DB 9; Length 506;
Best Local Similarity 60.4%; Pred. No. 0.015;
RESULT 857
ID ABV56485 standard; cDNA; 543 BP.
DE Human prostate expression marker cDNA 56476.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 543;
Best Local Similarity 57.3%; Pred. No. 0.016;
RESULT 858
ID AAH70126 standard; cDNA; 545 BP.
DE Human cervical cancer marker nucleic acid 1400.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 4; Length 545;
Best Local Similarity 53.9%; Pred. No. 0.016;
RESULT 859
ID ACN53724 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-H4, SEQ:8505.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.0%; Score 49.8; DB 13; Length 571;
Best Local Similarity 64.1%; Pred. No. 0.016;
RESULT 860
ID AA26373 standard; cDNA; 1048 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 3; Length 1048;
Best Local Similarity 59.6%; Pred. No. 0.022;
RESULT 861
ID ADL71434 standard; cDNA; 1048 BP.
DE Novel human secreted protein cDNA seqid 38.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSOUIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (WEIY/) WEI Y.
Query Match 3.0%; Score 49.8; DB 12; Length 1048;
Best Local Similarity 59.6%; Pred. No. 0.022;
RESULT 862
ID ADH02701 standard; DNA; 1317 BP.
DE Human elongation factor EEF1A1 cDNA fragment, SEQ ID NO:7.
PN WO2003104488-A1.
PD 18-DEC-2003.
PA (CANC-) CANCER CARE ONTARIO.

Query Match 3.0%; Score 49.8; DB 12; Length 1317;
Best Local Similarity 58.4%; Pred. No. 0.025;
RESULT 863
ID ACF34510 standard; DNA; 1833 BP.
DE Gene encoding angiogenesis protein BNO144.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 3.0%; Score 49.8; DB 8; Length 1833;
Best Local Similarity 58.4%; Pred. No. 0.029;
RESULT 864
ID ADL35468 standard; DNA; 1833 BP.
DE Human eukaryotic translation elongation factor 1 alpha 1 (EBF1A1) DNA.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 3.0%; Score 49.8; DB 12; Length 1833;
Best Local Similarity 58.4%; Pred. No. 0.029;
RESULT 865
ID ADS98611 standard; cDNA; 1833 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:154.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIGA-) NGK INSULATORS LTD.
Query Match 3.0%; Score 49.8; DB 13; Length 1833;
Best Local Similarity 58.4%; Pred. No. 0.029;
RESULT 866
ID ADJ62805 standard; cDNA; 1837 BP.
DE Human cDNA differentially expressed in response to docetaxel #75.
PN US2004018527-A1.
PD 29-JAN-2004.
PA (CHAN/) CHANG J C.
PA (OCON/) O'CONNELL P.
Query Match 3.0%; Score 49.8; DB 12; Length 1837;
Best Local Similarity 58.4%; Pred. No. 0.029;
RESULT 867
ID ADP10528 standard; DNA; 1837 BP.
DE Reference mRNA sequences for marker probe #205.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 3.0%; Score 49.8; DB 12; Length 1837;
Best Local Similarity 58.4%; Pred. No. 0.029;
RESULT 868
ID AAF18296 standard; DNA; 2044 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 315.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 3.0%; Score 49.8; DB 3; Length 2044;
Best Local Similarity 57.3%; Pred. No. 0.031;
RESULT 869
ID AAA95790 standard; cDNA; 2045 BP.
DE Apoptosis related gene 1 clone HLDOK36.
PN WO200056752-A2.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 3; Length 2045;
Best Local Similarity 57.3%; Pred. No. 0.031;
RESULT 870
ID AAH3283 standard; cDNA; 2045 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 4; Length 2045;
Best Local Similarity 57.3%; Pred. No. 0.031;
RESULT 871
ID AAV63189 standard; cDNA; 2496 BP.
DE cDNA from clone cr1162_25 which encodes a secreted protein.
PN WO9844113-A1.
PD 08-OCT-1998.

PA (GEMY) GENETICS INST INC.
Query Match 3.0%; Score 49.8; DB 2; Length 2496;
Best Local Similarity 60.9%; Pred. No. 0.034;
RESULT 872
ID ABQ92039 standard; cDNA; 2496 BP.
DE Human polynucleotide SEQ ID NO 36.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 3.0%; Score 49.8; DB 6; Length 2496;
Best Local Similarity 60.9%; Pred. No. 0.034;
RESULT 873
ID ADI03925 standard; DNA; 2496 BP.
DE Human B7-L1 polypeptide encoding DNA.
PN WO2003105887-A1.
PD 24-DEC-2003.
PA (AMHP) WYETH.
Query Match 3.0%; Score 49.8; DB 12; Length 2496;
Best Local Similarity 60.9%; Pred. No. 0.034;
RESULT 874
ID AAF91859 standard; cDNA; 3436 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HDPFB02, SEQ ID NO:12.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 4; Length 3436;
Best Local Similarity 59.6%; Pred. No. 0.04;
RESULT 875
ID AAS00767 standard; cDNA; 3436 BP.
DE Human B7-H3 cDNA clone.
PN WO200118021-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MAYO-) MAYO CLINIC.
Query Match 3.0%; Score 49.8; DB 4; Length 3436;
Best Local Similarity 59.6%; Pred. No. 0.04;
RESULT 876
ID ADA39737 standard; cDNA; 3436 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 8; Length 3436;
Best Local Similarity 59.6%; Pred. No. 0.04;
RESULT 877
ID ADC73453 standard; DNA; 3436 BP.
DE Human secreted protein-related DNA - SEQ ID 86.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 10; Length 3436;
Best Local Similarity 59.6%; Pred. No. 0.04;
RESULT 878
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 49.8; DB 6; Length 7346;
Best Local Similarity 59.6%; Pred. No. 0.059;
RESULT 879
ID ABR80102 standard; DNA; 8712 BP.
DE Human chemically modified disease associated gene SEQ ID NO 119.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.0%; Score 49.8; DB 6; Length 8712;
Best Local Similarity 60.9%; Pred. No. 0.064;
RESULT 880
ID AAI92106 standard; cDNA; 425 BP.
DE Human polynucleotide SEQ ID NO 12166.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 49.6; DB 4; Length 425;
Best Local Similarity 57.9%; Pred. No. 0.016;
RESULT 881
ID ACN60136 standard; cDNA; 481 BP.
DE Cotton gynecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.0%; Score 49.6; DB 13; Length 481;
Best Local Similarity 59.0%; Pred. No. 0.017;
RESULT 882
ID ADQ22716 standard; DNA; 1486 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5536.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.0%; Score 49.6; DB 12; Length 1486;
Best Local Similarity 58.6%; Pred. No. 0.03;
RESULT 883
ID ACS59907 standard; cDNA; 1678 BP.
DE Human REMAP-20 encoding cDNA SEQ ID NO:56.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.0%; Score 49.6; DB 9; Length 1678;
Best Local Similarity 59.0%; Pred. No. 0.032;
RESULT 884
ID ADL63386 standard; DNA; 2161 BP.
DE Human ovarian cancer DNA marker #21598.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.6; DB 5; Length 2161;
Best Local Similarity 56.9%; Pred. No. 0.036;
RESULT 885
ID ADG32748 standard; DNA; 2870 BP.
DE Human DNA differentially expressed in patients with SLE SeqID72.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 3.0%; Score 49.6; DB 10; Length 2870;
Best Local Similarity 61.7%; Pred. No. 0.041;
RESULT 886
ID ADD18806 standard; DNA; 3232 BP.
DE Human disease related protein DNA sequence SeqID238.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 3.0%; Score 49.6; DB 10; Length 3232;
Best Local Similarity 60.3%; Pred. No. 0.044;
RESULT 887
ID ADH61306 standard; DNA; 3420 BP.
DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.0%; Score 49.6; DB 12; Length 3420;
Best Local Similarity 59.0%; Pred. No. 0.045;
RESULT 888
ID ABL333518 standard; DNA; 5520 BP.
DE Human immune system associated gene SEQ ID NO: 1491.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 49.6; DB 6; Length 5520;
Best Local Similarity 59.0%; Pred. No. 0.058;
RESULT 889
ID ABL32677 standard; DNA; 6015 BP.
DE Human immune system associated gene SEQ ID NO: 650.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 49.6; DB 6; Length 6015;
Best Local Similarity 63.3%; Pred. No. 0.06;
RESULT 890
ID AAI87537 standard; cDNA; 366 BP.
DE Human polynucleotide SEQ ID NO 7597.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.4; DB 4; Length 366;
Best Local Similarity 61.1%; Pred. No. 0.017;
RESULT 891
ID ABV56666 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 56657.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 408;
Best Local Similarity 54.9%; Pred. No. 0.017;
RESULT 892
ID AAI82260 standard; cDNA; 412 BP.
DE Human polynucleotide SEQ ID NO 2320.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.4; DB 4; Length 412;
Best Local Similarity 63.8%; Pred. No. 0.018;
RESULT 893
ID ABV45890 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 45881.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 438;
Best Local Similarity 62.6%; Pred. No. 0.018;
RESULT 894
ID AAI82206 standard; cDNA; 480 BP.
DE Human polynucleotide SEQ ID NO 2266.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.4; DB 4; Length 480;
Best Local Similarity 54.0%; Pred. No. 0.019;
RESULT 895
ID ACH25146 standard; cDNA; 561 BP.
DE Human adult ovary cDNA #3526.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CHAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.9%; Score 49.4; DB 9; Length 561;
Best Local Similarity 58.5%; Pred. No. 0.02;
RESULT 896
ID ABV58690 standard; cDNA; 579 BP.
DE Human prostate expression marker cDNA 58681.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 579;
Best Local Similarity 58.5%; Pred. No. 0.021;
RESULT 897

ID AAL20340 standard; cDNA; 622 BP.
DE Human breast cancer expressed polynucleotide 12797.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 4; Length 622;
Best Local Similarity 57.4%; Pred. No. 0.022;
RESULT 898
ID AAC80551 standard; cDNA; 658 BP.
DE Human secreted protein gene 21 SEQ ID NO:31.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 3; Length 658;
Best Local Similarity 57.4%; Pred. No. 0.022;
RESULT 899
ID AAH35003 standard; cDNA; 788 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2085.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 788;
Best Local Similarity 58.5%; Pred. No. 0.024;
RESULT 900
ID AAS02414 standard; cDNA; 797 BP.
DE Human secreted protein, cDNA #20.
PN WO200123546-A1.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 797;
Best Local Similarity 58.5%; Pred. No. 0.024;
RESULT 901
ID ABV28953 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 28944.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 902
ID ABV22100 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 22091.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 903
ID ABV23114 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 23105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 904
ID ABV27940 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 27931.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 905
ID AAS31262 standard; cDNA; 2645 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 906
ID ABQ66586 standard; cDNA; 2645 BP.
DE Human polynucleotide SEQ ID NO 76.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.9%; Score 49.4; DB 6; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 907
ID ADC10608 standard; cDNA; 2645 BP.
DE Human cDNA from extracellular matrix gene 66.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 10; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 908
ID ADQ23227 standard; DNA; 3480 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6047.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.4; DB 12; Length 3480;
Best Local Similarity 57.4%; Pred. No. 0.052;
RESULT 909
ID ADQ24537 standard; DNA; 3480 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.4; DB 12; Length 3480;
Best Local Similarity 57.4%; Pred. No. 0.052;
RESULT 910
ID AAI88514 standard; cDNA; 396 BP.
DE Human polynucleotide SEQ ID NO 8574.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 389;
Best Local Similarity 57.0%; Pred. No. 0.019;
RESULT 911
ID AAI88643 standard; cDNA; 396 BP.
DE Human polynucleotide SEQ ID NO 8703.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 396;
Best Local Similarity 57.0%; Pred. No. 0.019;
RESULT 912
ID AAI87424 standard; cDNA; 429 BP.
DE Human polynucleotide SEQ ID NO 7484.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 429;
Best Local Similarity 60.0%; Pred. No. 0.02;
RESULT 913
ID ABV58527 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 58518.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 442;
Best Local Similarity 57.0%; Pred. No. 0.021;
RESULT 914
ID ACH25161 standard; cDNA; 448 BP.
DE Human adult ovary cDNA #3541.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.
Query Match 2.9%; Score 49.2; DB 9; Length 448;
Best Local Similarity 59.1%; Pred. No. 0.021;
RESULT 915
ID AAI84689 standard; cDNA; 453 BP.
DE Human polynucleotide SEQ ID NO 4749.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 453;
Best Local Similarity 60.4%; Pred. No. 0.021;
RESULT 916
ID ABV58840 standard; cDNA; 539 BP.
DE Human prostate expression marker cDNA 58831.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 539;
Best Local Similarity 59.2%; Pred. No. 0.023;
RESULT 917
ID ABV56624 standard; cDNA; 544 BP.
DE Human prostate expression marker cDNA 56615.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 544;
Best Local Similarity 60.4%; Pred. No. 0.023;
RESULT 918
ID ABV58620 standard; cDNA; 554 BP.
DE Human prostate expression marker cDNA 58611.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 554;
Best Local Similarity 61.9%; Pred. No. 0.023;
RESULT 919
ID ABV58414 standard; cDNA; 575 BP.
DE Human prostate expression marker cDNA 58405.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 575;
Best Local Similarity 57.0%; Pred. No. 0.023;
RESULT 920
ID AAH71551 standard; cDNA; 621 BP.
DE Human cervical cancer marker nucleic acid 2825.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 4; Length 621;
Best Local Similarity 57.0%; Pred. No. 0.024;
RESULT 921
ID AAH34312 standard; cDNA; 712 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1394.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.2; DB 4; Length 712;
Best Local Similarity 59.2%; Pred. No. 0.026;
RESULT 922
ID ADJ80203 standard; cDNA; 877 BP.
DE Novel human nucleic acid-associated protein coding sequence #21.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.9%; Score 49.2; DB 10; Length 877;
Best Local Similarity 59.2%; Pred. No. 0.029;
RESULT 923
ID AAK58876 standard; cDNA; 1503 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3936.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.9%; Score 49.2; DB 4; Length 1503;
Best Local Similarity 59.6%; Pred. No. 0.038;
RESULT 924
ID ABA93758 standard; cDNA; 1537 BP.
DE Human testis derived cDNA clone tes3_22124.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 2.9%; Score 49.2; DB 6; Length 1537;
Best Local Similarity 63.6%; Pred. No. 0.039;
RESULT 925
ID ADQ22988 standard; DNA; 1576 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.2; DB 12; Length 1576;
Best Local Similarity 57.0%; Pred. No. 0.039;
RESULT 926
ID ADQ23425 standard; DNA; 2408 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6245.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.2; DB 12; Length 2408;
Best Local Similarity 61.9%; Pred. No. 0.048;
RESULT 927
ID ABZ10224 standard; DNA; 2501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #364.
PN WO200272722-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 8; Length 2501;
Best Local Similarity 58.0%; Pred. No. 0.049;
RESULT 928
ID ADQ08601 standard; DNA; 3030 BP.
DE Ciona intestinalis nervous system associated gene SeqID3.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 2.9%; Score 49.2; DB 12; Length 3030;
Best Local Similarity 60.4%; Pred. No. 0.054;
RESULT 929
ID AAX33181 standard; DNA; 6644 BP.
DE Base sequence of the plasmid prx-ires-bar.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 6644;
Best Local Similarity 60.4%; Pred. No. 0.081;
RESULT 930
ID ABK40051 standard; DNA; 7058 BP.
DE Human chemically pretreated gene sequence #67 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 6; Length 7058;
Best Local Similarity 63.6%; Pred. No. 0.083;
RESULT 931
ID AAX33182 standard; DNA; 7372 BP.
DE Base sequence of the plasmid prx-Bcl-xl-bsr.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 7372;
Best Local Similarity 60.4%; Pred. No. 0.085;
RESULT 932
ID AAX33180 standard; DNA; 7797 BP.
DE Cowpox virus bsr full length gene sequence.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 7797;

Best Local Similarity 60.4%; Pred. No. 0.088;
RESULT 933
ID AAX33184 standard; DNA; 7996 BP.
DE Base sequence of the plasmid pRx-Bcl 2-i-hCD 25.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 7996;
Best Local Similarity 60.4%; Pred. No. 0.089;
RESULT 934
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 6; Length 11394;
Best Local Similarity 57.0%; Pred. No. 0.11;
RESULT 935
ID AB210104 standard; DNA; 35962 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #244.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 8; Length 35962;
Best Local Similarity 58.0%; Pred. No. 0.19;
RESULT 936
ID AAS07790 standard; DNA; 256 BP.
DE Cervical cancer pre-malignant condition DNA marker #89.
PN WO200142792-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 4; Length 256;
Best Local Similarity 59.0%; Pred. No. 0.018;
RESULT 937
ID ACN55002 standard; cDNA; 342 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 342;
Best Local Similarity 57.5%; Pred. No. 0.02;
RESULT 938
ID ABV58528 standard; cDNA; 347 BP.
DE Human prostate expression marker cDNA 58519.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 347;
Best Local Similarity 57.5%; Pred. No. 0.02;
RESULT 939
ID AAI84446 standard; cDNA; 348 BP.
DE Human polynucleotide SEQ ID NO 4506.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49; DB 4; Length 348;
Best Local Similarity 59.9%; Pred. No. 0.021;
RESULT 940
ID AAI85202 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 5262.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49; DB 4; Length 390;
Best Local Similarity 58.6%; Pred. No. 0.022;
RESULT 941
ID ACN53426 standard; cDNA; 403 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 403;
Best Local Similarity 57.5%; Pred. No. 0.022;
RESULT 942
ID ACH23125 standard; cDNA; 426 BP.
DE Human adult ovary cDNA #1505.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.9%; Score 49; DB 9; Length 426;
Best Local Similarity 58.6%; Pred. No. 0.023;
RESULT 943
ID ABV57380 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 57371.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 429;
Best Local Similarity 59.9%; Pred. No. 0.023;
RESULT 944
ID ABV56638 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 56629.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 469;
Best Local Similarity 58.6%; Pred. No. 0.024;
RESULT 945
ID ACN51887 standard; cDNA; 469 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 469;
Best Local Similarity 57.5%; Pred. No. 0.024;
RESULT 946
ID ACN58415 standard; cDNA; 469 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-009-Q6-K6-H8, SEQ:13196.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 469;
Best Local Similarity 57.5%; Pred. No. 0.024;
RESULT 947
ID ABV57020 standard; cDNA; 472 BP.
DE Human prostate expression marker cDNA 57011.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 472;
Best Local Similarity 55.6%; Pred. No. 0.024;
RESULT 948
ID ABV54546 standard; cDNA; 541 BP.
DE Human prostate expression marker cDNA 54537.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 541;
Best Local Similarity 58.6%; Pred. No. 0.026;
RESULT 949

ID ACN53890 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FENG P C C.
PA (FENG/) FENG P C C.
PA (FENG/) FENG P C C.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 547;
Best Local Similarity 56.2%; Pred. No. 0.026;
RESULT 950
ID ABQ52063 standard; DNA; 553 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38654.
PN WO2002186332-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 553;
Best Local Similarity 62.3%; Pred. No. 0.026;
RESULT 951
ID ABQ52062 standard; DNA; 553 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38653.
PN WO2002186332-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 553;
Best Local Similarity 62.3%; Pred. No. 0.026;
RESULT 952
ID ADRG3596 standard; cDNA; 1041 BP.
DE Cotton cDNA sequence, SEQ ID 4377.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAO/) CAO Y.
Query Match 2.9%; Score 49; DB 13; Length 1041;
Best Local Similarity 58.6%; Pred. No. 0.036;
RESULT 953
ID ADQ24168 standard; DNA; 1698 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6988.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 1698;
Best Local Similarity 61.2%; Pred. No. 0.046;
RESULT 954
ID ADM47920 standard; DNA; 1882 BP.
DE Polynucleotide sequence #338 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCEITI L B.
Query Match 2.9%; Score 49; DB 12; Length 1882;
Best Local Similarity 59.9%; Pred. No. 0.048;
RESULT 955
ID AAA23441 standard; cDNA; 1954 BP.
DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 2.9%; Score 49; DB 3; Length 1954;
Best Local Similarity 59.9%; Pred. No. 0.049;
RESULT 956
ID ACN88781 standard; DNA; 2024 BP.
DE Breast cancer related marker, seq id 9931.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 49; DB 11; Length 2024;
Best Local Similarity 58.6%; Pred. No. 0.05;
RESULT 957
ID AA243781 standard; cDNA; 2685 BP.
DE Human fetal brain cDNA clone vb6_1.
PN WO200200928-A2.

PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 2.9%; Score 49; DB 3; Length 2685;
Best Local Similarity 59.9%; Pred. No. 0.058;
RESULT 958
ID ADQ24699 standard; DNA; 2936 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7519.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 2936;
Best Local Similarity 57.5%; Pred. No. 0.06;
RESULT 959
ID ADQ24532 standard; DNA; 2936 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7352.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 2936;
Best Local Similarity 57.5%; Pred. No. 0.06;
RESULT 960
ID ABQ54675 standard; cDNA; 3044 BP.
DE Human ovarian antigen HVCAR76 cDNA, SEQ ID NO:555.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49; DB 6; Length 3044;
Best Local Similarity 59.0%; Pred. No. 0.062;
RESULT 961
ID ABL33662 standard; DNA; 5845 BP.
DE Human immune system associated gene SEQ ID NO: 1635.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 5845;
Best Local Similarity 59.9%; Pred. No. 0.086;
RESULT 962
ID ADL45710 standard; DNA; 5930 BP.
DE Human ovarian cancer DNA marker #19600.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 5930;
Best Local Similarity 58.6%; Pred. No. 0.086;
RESULT 963
ID ABL34058 standard; DNA; 6012 BP.
DE Human immune system associated gene SEQ ID NO: 2031.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6012;
Best Local Similarity 59.9%; Pred. No. 0.087;
RESULT 964
ID ABL32411 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 384.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6161;
Best Local Similarity 64.6%; Pred. No. 0.088;
RESULT 965
ID ABL32806 standard; DNA; 6211 BP.
DE Human immune system associated gene SEQ ID NO: 779.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6211;
Best Local Similarity 59.9%; Pred. No. 0.088;
RESULT 966
ID ABL33050 standard; DNA; 6522 BP.
DE Human immune system associated gene SEQ ID NO: 1023.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6522;
Best Local Similarity 59.9%; Pred. No. 0.09;
RESULT 967
ID ABL32118 standard; DNA; 11416 BP.
DE Human immune system associated gene SEQ ID NO: 91.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 968
ID ABL70135 standard; DNA; 11416 BP.
DE Chemically treated cell signalling DNA sequence#13.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 969
ID AAS61063 standard; DNA; 11416 BP.
DE Human gene regulation-associated gene oligonucleotide #18.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 970
ID ABL34072 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2045.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 40862;
Best Local Similarity 59.9%; Pred. No. 0.23;
RESULT 971
ID ADI72102 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #4844.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 299;
Best Local Similarity 56.0%; Pred. No. 0.021;
RESULT 972
ID ADI37251 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #1141.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 299;
Best Local Similarity 56.0%; Pred. No. 0.021;
RESULT 973
ID ABV49426 standard; cDNA; 308 BP.
DE Human prostate expression marker cDNA 49417.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 308;
Best Local Similarity 57.1%; Pred. No. 0.022;
RESULT 974
ID ABV55289 standard; cDNA; 313 BP.
DE Human prostate expression marker cDNA 55280.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 313;
Best Local Similarity 63.8%; Pred. No. 0.022;
RESULT 975
ID ABV04395 standard; cDNA; 326 BP.
DE Human prostate expression marker cDNA 4386.
PN WO200160860-A2.
PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 326;
Best Local Similarity 61.2%; Pred. No. 0.022;
RESULT 976
ID AAI89034 standard; cDNA; 413 BP.
DE Human polynucleotide SEQ ID NO 9094.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.8; DB 4; Length 413;
Best Local Similarity 57.1%; Pred. No. 0.025;
RESULT 977
ID AAI91775 standard; cDNA; 421 BP.
DE Human polynucleotide SEQ ID NO 11835.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.8; DB 4; Length 421;
Best Local Similarity 60.6%; Pred. No. 0.026;
RESULT 978
ID ACN56150 standard; cDNA; 436 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D9, SEQ:10931.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.8; DB 13; Length 436;
Best Local Similarity 53.7%; Pred. No. 0.026;
RESULT 979
ID ABV19606 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 19597.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 446;
Best Local Similarity 59.2%; Pred. No. 0.026;
RESULT 980
ID AAI80552 standard; cDNA; 448 BP.
DE Human polynucleotide SEQ ID NO 612.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.8; DB 4; Length 448;
Best Local Similarity 59.3%; Pred. No. 0.026;
RESULT 981
ID ACN45690 standard; cDNA; 486 BP.
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-F5, SEQ:471.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.8; DB 13; Length 486;
Best Local Similarity 62.1%; Pred. No. 0.027;
RESULT 982
ID ABV23693 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 23684.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 489;
Best Local Similarity 59.3%; Pred. No. 0.028;
RESULT 983
ID ABV29562 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 29553.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 489;
Best Local Similarity 59.3%; Pred. No. 0.028;

RESULT 984
ID ABV58114 standard; cDNA; 510 BP.
DE Human prostate expression marker cDNA 58105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 510;
Best Local Similarity 59.3%; Pred. No. 0.028;
RESULT 985
ID AAC74364 standard; cDNA; 639 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200058340-A2.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 3; Length 639;
Best Local Similarity 63.8%; Pred. No. 0.032;
RESULT 986
ID AAD05366 standard; cDNA; 655 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLQ64, SEQ ID NO:77.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 4; Length 655;
Best Local Similarity 62.1%; Pred. No. 0.032;
RESULT 987
ID AAH34055 standard; cDNA; 673 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1137.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 4; Length 673;
Best Local Similarity 59.3%; Pred. No. 0.032;
RESULT 988
ID ABZ76269 standard; cDNA; 836 BP.
DE Human GENSET cDNA clone name NBART.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 2.9%; Score 48.8; DB 8; Length 836;
Best Local Similarity 59.3%; Pred. No. 0.036;
RESULT 989
ID ADQ22074 standard; DNA; 980 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.8; DB 12; Length 980;
Best Local Similarity 57.1%; Pred. No. 0.039;
RESULT 990
ID AAV70895 standard; cDNA; 1813 BP.
DE cDNA encoding an allelic variant of human Zcytor5.
PN WO9849307-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 2.9%; Score 48.8; DB 2; Length 1813;
Best Local Similarity 56.1%; Pred. No. 0.053;
RESULT 991
ID ABL33879 standard; DNA; 5378 BP.
DE Human immune system associated gene SEQ ID NO: 1852.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.8; DB 6; Length 5378;
Best Local Similarity 57.1%; Pred. No. 0.093;
RESULT 992
ID ABQ67094 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.8; DB 6; Length 83391;
Best Local Similarity 58.1%; Pred. No. 0.37;
RESULT 993

ID ADI72391 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #5133.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 291;
Best Local Similarity 52.2%; Pred. No. 0.024;
RESULT 994
ID ADL37534 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #11424.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 291;
Best Local Similarity 52.2%; Pred. No. 0.024;
RESULT 995
ID ABV49069 standard; cDNA; 320 BP.
DE Human prostate expression marker cDNA 49060.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 320;
Best Local Similarity 56.5%; Pred. No. 0.025;
RESULT 996
ID AAI86367 standard; cDNA; 379 BP.
DE Human polynucleotide SEQ ID NO 6427.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.6; DB 4; Length 379;
Best Local Similarity 54.9%; Pred. No. 0.027;
RESULT 997
ID ACH19935 standard; cDNA; 423 BP.
DE Human adult lung cDNA #938.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.9%; Score 48.6; DB 9; Length 423;
Best Local Similarity 52.5%; Pred. No. 0.029;
RESULT 998
ID ABV38062 standard; cDNA; 425 BP.
DE Human prostate expression marker cDNA 38053.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 425;
Best Local Similarity 57.6%; Pred. No. 0.029;
RESULT 999
ID ABV47755 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 47746.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 471;
Best Local Similarity 58.7%; Pred. No. 0.031;
RESULT 1000
ID ACN54837 standard; cDNA; 489 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D11, SEQ:9618.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.6; DB 13; Length 489;
Best Local Similarity 57.6%; Pred. No. 0.031;
RESULT 1001
ID ABVI7965 standard; cDNA; 816 BP.
DE Human prostate expression marker cDNA 17956.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 816;
Best Local Similarity 58.7%; Pred. No. 0.04;
RESULT 1002
ID ABA93702 standard; cDNA; 835 BP.
DE Human signal transduction cDNA clone amy2_10h17.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GSHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 2.9%; Score 48.6; DB 6; Length 835;
Best Local Similarity 61.4%; Pred. No. 0.041;
RESULT 1003
ID AAC98083 standard; cDNA; 1377 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:93.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.6; DB 3; Length 1377;
Best Local Similarity 58.3%; Pred. No. 0.053;
RESULT 1004
ID ABX92004 standard; cDNA; 1808 BP.
DE Lung specific nucleic acid (LSNA) #46.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.9%; Score 48.6; DB 6; Length 1808;
Best Local Similarity 58.7%; Pred. No. 0.06;
RESULT 1005
ID ABS57347 standard; cDNA; 1851 BP.
DE cDNA encoding human cancer cell growth suppressing protein PP6068.
PN CN1351080-A.
PD 29-MAY-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.9%; Score 48.6; DB 6; Length 1851;
Best Local Similarity 58.7%; Pred. No. 0.061;
RESULT 1006
ID AAD06011 standard; DNA; 2034 BP.
DE Human neuronal apoptosis regulated candidate (NARC) 10C DNA.
PN WO200131007-A2.
PD 03-MAY-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 4; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1007
ID ABS56722 standard; cDNA; 2034 BP.
DE Human NARC10 cDNA.
PN WO200281516-A2.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 8; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1008
ID ADJ57918 standard; cDNA; 2034 BP.
DE Human NARC 10C cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 12; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1009
ID ADQ23617 standard; DNA; 2050 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.6; DB 12; Length 2050;
Best Local Similarity 60.0%; Pred. No. 0.064;
RESULT 1010
ID ABL32778 standard; DNA; 5532 BP.
DE Human immune system associated gene SEQ ID NO: 751.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 6; Length 5532;
Best Local Similarity 63.0%; Pred. No. 0.11;
RESULT 1011
ID ABL32911 standard; DNA; 8946 BP.
DE Human immune system associated gene SEQ ID NO: 884.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 6; Length 8946;
Best Local Similarity 57.6%; Pred. No. 0.14;
RESULT 1012
ID AAS46704 standard; DNA; 14615 BP.
DE Tumor suppressor gene derived chemically modified sequence #427.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 4; Length 14615;
Best Local Similarity 57.6%; Pred. No. 0.17;
RESULT 1013
ID ABX47137 standard; cDNA; 341 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12302.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48.4; DB 8; Length 341;
Best Local Similarity 62.3%; Pred. No. 0.029;
RESULT 1014
ID AAI87525 standard; cDNA; 367 BP.
DE Human polynucleotide SEQ ID NO 7585.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 367;
Best Local Similarity 64.0%; Pred. No. 0.03;
RESULT 1015
ID AAI84785 standard; cDNA; 388 BP.
DE Human polynucleotide SEQ ID NO 4845.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 388;
Best Local Similarity 60.8%; Pred. No. 0.031;
RESULT 1016
ID ADL43635 standard; DNA; 388 BP.
DE Human ovarian cancer DNA marker #17525.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.4; DB 5; Length 388;
Best Local Similarity 57.1%; Pred. No. 0.031;
RESULT 1017
ID AAI89093 standard; cDNA; 415 BP.
DE Human polynucleotide SEQ ID NO 9153.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 415;
Best Local Similarity 65.4%; Pred. No. 0.032;
RESULT 1018
ID ABV56837 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 56828.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.4; DB 5; Length 432;
Best Local Similarity 64.0%; Pred. No. 0.033;
RESULT 1019
ID ABX47746 standard; cDNA; 442 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #12911.
PN US20021317139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 8; Length 442;
RESULT 1020
ID ABV56778 standard; cDNA; 451 BP.
DE Human prostate expression marker cDNA 56769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 5; Length 451;
RESULT 1021
ID ACN45855 standard; cDNA; 608 BP.
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 13; Length 608;
RESULT 1022
ID ACN53565 standard; cDNA; 619 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 13; Length 619;
RESULT 1023
ID AA59475 standard; DNA; 1117 BP.
DE Nucleotide sequence of a soybean type III glutathione-S-transferase.
PN WO200047728-A2.
PD 17-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 3; Length 1117;
RESULT 1024
ID ADQ22714 standard; DNA; 1661 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 1661;
RESULT 1025
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2136;
RESULT 1026
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 8; Length 2153;
RESULT 1027
ID ADH72101 standard; DNA; 2153 BP.

DE Human gene of the invention NOV43a SEQ ID NO:997.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2153;
RESULT 1028
ID ADO08270 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOGF L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2153;
RESULT 1029
ID ADQ25384 standard; DNA; 2176 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8204.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2176;
RESULT 1030
ID ADQ22511 standard; DNA; 2179 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5331.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2179;
RESULT 1031
ID ADQ22185 standard; DNA; 2857 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5005.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 12; Length 2857;
RESULT 1032
ID AAS68120 standard; cDNA; 3910 BP.
DE DNA encoding novel human diagnostic protein #3924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.9%; Score 48.4; DB 5; Length 3910;

Best Local Similarity 49.4%; Pred. No. 0.1;
RESULT 1033
ID ADQ23023 standard; DNA; 4046 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 4046;
Best Local Similarity 58.2%; Pred. No. 0.1;
RESULT 1034
ID AAI72024 standard; cDNA; 4073 BP.
DE Human thrombospondin protein, BTL012, coding sequence.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Query Match 2.9%; Score 48.4; DB 6; Length 4073;
Best Local Similarity 49.4%; Pred. No. 0.1;
RESULT 1035
ID ADB54096 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 20.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1036
ID ADB54224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1037
ID ADS9522 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:538.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 13; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1038
ID ADS9248 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:264.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 13; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1039
ID ABL32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 5195;
Best Local Similarity 62.3%; Pred. No. 0.12;
RESULT 1040
ID ADL93996 standard; cDNA; 5877 BP.
DE Human G-coupled protein receptor-related gene #44.
PN US200406205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON J.
PA (CASW/) CASMAN S J.

PA (BOLD/) BOLDOS F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 2.9%; Score 48.4; DB 12; Length 5877;
Best Local Similarity 49.4%; Pred. No. 0.12;
RESULT 1041
ID ADE16057 standard; DNA; 5935 BP.
DE G-coupled protein receptor related polypeptide DNA, SEQ ID NO 87.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 10; Length 5935;
Best Local Similarity 49.4%; Pred. No. 0.12;
RESULT 1042
ID ABL33679 standard; DNA; 6070 BP.
DE Human immune system associated gene SEQ ID NO: 1652.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1043
ID ABL34579 standard; DNA; 6070 BP.
DE Human metastasis associated gene SEQ ID NO: 132.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1044
ID ABL70372 standard; DNA; 6070 BP.
DE Chemically treated cell signalling DNA sequence complementary to#131.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1045
ID ABQ67130 standard; DNA; 6070 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1046
ID ADS99840 standard; DNA; 6070 BP.
DE Complement of bisulphite treated metastasis-associated human gene #66.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.9%; Score 48.4; DB 7; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1047
ID ABX56304 standard; DNA; 6343 BP.
DE Human NOV2sc CG56914-03 DNA SEQ ID 87.
PN WO200281625-A2.
PD 17-OCT-2002.

PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 8; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.13;
RESULT 1048
ID ADH72107 standard; DNA; 6343 BP.
DE Human gene of the invention NOV43d SEQ ID NO:1003.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 12; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.13;
RESULT 1049
ID ABL33356 standard; DNA; 6577 BP.
DE Human immune system associated gene SEQ ID NO: 1329.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1050
ID ABL70561 standard; DNA; 6577 BP.
DE Chemically treated cell signalling DNA sequence#226.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1051
ID AAS61221 standard; DNA; 6577 BP.
DE Human gene regulation-associated gene oligonucleotide #176.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1052
ID ABK34027 standard; DNA; 6944 BP.
DE Human DNA for staging of Astrocytomas, complement, #57.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1053
ID ADA20447 standard; DNA; 6944 BP.
DE Prostate tumour related genomic DNA complement sample #56.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 8; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1054
ID ADA84254 standard; DNA; 6944 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 8; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1055
ID ADQ22776 standard; DNA; 7281 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5596.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 7281;
Best Local Similarity 57.1%; Pred. No. 0.14;
RESULT 1056
ID ADS89706 standard; DNA; 7467 BP.
DE Oligonucleotide of the invention SEQ ID NO:722.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 48.4; DB 13; Length 7467;
Best Local Similarity 60.8%; Pred. No. 0.14;
RESULT 1057
ID ADK60477 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1058
ID ADK60778 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1059
ID ADP73100 standard; DNA; 8546 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1060
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.9%; Score 48.4; DB 13; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1061
ID ABL33068 standard; DNA; 9117 BP.
DE Human immune system associated gene SEQ ID NO: 1041.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 9117;
Best Local Similarity 62.3%; Pred. No. 0.15;
RESULT 1062
ID ADF50896 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 4).
PN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 11097;
Best Local Similarity 62.3%; Pred. No. 0.17;
RESULT 1063
ID ADF50894 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 2).
PN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 11097;
Best Local Similarity 62.3%; Pred. No. 0.17;
RESULT 1064
ID ADO08272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.

PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALI/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 2.9%; Score 48.4; DB 12; Length 15659;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1065
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 8; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1066
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 12; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1067
ID ABO86156 standard; DNA; 16908 BP.
DE Novel human gene. SEQ ID 27.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.9%; Score 48.4; DB 6; Length 16908;
Best Local Similarity 49.4%; Pred. No. 0.21;
RESULT 1068
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1069
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1070
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 385;
PA (ALMS/) AL M S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1071
ID ADQ22570 standard; DNA; 18248 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 18248;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1072
ID ABL37453 standard; cDNA; 153 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:1042.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.9%; Score 48.2; DB 6; Length 153;
Best Local Similarity 59.3%; Pred. No. 0.022;
RESULT 1073
ID AAH70080 standard; cDNA; 268 BP.
DE Human cervical cancer marker nucleic acid 1354.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 4; Length 268;
Best Local Similarity 51.9%; Pred. No. 0.029;
RESULT 1074
ID ACN45531 standard; cDNA; 272 BP.
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-K6-E5, SEQ:312.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 272;
Best Local Similarity 63.2%; Pred. No. 0.03;
RESULT 1075
ID ABV58763 standard; cDNA; 317 BP.
DE Human prostate expression marker cDNA 58754.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 317;
Best Local Similarity 57.7%; Pred. No. 0.032;
RESULT 1076
ID ACN50558 standard; cDNA; 325 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-K6-E8, SEQ:5339.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 325;
Best Local Similarity 62.2%; Pred. No. 0.032;
RESULT 1077
ID AAL23694 standard; cDNA; 359 BP.
DE Human breast cancer expressed polynucleotide 16151.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 4; Length 359;
Best Local Similarity 61.6%; Pred. No. 0.034;
RESULT 1078
ID ADL37765 standard; DNA; 385 BP.
DE Human ovarian cancer DNA marker #11655.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 385;

Best Local Similarity 53.5%; Pred. No. 0.035;
RESULT 1079
ID ADI72626 standard; DNA; 385 BP.
DE Human ovarian cancer DNA marker #5368.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 385;
Best Local Similarity 53.5%; Pred. No. 0.035;
RESULT 1080
ID AAI84791 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 4851.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 390;
Best Local Similarity 57.7%; Pred. No. 0.035;
RESULT 1081
ID AAI83999 standard; cDNA; 411 BP.
DE Human polynucleotide SEQ ID NO 4059.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 411;
Best Local Similarity 60.2%; Pred. No. 0.036;
RESULT 1082
ID AAI88617 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 8677.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 416;
Best Local Similarity 58.9%; Pred. No. 0.037;
RESULT 1083
ID AAI89032 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 9092.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 416;
Best Local Similarity 61.6%; Pred. No. 0.037;
RESULT 1084
ID ABV49374 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 49365.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 453;
Best Local Similarity 63.2%; Pred. No. 0.038;
RESULT 1085
ID ACN57722 standard; cDNA; 492 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-005-Q6-N6-B12, SEQ:12503.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 492;
Best Local Similarity 60.2%; Pred. No. 0.04;
RESULT 1086
ID ABV57520 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 57511.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 504;
Best Local Similarity 58.9%; Pred. No. 0.04;
RESULT 1087
ID ACN55029 standard; cDNA; 518 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-D8, SEQ:9810.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 518;
Best Local Similarity 55.3%; Pred. No. 0.041;
RESULT 1088
ID ACN60563 standard; cDNA; 585 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-B11, SEQ:15344.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 585;
Best Local Similarity 56.7%; Pred. No. 0.043;
RESULT 1089
ID ACN62771 standard; cDNA; 594 BP.
DE Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-K6-CS, SEQ:17552.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 594;
Best Local Similarity 61.6%; Pred. No. 0.044;
RESULT 1090
ID AAD34114 standard; cDNA; 921 BP.
DE Human secreted protein-encoding gene 9 cDNA clone HB8NQ42, SEQ ID NO:19.
PN WO200222654-A1.
PD 21-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.2; DB 6; Length 921;
Best Local Similarity 63.2%; Pred. No. 0.055;
RESULT 1091
ID AAD54409 standard; cDNA; 990 BP.
DE Lolium perenne defensin a (LpDEFA) cDNA.
PN WO200288359-A1.
PD 07-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 2.9%; Score 48.2; DB 8; Length 990;
Best Local Similarity 54.1%; Pred. No. 0.057;
RESULT 1092
ID AAL57070 standard; DNA; 1040 BP.
DE Human G-protein coupled receptor GAV18 DNA sequence.
PN WO2003042399-A2.
PD 22-MAY-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 2.9%; Score 48.2; DB 9; Length 1040;
Best Local Similarity 63.2%; Pred. No. 0.059;
RESULT 1093
ID ADG73631 standard; cDNA; 1259 BP.
DE Human cDNA of the invention SEQ ID NO:16.
PN CN1369506-A.
PD 18-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.9%; Score 48.2; DB 10; Length 1259;
Best Local Similarity 65.1%; Pred. No. 0.064;
RESULT 1094
ID ADF94940 standard; cDNA; 1311 BP.
DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.
PN WO2003031586-A2.
PD 17-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (BLON-) BLONDEL O.
PA (RUBE/) RUBEN S M.
Query Match 2.9%; Score 48.2; DB 10; Length 1311;
Best Local Similarity 62.2%; Pred. No. 0.065;
RESULT 1095
ID ABS53034 standard; DNA; 2038 BP.

DE Arabidopsis thaliana squalene epoxidase polynucleotide #4.
PN WO200261072-A2.
PD 08-AUG-2002.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 2.9%; Score 48.2; DB 6; Length 2038;
Best Local Similarity 58.9%; Pred. No. 0.082;
RESULT 1096
ID ADQ23275 standard; DNA; 3056 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6095.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.2; DB 12; Length 3056;
Best Local Similarity 63.2%; Pred. No. 0.1;
RESULT 1097
ID ABL33751 standard; DNA; 7037 BP.
DE Human immune system associated gene SEQ ID NO: 1724.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 7037;
Best Local Similarity 60.2%; Pred. No. 0.15;
RESULT 1098
ID ABL32448 standard; DNA; 7238 BP.
DE Human immune system associated gene SEQ ID NO: 421.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 7238;
Best Local Similarity 60.2%; Pred. No. 0.16;
RESULT 1099
ID ABL32332 standard; DNA; 8895 BP.
DE Human immune system associated gene SEQ ID NO: 305.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 8895;
Best Local Similarity 58.9%; Pred. No. 0.17;
RESULT 1100
ID ABL34492 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 45.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 11996;
Best Local Similarity 65.1%; Pred. No. 0.2;
RESULT 1101
ID ADS99753 standard; DNA; 11996 BP.
DE Bisulphite treated human gene associated with metastasis #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.9%; Score 48.2; DB 7; Length 11996;
Best Local Similarity 65.1%; Pred. No. 0.2;
RESULT 1102
ID ACN50958 standard; cDNA; 139 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-E3, SEQ:5739.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 139;
Best Local Similarity 64.3%; Pred. No. 0.024;
RESULT 1103
ID ABX46273 standard; cDNA; 239 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11438.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 2.9%; Score 48; DB 8; Length 239;
Query Match 59.6%; Pred. No. 0.031;
Best Local Similarity 59.6%; Pred. No. 0.031;
RESULT 1104
ID ABX42739 standard; cDNA; 241 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7904.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 2.9%; Score 48; DB 8; Length 241;
Query Match 59.6%; Pred. No. 0.031;
Best Local Similarity 59.6%; Pred. No. 0.031;
RESULT 1105
ID ADS72366 standard; cDNA; 269 BP.
DE Human kidney tumour specific cDNA, SEQ ID 963.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.9%; Score 48; DB 7; Length 269;
Best Local Similarity 56.2%; Pred. No. 0.033;
RESULT 1106
ID ABX43930 standard; cDNA; 283 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9095.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 2.9%; Score 48; DB 8; Length 283;
Query Match 64.3%; Pred. No. 0.034;
Best Local Similarity 64.3%; Pred. No. 0.034;
RESULT 1107
ID ABV56758 standard; cDNA; 323 BP.
DE Human prostate expression marker cDNA 56749.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 323;
Best Local Similarity 56.2%; Pred. No. 0.036;
RESULT 1108
ID ABX38490 standard; cDNA; 373 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3655.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 2.9%; Score 48; DB 8; Length 373;
Query Match 58.3%; Pred. No. 0.039;
Best Local Similarity 58.3%; Pred. No. 0.039;
RESULT 1109
ID AAI89019 standard; cDNA; 386 BP.
DE Human polynucleotide SEQ ID NO 9079.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 386;
Best Local Similarity 64.3%; Pred. No. 0.04;
RESULT 1110
ID AAI85430 standard; cDNA; 401 BP.
DE Human polynucleotide SEQ ID NO 5490.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 401;
Best Local Similarity 55.6%; Pred. No. 0.041;
RESULT 1111
ID AAI85304 standard; cDNA; 404 BP.
DE Human polynucleotide SEQ ID NO 5364.

PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 404;
Best Local Similarity 64.3%; Pred. No. 0.041;
RESULT 1112
ID AAI83194 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 3254.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 407;
Best Local Similarity 64.3%; Pred. No. 0.041;
RESULT 1113
ID AAI83744 standard; cDNA; 408 BP.
DE Human polynucleotide SEQ ID NO 3804.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 408;
Best Local Similarity 57.9%; Pred. No. 0.041;
RESULT 1114
ID ABV59282 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 59273.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 452;
Best Local Similarity 64.3%; Pred. No. 0.043;
RESULT 1115
ID AAI82085 standard; cDNA; 466 BP.
DE Human polynucleotide SEQ ID NO 2145.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 466;
Best Local Similarity 64.3%; Pred. No. 0.044;
RESULT 1116
ID AAI88612 standard; cDNA; 478 BP.
DE Human polynucleotide SEQ ID NO 8672.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 478;
Best Local Similarity 64.3%; Pred. No. 0.044;
RESULT 1117
ID ACN61416 standard; cDNA; 490 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 490;
Best Local Similarity 49.6%; Pred. No. 0.045;
RESULT 1118
ID ABV58419 standard; cDNA; 515 BP.
DE Human prostate expression marker cDNA 58410.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 515;
Best Local Similarity 56.2%; Pred. No. 0.046;
RESULT 1119
ID ABV57482 standard; cDNA; 533 BP.
DE Human prostate expression marker cDNA 57473.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 533;
Best Local Similarity 56.2%; Pred. No. 0.047;
RESULT 1120

ID ABV58372 standard; cDNA; 540 BP.
DE Human prostate expression marker cDNA 58363.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 540;
Best Local Similarity 56.2%; Pred. No. 0.047;
RESULT 1121
ID ABV58085 standard; cDNA; 585 BP.
DE Human prostate expression marker cDNA 58076.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 585;
Best Local Similarity 56.2%; Pred. No. 0.049;
RESULT 1122
ID ADF76609 standard; cDNA; 602 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 283.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 10; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1123
ID ADL83210 standard; cDNA; 602 BP.
DE Human PRO52174 cDNA, SEQ ID 412.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1124
ID ADL91506 standard; cDNA; 602 BP.
DE Human immune-related polypeptide PRO52174-encoding cDNA, SEQ ID NO:21.
PN WO2004024072-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1125
ID ADM41666 standard; cDNA; 602 BP.
DE PRO52174 cDNA, associated with B-cell activation.
PN WO2004024069-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1126
ID ABV43916 standard; cDNA; 606 BP.
DE Human prostate expression marker cDNA 43907.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 606;
Best Local Similarity 58.3%; Pred. No. 0.05;
RESULT 1127
ID ACN54555 standard; cDNA; 627 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-C2, SEQ:93356.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 627;
Best Local Similarity 64.3%; Pred. No. 0.051;
RESULT 1128
ID ADP04748 standard; cDNA; 1352 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 343.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 2.9%; Score 48; DB 12; Length 1352;

Best Local Similarity 59.6%; Pred. No. 0.075;
RESULT 1129
ID AAG32734 standard; DNA; 1483 BP.
DE Human DNA differentially expressed in patients with SLE SeqID58.
FN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.9%; Score 48; DB 10; Length 1483;
Best Local Similarity 59.6%; Pred. No. 0.079;
RESULT 1130
ID AAI72316 standard; cDNA; 1637 BP.
DE Human transporter protein cDNA.
FN WO200202635-A2.
PD 10-JAN-2002.
PA (APPL-) APPLERA CORP.
Query Match 2.9%; Score 48; DB 6; Length 1637;
Best Local Similarity 58.3%; Pred. No. 0.083;
RESULT 1131
ID AAZ90632 standard; DNA; 1690 BP.
DE Human adipose tissue protein #2 encoding DNA.
FN JP2000037190-A.
PD 08-FEB-2000.
PA (NTSB-) JAPAN TOBACCO INC.
Query Match 2.9%; Score 48; DB 3; Length 1690;
Best Local Similarity 64.3%; Pred. No. 0.084;
RESULT 1132
ID AAD32523 standard; DNA; 1726 BP.
DE Human B7-H10 gene.
FN WO200202587-A1.
PD 10-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48; DB 6; Length 1726;
Best Local Similarity 59.6%; Pred. No. 0.085;
RESULT 1133
ID AAX52252 standard; DNA; 1984 BP.
DE Protein PRO271 cDNA clone DNA39423-1182.
FN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 2; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1134
ID ADC78532 standard; cDNA; 1984 BP.
DE Human PRO271 cDNA.
FN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 3; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1135
ID ADL18008 standard; cDNA; 1984 BP.
DE Human secreted/transmembrane protein cDNA, #42.
FN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATH J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.9%; Score 48; DB 13; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1136
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
FN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 4; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1137
ID AAS45938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
FN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 4; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1138
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
FN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1139
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003036141-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1140
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1141
ID ACA05713 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1142
ID ACA66547 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
FN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1143
ID ACD07574 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1144
ID ACF20122 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1145
ID ACF19508 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1146
ID ACD21796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1147
ID ACF12961 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1148
ID ACD25064 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1149
ID ACF00113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1150
ID ACF2170 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1151
ID ACD04694 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1152
ID ACD18155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1153
ID ACD08162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1154
ID ABX71622 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1155
ID ACF88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1156
ID ACF70038 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1157
ID ACD12260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1158
ID ACF74175 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1159
ID ACD15803 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1160
ID ACD25371 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1161
ID ACD17848 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1162
ID ACF88135 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1163
ID ACD21489 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1164
ID ACD18556 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1165
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032130-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1166
ID ABX98166 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
FN US2003036156-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1167
ID ACD13917 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032117-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1168
ID ACD09697 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036128-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1169
ID ACC88442 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027266-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1170
ID ACD21182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1171
ID ABX75554 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO271.
FN US2003022298-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1172
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032102-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1173
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2003036117-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1174
ID ACA57696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
FN US2003036143-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1175
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032130-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1176
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1177
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036132-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1178
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1179
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003017542-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1180
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032137-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1181
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027269-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1182
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027268-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1183
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027274-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1184
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1185
ID ACA72477 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1186
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1187
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1188
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1189
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1190
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1191
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1192
ID ACC86105 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1193
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1194
ID ACD12585 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ACF19815 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1196
ID ABX76759 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1197
ID ABX96191 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1198
ID ACA73091 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1199
ID ACA05512 standard; cDNA; 1985 BP.
DE cDNA encoding human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1200
ID ACA68634 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1201
ID ACA74478 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1202
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1203
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1204
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1205
ID ACA68203 standard; cDNA; 1985 BP.

DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1206
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1207
ID ACC61145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1208
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1209
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1210
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1211
ID ACF12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1212
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1213
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1214
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1215
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.

PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1216
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1217
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1218
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1219
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1220
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1221
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1222
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1223
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1224
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1225
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1226
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US20030316153-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1227
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1228
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US20030316150-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1229
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1230
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US200302293-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1231
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1232
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1233
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1234
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US20030316139-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1235
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1236

ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1237
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1238
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US20030316152-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1239
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1240
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1241
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1242
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1243
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1244
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1245
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1246
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1247
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1248
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1249
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1250
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1251
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1252
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1253
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1254
ID ACD46632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1256
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1257
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1258
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1259
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1260
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1261
ID ACF48763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1262
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1263
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1264
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1265
ID ACF41110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1266
ID ACF15724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1267
ID ACF16031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1268
ID ACD31858 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1269
ID ACF18666 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1270
ID ACF09113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1271
ID ACF78234 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1272
ID ACP51833 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1273
ID ACF6320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1274
ID ACF24113 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1275
ID ACF63424 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1276
ID ACF50298 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1277
ID ACH07769 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1278
ID ACF13575 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1279
ID ACD41501 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1280
ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1281
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1282
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1283
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

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PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1284
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1285
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1286
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1287
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1288
ID ACD84554 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1289
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1290
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1291
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1292
ID ACF76699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1293
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1294
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1295
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1296
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1297
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1298
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1299
ID ACD22410 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1300
ID ACF15110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1301
ID ACC97205 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1302
ID ADA18273 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
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PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1303
ID ACD66964 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1304
ID ACC92235 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1305
ID ACF13882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1306
ID ACF14189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1307
ID ACF09420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1308
ID ACD45711 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1309
ID ACD47860 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1310
ID ACD67591 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1311
ID ACP25399 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1312
ID ACP29083 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1313
ID ACD84861 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1314
ID ACD83940 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1315
ID ACD87931 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1316
ID ACF30618 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1317
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1318
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1319
ID ACH12188 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1320
ID ACD40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

ID	ACF27855 standard; cDNA; 1985 BP.
DE	Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN	US2003068751-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1331	
ID	ACD89159 standard; cDNA; 1985 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #14.
PN	US2003068684-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1332	
ID	ACF63731 standard; cDNA; 1985 BP.
DE	Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN	US2003073179-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1333	
ID	ACF60371 standard; cDNA; 1985 BP.
DE	Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN	US2003087374-A1.
PD	08-MAY-2003.
PA	
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1334	
ID	ACH12495 standard; cDNA; 1985 BP.
DE	cDNA encoding human PRO polypeptide #14.
PN	US2003049773-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1335	
ID	ACH09918 standard; cDNA; 1985 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #14.
PN	US2003049777-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1336	
ID	ADC03773 standard; cDNA; 1985 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #14.
PN	US2003040055-A1.
PD	27-FEB-2003.
PA	
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1337	
ID	ADC10311 standard; cDNA; 1985 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #14.
PN	US2003036164-A1.
PD	20-FEB-2003.
PA	
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1338	
ID	ADC11953 standard; cDNA; 1985 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #14.
PN	US2003040074-A1.
PD	27-FEB-2003.
PA	
Query Match	2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity	56.2%; Pred. No. 0.091;
RESULT 1339	
ID	ACD83125 standard; cDNA; 1985 BP.
DE	Human PRO polynucleotide #38.
PN	US2003044793-A1.
PD	06-MAR-2003.
PA	(GETH) GENENTECH INC.

Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1340
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1341
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1342
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1343
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1344
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1345
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1346
ID ACF33793 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1347
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1348
ID ACD90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1349
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1350
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1351
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1352
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1353
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1354
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1355
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1356
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1357
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1358
ID ACF07885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1359
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1360
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1361
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068693-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1362
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1363
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1364
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1365
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1366
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 56.2%; Score 48; DB 9; Length 1985;
RESULT 1367
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1368
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1369
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1370
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1371
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1372
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1373
ID ACD30630 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1374
ID ACD31551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1375
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1376
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1377
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1378
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1379
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1380
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1381
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1382
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1383
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1384
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1385
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1386
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1387
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1388
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1389
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1390
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1391
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1392
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1393
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1394
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1395
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.9%; Score 48; DB 9; Length 1985;
Query Match Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1396
ID ACF78541 standard; cDNA; 1985 BP.

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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1397
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1398
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1399
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1400
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1401
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1402
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1403
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1404
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1405
ID ACD90080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1406
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1407
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1408
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1409
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1410
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1411
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1412
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1413
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1414
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
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RESULT 1415
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1416
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1417
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1418
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1419
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1420
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1421
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1422
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1423
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1424
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1425
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1426
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1427
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1428
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1429
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1430
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1431
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1432
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1433
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
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RESULT 1434
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US20030321136-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1435
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036129-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1436
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003040053-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1437
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040057-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1438
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1439
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044932-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1440
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027270-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1441
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1442
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032126-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1443
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1444
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1445
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1446
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049738-A1.
PD 13-MAR-2003.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1447
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1448
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1449
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1450
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1451
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1452
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1453
ID ACF25706 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003045700-A1.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1454
ID ACF39019 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1455
ID ACF28776 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1456
ID ACD90693 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1457
ID ACD86396 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1458
ID ACH05258 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PD US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1459
ID ACF65054 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1460
ID ADB20139 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003082767-A1.
PD 01-MAY-2003.
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RESULT 1461
ID ACF43527 standard; cDNA; 1985 BP.
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PD US2003104552-A1.
PD 05-JUN-2003.
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RESULT 1462
ID ACH08997 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003049774-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1463
ID ACH09304 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1464
ID ADA78391 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1465
ID ACF09727 standard; cDNA; 1985 BP.
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PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1466
ID ACF50912 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1467
ID ACF23806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1468
ID ACD8238 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1469
ID ACH09611 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1470
ID ACH10532 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1471
ID ACD11339 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003036126-A1.
PD 20-FEB-2003.

Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1491
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1492
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1493
ID ADA41969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1494
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1495
ID ACF10648 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1496
ID ACC93463 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1497
ID ACC96082 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1498
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1499
ID ADA17316 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1500
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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OM nucleic - nucleic search, using sw model

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(without alignments)
9026.128 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1032	61.5	1032	4	US-09-700-397-1
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4	343	20.4	1238	2	US-08-414-657D-3
5	343	20.4	1238	3	US-09-135-080-3
6	341.6	20.3	1195	4	US-09-976-594-403
7	340.6	20.3	924	2	US-08-414-657D-7
8	340.6	20.3	977	2	US-08-414-657D-1
9	340.6	20.3	977	3	US-09-135-080-1
10	340.6	20.3	1014	2	US-08-414-657D-5
11	340.6	20.3	1014	3	US-09-135-080-7
12	338.6	20.2	861	2	US-08-414-657D-9
13	338.6	20.2	912	2	US-08-414-657D-6
14	337.4	20.1	945	2	US-08-414-657D-8
15	333.8	19.9	861	2	US-08-414-657D-10
16	316.2	18.8	333	4	US-09-513-999C-23289
17	303.6	18.1	756	2	US-08-414-657D-17
18	301	17.9	309	4	US-09-621-976-3309
19	298.2	17.8	756	2	US-08-414-657D-18
20	281	16.7	1030	4	US-09-949-016-4587
21	193.6	11.5	352	4	US-09-513-999C-2775
22	174.4	10.4	182	4	US-09-621-976-967
23	146	8.7	200	4	US-09-513-999C-14430
24	105.6	6.3	913	4	US-09-774-528-410
25	100	6.0	219	2	US-08-414-657D-11
26	95.2	5.7	219	2	US-08-414-657D-12
27	87	5.2	438	4	US-09-621-976-8385

4.7	113538	4	US-09-949-016-16329	Sequence 16329, A
4.6	177	2	US-08-414-657D-13	Sequence 13, Appl
4.6	177	2	US-08-414-657D-14	Sequence 14, Appl
4.6	601	4	US-09-949-016-163724	Sequence 163724,
3.9	198	2	US-08-414-657D-15	Sequence 15, Appl
3.8	198	2	US-08-414-657D-16	Sequence 16, Appl
3.0	612	4	US-09-902-540-1357	Sequence 1357, Ap
3.0	240	1	US-08-628-417-6	Sequence 6, Appl
3.0	1039	4	US-09-902-540-1280	Sequence 1280, Ap
3.0	1048	4	US-09-489-847-38	Sequence 38, Appl
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2.9	147	4	US-09-621-976-10383	Sequence 10383, A
2.9	1117	3	US-09-247-373B-33	Sequence 33, Appl
2.9	2038	4	US-09-885-723-6	Sequence 6, Appl
2.9	1985	4	US-09-907-794A-212	Sequence 212, App
2.9	1985	4	US-09-905-125A-212	Sequence 212, App
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2.9	1985	4	US-09-906-700-212	Sequence 212, App
2.9	1985	4	US-09-903-603A-212	Sequence 212, App
2.9	1985	4	US-09-904-920A-212	Sequence 212, App
2.9	1985	4	US-09-909-064-212	Sequence 212, App
2.9	1985	4	US-09-905-381A-212	Sequence 212, App
2.9	1985	4	US-09-906-618-212	Sequence 212, App
2.8	441	4	US-09-601-537-10	Sequence 10, Appl
2.8	4121	4	US-09-601-537-9	Sequence 9, Appl
2.8	147	4	US-09-621-976-10254	Sequence 10254, A
2.8	2447	2	US-09-014-969-14	Sequence 14, Appl
2.8	2674	3	US-09-817-180-1	Sequence 1, Appl
2.8	2674	4	US-10-003-295-1	Sequence 1, Appl
2.8	1696	4	US-09-835-811-1	Sequence 1, Appl
2.8	1738	4	US-09-918-909A-27	Sequence 27, Appl
2.8	76164	4	US-09-949-016-13288	Sequence 12288, A
2.8	76165	4	US-09-949-016-14005	Sequence 14005, A
2.8	268	4	US-09-621-976-73	Sequence 73, Appl
2.8	2608	4	US-09-904-615-16	Sequence 16, Appl
2.8	569	4	US-09-461-325-44	Sequence 44, Appl
2.8	569	4	US-10-012-542-44	Sequence 44, Appl
2.8	630	1	US-08-115-123-44	Sequence 1, Appl
2.8	630	1	US-08-185-414E-1	Sequence 1, Appl
2.8	674	4	US-09-620-405B-465	Sequence 465, App
2.8	674	4	US-09-433-826B-465	Sequence 465, App
2.8	674	4	US-09-604-287A-465	Sequence 465, App
2.8	674	4	US-09-834-759-465	Sequence 465, App
2.8	674	4	US-09-590-751A-465	Sequence 465, App
2.8	674	4	US-09-551-621-465	Sequence 465, App
2.8	1411	3	US-08-964-127-5	Sequence 5, Appl
2.8	1411	3	US-09-496-692-5	Sequence 5, Appl
2.8	1411	3	US-10-000-273-5	Sequence 5, Appl
2.8	3275	3	US-09-370-838-151	Sequence 151, App
2.8	3275	4	US-09-854-133-151	Sequence 151, App
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2.8	193	4	US-09-621-976-10543	Sequence 10543, A
2.8	578	3	US-09-602-877A-95	Sequence 95, Appl
2.8	1020	4	US-09-328-475C-43	Sequence 43, Appl
2.8	1034	4	US-09-311-021-105	Sequence 105, App
2.8	2246	3	US-09-363-708-3	Sequence 3, Appl
2.8	2246	4	US-09-083-587-3	Sequence 3, Appl
2.8	2280	3	US-08-813-150-1	Sequence 1, Appl
2.8	2280	4	US-09-546-553-1	Sequence 1, Appl
2.8	3438	4	US-10-164-595-29	Sequence 29, Appl
2.8	614	4	US-09-902-540-1318	Sequence 1318, Ap
2.8	790	3	US-09-363-970-4	Sequence 4, Appl
2.8	1024	4	US-09-328-475C-50	Sequence 50, Appl
2.7	4064	4	US-09-873-737A-3	Sequence 3, Appl
2.7	249	4	US-09-621-976-1322	Sequence 1322, Ap
2.7	365	4	US-09-621-976-16042	Sequence 16042, A
2.7	601	4	US-09-949-016-47248	Sequence 47248, A
2.7	903	5	PCT-US95-06406A-21	Sequence 21, Appl
2.7	1447	3	US-09-443-041A-27	Sequence 27, Appl
2.7	2394	4	US-09-800-729-33	Sequence 33, Appl
2.7	5481	4	US-09-949-016-12049	Sequence 12049, A
2.7	5484	4	US-09-949-016-15589	Sequence 15589, A
2.7	12797	4	US-09-949-016-13123	Sequence 13123, A

101	45.8	2.7	96327	4	US-09-949-016-16541	Sequence 16541, A	c 174	44.6	2.7	396	4	US-09-970-966-33	Sequence 33, Appl
102	45.6	2.7	282	4	US-09-621-976-18648	Sequence 18648, A	175	44.6	2.7	601	4	US-09-949-016-204599	Sequence 204599,
c 103	45.4	2.7	260	2	US-08-520-678A-29	Sequence 29, Appl	176	44.6	2.7	601	4	US-09-949-016-204600	Sequence 204600,
c 104	45.4	2.7	260	3	US-08-897-126-29	Sequence 29, Appl	177	44.6	2.7	601	4	US-09-949-016-204601	Sequence 204601,
105	45.4	2.7	2198	3	US-09-248-335-35	Sequence 35, Appl	178	44.6	2.7	601	4	US-09-949-016-204602	Sequence 204602,
106	45.4	2.7	1046	4	US-10-003-392-3	Sequence 3, Appl	179	44.6	2.7	601	4	US-09-949-016-204603	Sequence 204603,
c 107	45.4	2.7	7218	1	US-08-233-463-14	Sequence 14, Appl	180	44.6	2.7	601	4	US-09-949-016-204604	Sequence 204604,
c 108	45.4	2.7	54246	4	US-09-949-016-16206	Sequence 16206, A	181	44.6	2.7	601	4	US-09-949-016-204605	Sequence 204605,
c 109	45.4	2.7	22452	4	US-09-949-016-12968	Sequence 12968, A	182	44.6	2.7	601	4	US-09-949-016-204606	Sequence 204606,
110	45.2	2.7	176	4	US-09-621-976-13903	Sequence 13903, A	183	44.6	2.7	708	4	US-09-949-016-204607	Sequence 204607,
111	45.2	2.7	359	4	US-09-621-976-16008	Sequence 16008, A	184	44.6	2.7	708	4	US-09-270-767-13081	Sequence 13081, A
112	45.2	2.7	359	4	US-09-621-976-16019	Sequence 16019, A	185	44.6	2.7	2184	3	US-08-955-916C-1	Sequence 1, Appl
113	45.2	2.7	362	4	US-09-621-976-16010	Sequence 16010, A	186	44.6	2.7	2184	3	US-08-697-786A-1	Sequence 1, Appl
c 114	45.2	2.7	396	4	US-09-640-173-53	Sequence 53, Appl	187	44.6	2.7	2527	4	US-09-244-805-29	Sequence 29, Appl
c 115	45.2	2.7	396	4	US-09-713-550-53	Sequence 53, Appl	188	44.6	2.7	2806	3	US-09-653-839-9	Sequence 9, Appl
c 116	45.2	2.7	396	4	US-09-825-294-53	Sequence 53, Appl	189	44.6	2.7	2806	3	US-10-202-619-9	Sequence 9, Appl
c 117	45.2	2.7	396	4	US-09-970-966-53	Sequence 53, Appl	190	44.6	2.7	87734	4	US-09-949-016-17521	Sequence 17521, A
c 118	45.2	2.7	537	4	US-09-720-201A-4	Sequence 4, Appl	191	44.6	2.7	118143	4	US-09-949-016-17196	Sequence 17196, A
c 119	45.2	2.7	644	4	US-09-720-201A-6	Sequence 6, Appl	192	44.4	2.6	127	4	US-09-621-976-13933	Sequence 13933, A
120	45.2	2.7	1091	4	US-09-328-965-1	Sequence 1, Appl	193	44.4	2.6	196	4	US-09-442-054A-42	Sequence 42, Appl
121	45.2	2.7	1273	4	US-09-270-767-14731	Sequence 14731, A	c 134	44.4	2.6	196	4	US-03-442-054A-42	Sequence 42, Appl
c 122	45.2	2.7	9589	1	US-07-925-695-1	Sequence 1, Appl	c 135	44.4	2.6	356	2	US-08-520-678A-22	Sequence 22, Appl
c 123	45.2	2.7	9589	1	US-07-925-695-2	Sequence 2, Appl	c 136	44.4	2.6	356	3	US-08-897-126-22	Sequence 22, Appl
c 124	45	2.7	371	4	US-09-621-976-16048	Sequence 16048, A	c 137	44.4	2.6	582	4	US-09-787-292-3	Sequence 3, Appl
125	45	2.7	1459	4	US-09-537-654-3	Sequence 3, Appl	138	44.4	2.6	601	4	US-09-949-016-38491	Sequence 38491, A
126	45	2.7	1798	3	US-09-797-906-1	Sequence 1, Appl	139	44.4	2.6	601	4	US-09-949-016-48520	Sequence 48520, A
127	45	2.7	2010	1	US-07-864-475A-4	Sequence 4, Appl	200	44.4	2.6	601	4	US-09-949-016-170716	Sequence 170716,
c 128	45	2.7	2010	1	US-08-468-249A-4	Sequence 4, Appl	201	44.4	2.6	601	4	US-09-949-016-170759	Sequence 170759,
c 129	44.8	2.7	224	2	US-08-731-272A-26	Sequence 26, Appl	202	44.4	2.6	601	4	US-09-949-016-170802	Sequence 170802,
130	44.8	2.7	357	4	US-09-621-976-16058	Sequence 16058, A	203	44.4	2.6	601	4	US-09-949-016-170843	Sequence 170843,
131	44.8	2.7	554	4	US-09-696-169A-14	Sequence 14, Appl	204	44.4	2.6	1051	3	US-09-245-041-10	Sequence 10, Appl
132	44.8	2.7	601	4	US-09-949-016-38490	Sequence 38490, A	205	44.4	2.6	1051	4	US-09-358-055B-10	Sequence 10, Appl
133	44.8	2.7	601	4	US-09-949-016-170715	Sequence 170715, A	206	44.4	2.6	1051	4	US-09-893-238-10	Sequence 10, Appl
134	44.8	2.7	601	4	US-09-949-016-170758	Sequence 170758, A	207	44.4	2.6	1134	3	US-09-248-335-29	Sequence 29, Appl
135	44.8	2.7	601	4	US-09-949-016-170801	Sequence 170801, A	208	44.4	2.6	1141	4	US-09-800-729-78	Sequence 78, Appl
136	44.8	2.7	601	4	US-09-949-016-170842	Sequence 170842, A	209	44.4	2.6	2327	4	US-10-066-130-20	Sequence 20, Appl
137	44.8	2.7	601	4	US-09-949-016-182153	Sequence 182153, A	210	44.4	2.6	2674	4	US-10-066-130-19	Sequence 19, Appl
138	44.8	2.7	601	4	US-09-949-016-182154	Sequence 182154, A	211	44.4	2.6	2771	4	US-10-066-130-18	Sequence 18, Appl
139	44.8	2.7	1000	3	US-09-018-584A-34	Sequence 34, Appl	212	44.4	2.6	4456	3	US-09-095-443-1	Sequence 1, Appl
140	44.8	2.7	1000	4	US-09-199-542B-108	Sequence 108, Appl	213	44.4	2.6	5860	4	US-10-066-130-17	Sequence 17, Appl
141	44.8	2.7	1000	4	US-09-784-423-34	Sequence 34, Appl	c 214	44.4	2.6	9646	3	US-08-811-566-1	Sequence 1, Appl
142	44.8	2.7	1212	3	US-09-182-145-34	Sequence 34, Appl	c 215	44.4	2.6	9646	3	US-09-034-756-1	Sequence 1, Appl
c 143	44.8	2.7	1212	3	US-09-182-145-35	Sequence 35, Appl	c 216	44.4	2.6	12980	3	US-08-811-566-5	Sequence 5, Appl
144	44.8	2.7	1641	1	US-08-300-903A-8	Sequence 8, Appl	c 217	44.4	2.6	12980	3	US-09-034-756-5	Sequence 5, Appl
145	44.8	2.7	1641	4	US-08-988-197-8	Sequence 8, Appl	218	44.2	2.6	195	4	US-09-621-976-18062	Sequence 18062, A
146	44.8	2.7	1641	4	US-10-385-072-8	Sequence 8, Appl	219	44.2	2.6	244	4	US-09-621-976-484	Sequence 484, App
147	44.8	2.7	1771	4	US-09-907-794A-158	Sequence 158, App	220	44.2	2.6	272	4	US-09-270-767-11902	Sequence 11902, A
148	44.8	2.7	1771	4	US-09-866-028-36	Sequence 36, Appl	221	44.2	2.6	318	4	US-09-621-976-10247	Sequence 10247, A
149	44.8	2.7	1771	4	US-09-905-135A-158	Sequence 158, App	222	44.2	2.6	1066	1	US-08-157-101A-4	Sequence 4, Appl
150	44.8	2.7	1771	4	US-09-902-775A-158	Sequence 158, App	223	44.2	2.6	1193	3	US-09-372-422A-23	Sequence 23, Appl
151	44.8	2.7	1771	4	US-09-906-700-158	Sequence 158, App	224	44.2	2.6	1801	4	US-09-709-103-3	Sequence 3, Appl
152	44.8	2.7	1771	4	US-09-944-457-36	Sequence 36, Appl	225	44.2	2.6	1801	4	US-09-439-410A-3	Sequence 3, Appl
153	44.8	2.7	1771	4	US-09-903-603A-158	Sequence 158, App	226	44.2	2.6	1925	4	US-09-148-545-128	Sequence 128, App
154	44.8	2.7	1771	4	US-09-904-920A-158	Sequence 158, App	227	44.2	2.6	2202	3	US-09-465-558-59	Sequence 59, Appl
155	44.8	2.7	1771	4	US-09-909-064-158	Sequence 158, App	c 228	44.2	2.6	670689	4	US-09-949-016-12505	Sequence 12505, A
156	44.8	2.7	1771	4	US-09-905-381A-158	Sequence 158, App	c 229	44.2	2.6	670690	4	US-09-949-016-14207	Sequence 14207, A
157	44.8	2.7	1771	4	US-09-906-618-158	Sequence 158, App	230	44	2.6	123	4	US-09-621-976-12330	Sequence 12330, A
158	44.8	2.7	6671	1	US-08-280-443-1	Sequence 1, Appl	231	44	2.6	186	4	US-09-513-939C-18897	Sequence 18897, A
159	44.8	2.7	6671	1	US-08-457-459-1	Sequence 1, Appl	232	44	2.6	240	4	US-09-621-976-1324	Sequence 1324, Ap
160	44.8	2.7	6671	1	US-08-555-678-1	Sequence 1, Appl	233	44	2.6	601	4	US-09-949-016-204598	Sequence 204598,
161	44.8	2.7	6671	5	PCT-US95-02275-1	Sequence 1, Appl	234	44	2.6	882	4	US-09-311-021-107	Sequence 107, App
162	44.8	2.7	36075	4	US-09-949-016-16571	Sequence 16571, A	235	44	2.6	1342	4	US-09-489-847-89	Sequence 89, Appl
163	44.8	2.7	36075	4	US-09-949-016-16572	Sequence 16572, A	236	44	2.6	1882	3	US-09-370-253-1	Sequence 1, Appl
164	44.8	2.7	36625	4	US-09-949-016-12788	Sequence 12788, A	237	44	2.6	1921	2	US-08-557-128-11	Sequence 11, Appl
165	44.8	2.7	37133	4	US-09-949-016-16569	Sequence 16569, A	238	44	2.6	2269	3	US-09-394-645-1	Sequence 1, Appl
166	44.8	2.7	37133	4	US-09-949-016-16570	Sequence 16570, A	239	44	2.6	2269	3	US-09-243-650B-1	Sequence 1, Appl
167	44.8	2.7	74881	4	US-09-949-016-15545	Sequence 15545, A	240	44	2.6	6409	4	US-09-967-908A-1	Sequence 1, Appl
168	44.8	2.7	74914	4	US-09-949-016-12286	Sequence 12286, A	241	44	2.6	6409	4	US-10-159-151-1	Sequence 1, Appl
c 169	44.8	2.7	133358	4	US-09-949-016-15964	Sequence 15964, A	242	43.8	2.6	1248	4	US-09-489-847-101	Sequence 101, App
c 170	44.8	2.7	133360	4	US-09-949-016-16964	Sequence 16964, A	243	43.8	2.6	1636	4	US-09-578-194-6	Sequence 6, Appl
c 171	44.6	2.7	396	4	US-09-640-173-33	Sequence 33, Appl	244	43.8	2.6	1781	4	US-09-818-512-1	Sequence 1, Appl
c 172	44.6	2.7	396	4	US-09-713-550-33	Sequence 33, Appl	245	43.8	2.6	1872	3	US-09-801-052-1	Sequence 1, Appl
c 173	44.6	2.7	396	4	US-09-825-294-33	Sequence 33, Appl	246	43.8	2.6	1872	4	US-10-020-121-1	Sequence 1, Appl

247	43.8	2.6	2082	2	US-08-785-310A-2	Sequence 2, Appli	320	42.6	2.5	558	4	US-09-043-861-3	Sequence 3, Appli
248	43.8	2.6	2262	4	US-09-311-021-171	Sequence 171, App	321	42.6	2.5	601	4	US-09-949-016-161729	Sequence 161729,
c 249	43.8	2.6	31842	4	US-09-949-016-15123	Sequence 15123, A	322	42.6	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap
250	43.6	2.6	121	3	US-09-297-535-20	Sequence 20, Appl	323	42.6	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli
251	43.6	2.6	246	4	US-09-621-976-13617	Sequence 13617, A	324	42.6	2.5	2276	4	US-09-205-258-183	Sequence 183, App
c 252	43.6	2.6	396	4	US-09-640-173-16	Sequence 16, Appl	325	42.6	2.5	3334	4	US-09-668-119-2	Sequence 2, Appli
c 253	43.6	2.6	396	4	US-09-713-550-16	Sequence 16, Appl	326	42.6	2.5	5096	4	US-09-949-016-15105	Sequence 15105, A
c 254	43.6	2.6	396	4	US-09-825-294-16	Sequence 16, Appl	c 327	42.6	2.5	17836	4	US-09-949-016-16167	Sequence 16167, A
c 255	43.6	2.6	396	4	US-09-970-966-16	Sequence 16, Appl	c 328	42.6	2.5	39690	4	US-09-949-016-15079	Sequence 15079, A
256	43.6	2.6	550	4	US-09-010-147B-5	Sequence 5, Appli	329	42.4	2.5	194	4	US-09-621-976-9596	Sequence 9596, Ap
257	43.6	2.6	1507	3	US-09-453-323-1	Sequence 1, Appli	330	42.4	2.5	331	4	US-09-621-976-16100	Sequence 16100, A
258	43.6	2.6	2407	3	US-09-370-807-7	Sequence 7, Appli	331	42.4	2.5	1445	3	US-09-814-951A-1	Sequence 1, Appli
259	43.6	2.6	2407	3	US-09-921-259-7	Sequence 7, Appli	332	42.4	2.5	1474	3	US-08-821-954-64	Sequence 64, Appl
260	43.6	2.6	2634	3	US-09-463-238-3	Sequence 3, Appli	333	42.4	2.5	4548	4	US-09-571-479C-5	Sequence 5, Appli
261	43.6	2.6	18026	4	US-09-949-016-13309	Sequence 13309, A	c 334	42.4	2.5	44848	4	US-09-435-733-42	Sequence 42, Appl
262	43.6	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A	c 335	42.4	2.5	44848	4	US-09-988-113-42	Sequence 42, Appl
263	43.4	2.6	552	4	US-09-461-325-111	Sequence 111, App	c 336	42.4	2.5	61664	4	US-09-949-016-13308	Sequence 13308, A
264	43.4	2.6	552	4	US-10-012-542-111	Sequence 111, App	c 337	42.4	2.5	113379	4	US-09-949-016-17561	Sequence 17561, A
265	43.4	2.6	552	4	US-10-115-123-111	Sequence 111, App	c 338	42.4	2.5	113379	4	US-09-949-016-17562	Sequence 17562, A
266	43.4	2.6	1296	4	US-09-461-325-29	Sequence 29, Appl	c 339	42.2	2.5	105	4	US-09-621-976-13820	Sequence 13820, A
267	43.4	2.6	1296	4	US-10-012-542-29	Sequence 29, Appl	c 340	42.2	2.5	298	4	US-09-621-976-3871	Sequence 3871, Ap
268	43.4	2.6	1296	4	US-10-115-123-29	Sequence 29, Appl	c 341	42.2	2.5	370	4	US-09-513-999C-497	Sequence 497, App
269	43.4	2.6	2625	4	US-09-270-767-10080	Sequence 10080, A	c 342	42.2	2.5	370	4	US-09-471-276-222	Sequence 222, App
270	43.4	2.6	2625	3	US-08-971-089-5	Sequence 5, Appli	c 343	42.2	2.5	601	4	US-09-949-016-188357	Sequence 168357,
271	43.4	2.6	3715	4	US-09-234-245-1	Sequence 1, Appli	c 344	42.2	2.5	601	4	US-09-949-016-188358	Sequence 168358,
272	43.4	2.6	49931	4	US-09-949-016-13727	Sequence 13727, A	345	42.2	2.5	601	4	US-09-949-016-193087	Sequence 193087,
273	43.4	2.6	49931	4	US-09-949-016-13728	Sequence 13728, A	346	42.2	2.5	601	4	US-09-949-016-193088	Sequence 193088,
274	43.4	2.6	49931	4	US-09-949-016-13729	Sequence 13729, A	347	42.2	2.5	601	4	US-09-949-016-193180	Sequence 193180,
275	43.4	2.6	225127	4	US-09-949-016-16480	Sequence 16480, A	348	42.2	2.5	601	4	US-09-949-016-193181	Sequence 193181,
c 276	43.2	2.6	196	4	US-09-644-460-40	Sequence 40, Appl	349	42.2	2.5	601	4	US-09-949-016-193273	Sequence 193273,
277	43.2	2.6	358	4	US-09-621-976-927	Sequence 927, App	350	42.2	2.5	601	4	US-09-949-016-193274	Sequence 193274,
278	43.2	2.6	601	4	US-09-949-016-48516	Sequence 48516, A	351	42.2	2.5	601	4	US-09-949-016-193366	Sequence 193366,
279	43.2	2.6	601	4	US-09-949-016-48521	Sequence 48521, A	352	42.2	2.5	601	4	US-09-949-016-193367	Sequence 193367,
c 280	43.2	2.6	601	4	US-09-949-016-186016	Sequence 186016,	353	42.2	2.5	746	3	US-09-013-810-1	Sequence 1, Appli
281	43.2	2.6	763	4	US-09-743-207-3	Sequence 3, Appli	354	42.2	2.5	990	4	US-09-800-729-79	Sequence 79, Appl
282	43.2	2.6	812	3	US-09-091-097-7	Sequence 7, Appli	355	42.2	2.5	1023	1	US-08-252-966B-16	Sequence 16, Appl
283	43.2	2.6	931	4	US-09-482-273-31	Sequence 31, Appl	356	42.2	2.5	1114	3	US-09-152-060-41	Sequence 41, Appl
284	43.2	2.6	2434	4	US-09-489-847-67	Sequence 67, Appl	357	42.2	2.5	1277	4	US-09-270-767-25838	Sequence 25838, A
c 285	43.2	2.6	4419	4	US-09-620-312D-187	Sequence 187, App	358	42.2	2.5	1454	3	US-09-372-422A-19	Sequence 19, Appl
286	43.2	2.6	16600	4	US-09-949-016-13332	Sequence 13332, A	359	42.2	2.5	3156	4	US-09-311-021-187	Sequence 187, App
287	43.2	2.6	16600	4	US-09-949-016-13333	Sequence 13333, A	360	42.2	2.5	3556	4	US-09-270-767-10439	Sequence 10439, A
c 288	43.2	2.6	58768	4	US-09-949-016-11175	Sequence 13175, A	361	42.2	2.5	86213	4	US-09-949-016-17240	Sequence 17240, A
289	43.2	2.6	50724	4	US-09-949-016-16601	Sequence 16601, A	362	42.2	2.5	86213	4	US-09-949-016-17241	Sequence 17241, A
c 290	43.2	2.6	96922	4	US-09-949-016-17061	Sequence 17061, A	363	42.2	2.5	86213	4	US-09-949-016-17242	Sequence 17242, A
291	43	2.6	144	1	US-08-702-344-26	Sequence 26, Appl	364	42.2	2.5	118868	4	US-09-949-016-17243	Sequence 17243, A
292	43	2.6	166	4	US-09-621-976-18390	Sequence 18390, A	365	42.2	2.5	225127	4	US-09-949-016-15746	Sequence 15746, A
293	43	2.6	347	4	US-09-621-976-16026	Sequence 16026, A	c 366	42.2	2.5	678533	4	US-09-949-016-16480	Sequence 16480, A
294	43	2.6	635	1	US-08-455-633A-35	Sequence 35, Appl	c 367	42.2	2.5	678533	4	US-09-949-016-14577	Sequence 14577, A
295	43	2.6	635	2	US-08-416-336-5	Sequence 5, Appli	c 368	42.2	2.5	678533	4	US-09-949-016-14578	Sequence 14578, A
296	43	2.6	635	2	US-08-456-460C-35	Sequence 35, Appl	369	42	2.5	563	4	US-09-621-976-19183	Sequence 19183, A
297	43	2.6	635	5	PCT-US94-05354-35	Sequence 35, Appl	370	42	2.5	639	4	US-09-482-273-49	Sequence 49, Appl
c 298	43	2.6	711	4	US-09-270-767-9609	Sequence 9609, Ap	371	42	2.5	1013	4	US-09-322-409-6	Sequence 6, Appli
c 299	43	2.6	711	4	US-09-270-767-24891	Sequence 24891, A	c 372	42	2.5	1013	4	US-09-322-409-6	Sequence 8, Appli
300	43	2.6	1545	4	US-09-559-023-1	Sequence 1, Appli	373	42	2.5	1013	4	US-09-451-527-6	Sequence 6, Appli
301	43	2.6	1733	3	US-09-073-569-1	Sequence 1, Appli	c 374	42	2.5	1013	4	US-09-451-527-8	Sequence 8, Appli
302	43	2.6	2091	3	US-09-813-818-1	Sequence 1, Appli	375	42	2.5	1582	3	US-08-545-196B-10	Sequence 10, Appl
303	43	2.6	2091	4	US-10-199-333-1	Sequence 1, Appli	376	42	2.5	1582	3	US-08-545-196B-12	Sequence 12, Appl
304	43	2.6	2186	3	US-09-360-545-66	Sequence 66, Appl	377	42	2.5	1736	3	US-09-182-816-22	Sequence 22, Appl
305	43	2.6	2233	1	US-08-496-631-1	Sequence 1, Appli	c 378	42	2.5	1736	3	US-09-182-816-24	Sequence 24, Appl
306	43	2.6	4086	4	US-09-702-705-1801	Sequence 1801, Ap	379	42	2.5	1736	3	US-09-471-528-22	Sequence 22, Appl
307	43	2.6	4086	4	US-09-736-457-1801	Sequence 1801, Ap	c 380	42	2.5	1736	3	US-09-471-528-24	Sequence 24, Appl
308	43	2.6	4086	4	US-09-671-325-1801	Sequence 1801, Ap	381	42	2.5	1736	3	US-09-634-530-22	Sequence 22, Appl
309	43	2.6	12521	4	US-09-949-016-15988	Sequence 15988, A	c 382	42	2.5	1736	3	US-09-634-530-24	Sequence 24, Appl
310	42.8	2.5	177	4	US-09-621-976-1047	Sequence 1047, Ap	383	42	2.5	1927	3	US-09-336-536-66	Sequence 66, Appl
311	42.8	2.5	194	4	US-09-621-976-801	Sequence 801, App	384	42	2.5	5749	4	US-09-949-016-15441	Sequence 15441, A
312	42.8	2.5	601	4	US-09-949-016-48517	Sequence 48517, A	385	42	2.5	5749	4	US-09-949-016-15442	Sequence 15442, A
313	42.8	2.5	601	4	US-09-949-016-48518	Sequence 48518, A	386	42	2.5	13184	4	US-09-949-016-16573	Sequence 16573, A
314	42.8	2.5	601	4	US-09-949-016-48519	Sequence 48519, A	387	42	2.5	101349	4	US-09-949-016-17433	Sequence 17433, A
315	42.8	2.5	1378	3	US-09-149-476-208	Sequence 208, App	388	41.8	2.5	130	4	US-09-621-976-12892	Sequence 12892, A
316	42.8	2.5	2271	4	US-09-205-258-243	Sequence 243, App	c 389	41.8	2.5	227	2	US-08-520-678A-28	Sequence 28, Appl
317	42.8	2.5	2223	3	US-09-149-476-24	Sequence 24, Appl	c 390	41.8	2.5	227	3	US-08-897-126-28	Sequence 28, Appl
c 318	42.8	2.5	209210	4	US-09-949-016-15094	Sequence 15094, A	391	41.8	2.5	250	4	US-09-621-976-18893	Sequence 18893, A
319	42.6	2.5	323	4	US-09-621-976-10374	Sequence 10374, A	392	41.8	2.5	601	4	US-09-949-016-184918	Sequence 184918,

333	41.8	2.5	601	4	US-09-949-016-185073	Sequence 185073,	466	41.4	2.5	3410	4	US-09-688-489-110	Sequence 110, App
334	41.8	2.5	601	4	US-09-949-016-201490	Sequence 201490,	467	41.4	2.5	3410	4	US-09-679-426-110	Sequence 110, App
335	41.8	2.5	1008	4	US-09-780-641-1	Sequence 1, Appli	468	41.4	2.5	3410	4	US-09-759-143-110	Sequence 110, App
336	41.8	2.5	1192	4	US-09-439-554-23	Sequence 23, Appl	469	41.4	2.5	3410	4	US-09-651-236-110	Sequence 110, App
337	41.8	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	C 470	41.4	2.5	129778	4	US-09-949-016-12191	Sequence 12191, A
338	41.8	2.5	1461	3	US-08-722-126A-4	Sequence 4, Appli	C 471	41.4	2.5	129778	4	US-09-949-016-17075	Sequence 17075, A
339	41.8	2.5	1461	5	PCT-US95-04258-4	Sequence 4, Appli	472	41.4	2.5	132438	4	US-09-949-016-14349	Sequence 14349, A
400	41.8	2.5	1558	1	US-08-467-607-2	Sequence 2, Appli	473	41.4	2.5	132438	4	US-09-949-016-14350	Sequence 14350, A
401	41.8	2.5	1558	2	US-08-469-362-2	Sequence 2, Appli	474	41.4	2.5	131089	4	US-09-949-016-14348	Sequence 14348, A
402	41.8	2.5	1558	2	US-08-850-392-2	Sequence 2, Appli	C 475	41.4	2.5	151295	4	US-09-949-016-14568	Sequence 14568, A
403	41.8	2.5	1662	4	US-09-668-097A-13	Sequence 13, Appl	C 476	41.4	2.5	151295	4	US-09-949-016-14569	Sequence 14569, A
C 404	41.8	2.5	15666	4	US-09-949-016-15929	Sequence 15929, A	C 477	41.4	2.5	151295	4	US-09-949-016-14570	Sequence 14570, A
C 405	41.8	2.5	149543	4	US-09-949-016-15947	Sequence 15947, A	C 478	41.4	2.5	151295	4	US-09-949-016-14571	Sequence 14571, A
406	41.8	2.5	194937	4	US-09-949-016-17032	Sequence 17032, A	C 479	41.4	2.5	151295	4	US-09-949-016-14572	Sequence 14572, A
407	41.8	2.5	194937	4	US-09-949-016-17033	Sequence 17033, A	C 480	41.4	2.5	151605	4	US-09-949-016-11894	Sequence 11894, A
408	41.6	2.5	117	1	US-08-702-344-3	Sequence 3, Appli	481	41.4	2.5	237241	4	US-09-949-016-16101	Sequence 16101, A
409	41.6	2.5	164	4	US-09-621-976-16692	Sequence 16692, A	C 482	41.4	2.5	393753	4	US-09-949-016-14573	Sequence 14573, A
410	41.6	2.5	231	4	US-09-621-976-16317	Sequence 16317, A	C 483	41.4	2.5	393753	4	US-09-949-016-14574	Sequence 14574, A
411	41.6	2.5	242	4	US-09-621-976-16320	Sequence 16320, A	484	41.4	2.5	524032	4	US-09-949-016-16928	Sequence 16928, A
C 412	41.6	2.5	242	4	US-09-621-976-16324	Sequence 16324, A	485	41.4	2.5	524032	4	US-09-949-016-16929	Sequence 16929, A
C 413	41.6	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	486	41.4	2.5	524032	4	US-09-949-016-16930	Sequence 16930, A
C 414	41.6	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	487	41.4	2.5	524032	4	US-09-949-016-16931	Sequence 16931, A
C 415	41.6	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl	488	41.4	2.5	529885	4	US-09-949-016-14340	Sequence 14340, A
C 416	41.6	2.5	270	3	US-08-897-126-30	Sequence 30, Appl	489	41.4	2.5	529885	4	US-09-949-016-14341	Sequence 14341, A
C 417	41.6	2.5	601	4	US-09-949-016-37085	Sequence 37086, A	490	41.4	2.5	529885	4	US-09-949-016-14342	Sequence 14342, A
C 418	41.6	2.5	601	4	US-09-949-016-37087	Sequence 37087, A	491	41.4	2.5	529885	4	US-09-949-016-14343	Sequence 14343, A
C 419	41.6	2.5	601	4	US-09-949-016-161063	Sequence 161063, A	492	41.4	2.5	529885	4	US-09-949-016-14344	Sequence 14344, A
C 420	41.6	2.5	601	4	US-09-949-016-161064	Sequence 161064, A	493	41.4	2.5	529885	4	US-09-949-016-14345	Sequence 14345, A
421	41.6	2.5	664	4	US-09-904-635-66	Sequence 66, Appl	494	41.4	2.5	529885	4	US-09-949-016-14346	Sequence 14346, A
422	41.6	2.5	949	4	US-09-489-847-35	Sequence 35, Appl	495	41.4	2.5	529885	4	US-09-949-016-14347	Sequence 14347, A
423	41.6	2.5	1297	4	US-09-800-729-80	Sequence 80, Appl	C 496	41.4	2.5	818128	4	US-09-949-016-14546	Sequence 14546, A
424	41.6	2.5	1308	4	US-10-151-832-1	Sequence 1, Appli	C 497	41.4	2.5	818128	4	US-09-949-016-14547	Sequence 14547, A
425	41.6	2.5	1414	4	US-09-501-115-5	Sequence 5, Appli	C 498	41.4	2.5	818128	4	US-09-949-016-14548	Sequence 14548, A
426	41.6	2.5	1746	4	US-09-485-529-57	Sequence 57, Appl	C 499	41.4	2.5	818128	4	US-09-949-016-14549	Sequence 14549, A
427	41.6	2.5	1768	4	US-09-485-529-13	Sequence 13, Appl	C 500	41.4	2.5	818128	4	US-09-949-016-14550	Sequence 14550, A
428	41.6	2.5	1817	1	US-08-473-981A-5	Sequence 5, Appli	C 501	41.4	2.5	818128	4	US-09-949-016-14551	Sequence 14551, A
429	41.6	2.5	1817	2	US-08-474-087-5	Sequence 5, Appli	C 502	41.4	2.5	818128	4	US-09-949-016-14552	Sequence 14552, A
430	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	C 503	41.4	2.5	818128	4	US-09-949-016-14553	Sequence 14553, A
431	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	C 504	41.4	2.5	818128	4	US-09-949-016-14554	Sequence 14554, A
C 432	41.6	2.5	10877	4	US-09-674-311-1	Sequence 1, Appli	C 505	41.4	2.5	818128	4	US-09-949-016-14555	Sequence 14555, A
C 433	41.6	2.5	18107	4	US-09-949-016-13674	Sequence 13674, A	C 506	41.4	2.5	818128	4	US-09-949-016-14556	Sequence 14556, A
434	41.6	2.5	20721	4	US-09-949-016-16257	Sequence 16257, A	C 507	41.4	2.5	818128	4	US-09-949-016-14557	Sequence 14557, A
435	41.6	2.5	26684	4	US-09-949-016-15109	Sequence 15109, A	C 508	41.4	2.5	818128	4	US-09-949-016-14558	Sequence 14558, A
436	41.6	2.5	26684	4	US-09-949-016-15110	Sequence 15110, A	C 509	41.4	2.5	818128	4	US-09-949-016-14559	Sequence 14559, A
437	41.6	2.5	26684	4	US-09-949-016-17409	Sequence 17409, A	C 510	41.4	2.5	818128	4	US-09-949-016-14560	Sequence 14560, A
438	41.6	2.5	26684	4	US-09-949-016-17410	Sequence 17410, A	C 511	41.4	2.5	818128	4	US-09-949-016-14561	Sequence 14561, A
439	41.6	2.5	46823	4	US-09-949-016-12723	Sequence 12723, A	C 512	41.4	2.5	818128	4	US-09-949-016-14562	Sequence 14562, A
440	41.6	2.5	46940	4	US-09-949-016-16252	Sequence 16252, A	C 513	41.4	2.5	818128	4	US-09-949-016-14564	Sequence 14564, A
441	41.6	2.5	53332	4	US-09-801-861-3	Sequence 3, Appli	C 514	41.4	2.5	818128	4	US-09-949-016-14565	Sequence 14565, A
442	41.6	2.5	53332	4	US-10-224-562-3	Sequence 3, Appli	C 515	41.4	2.5	818128	4	US-09-949-016-14567	Sequence 14567, A
C 443	41.6	2.5	151088	4	US-09-949-016-16240	Sequence 16240, A	C 516	41.4	2.5	818128	4	US-09-949-016-14567	Sequence 14567, A
444	41.4	2.5	111	3	US-09-297-535-23	Sequence 23, Appl	517	41.2	2.5	98	4	US-09-621-976-11744	Sequence 11744, A
445	41.4	2.5	111	4	US-09-621-976-14677	Sequence 14677, A	518	41.2	2.5	250	4	US-09-621-976-17371	Sequence 17371, A
446	41.4	2.5	351	4	US-09-621-976-15134	Sequence 15134, A	519	41.2	2.5	333	3	US-09-018-584A-27	Sequence 27, Appl
447	41.4	2.5	510	4	US-09-248-796A-13735	Sequence 13735, A	520	41.2	2.5	333	4	US-09-784-423-27	Sequence 27, Appl
C 448	41.4	2.5	601	4	US-09-949-016-149677	Sequence 149677, A	C 521	41.2	2.5	396	4	US-09-640-173-10	Sequence 10, Appl
C 449	41.4	2.5	601	4	US-09-949-016-186673	Sequence 186673, A	C 522	41.2	2.5	396	4	US-09-713-550-10	Sequence 10, Appl
C 450	41.4	2.5	601	4	US-09-949-016-186674	Sequence 186674, A	C 523	41.2	2.5	396	4	US-09-825-234-10	Sequence 10, Appl
C 451	41.4	2.5	601	4	US-09-949-016-186675	Sequence 186675, A	C 524	41.2	2.5	396	4	US-09-970-966-10	Sequence 10, Appl
C 452	41.4	2.5	844	4	US-09-690-942-3	Sequence 3, Appli	C 525	41.2	2.5	1335	4	US-09-970-966-10	Sequence 10, Appl
453	41.4	2.5	890	4	US-09-621-976-2725	Sequence 2725, Ap	526	41.2	2.5	1508	3	US-09-270-767-13052	Sequence 13052, A
454	41.4	2.5	2239	3	US-09-196-390-1	Sequence 1, Appli	527	41.2	2.5	1544	4	US-09-039-046-1	Sequence 1, Appli
455	41.4	2.5	2239	4	US-09-952-677-1	Sequence 1, Appli	528	41.2	2.5	1835	3	US-09-187-999-14	Sequence 14, Appl
456	41.4	2.5	3410	3	US-09-020-956-110	Sequence 110, App	529	41.2	2.5	2599	4	US-09-485-549-1	Sequence 1, Appli
457	41.4	2.5	3410	3	US-09-030-607-110	Sequence 110, App	530	41.2	2.5	2633	4	US-09-949-016-4676	Sequence 4676, Ap
458	41.4	2.5	3410	3	US-09-439-313-110	Sequence 110, App	531	41.2	2.5	2852	3	US-09-023-655-950	Sequence 2, Appl
459	41.4	2.5	3410	3	US-09-352-616A-110	Sequence 110, App	532	41.2	2.5	2852	3	US-09-027-137-2	Sequence 2, Appl
460	41.4	2.5	3410	3	US-09-602-877A-100	Sequence 100, App	533	41.2	2.5	2852	3	US-09-344-441-2	Sequence 2, Appl
461	41.4	2.5	3410	3	US-09-232-149A-110	Sequence 110, App	C 534	41.2	2.5	5807	4	US-09-976-594-245	Sequence 245, App
462	41.4	2.5	3410	4	US-09-159-812-110	Sequence 110, App	C 535	41.2	2.5	23222	4	US-09-949-016-15949	Sequence 15949, A
463	41.4	2.5	3410	4	US-09-636-215-110	Sequence 110, App	C 536	41.2	2.5	29222	4	US-09-949-016-11874	Sequence 11874, A
464	41.4	2.5	3410	4	US-09-685-166A-110	Sequence 110, App	537	41.2	2.5	72604	3	US-09-268-952-7	Sequence 7, Appli
465	41.4	2.5	3410	4	US-09-115-453-110	Sequence 110, App	C 538	41.2	2.5	87608	4	US-09-657-474-7	Sequence 7, Appli
												US-09-949-016-17011	Sequence 17011, A

C 539	41.2	2.5	90428	4	US-09-949-016-12564	Sequence 12564, A	612	40.6	2.4	2718	4	US-09-667-135-1	Sequence 1, Appli
C 540	41.2	2.5	145928	4	US-09-949-016-15444	Sequence 15444, A	613	40.6	2.4	2989	6	5378464-1	Patent No. 5378464
C 541	41.2	2.5	251672	4	US-09-949-016-17296	Sequence 17296, A	614	40.6	2.4	2989	6	5378464-1	Patent No. 5378464
C 542	41.2	2.5	251682	4	US-09-949-016-11973	Sequence 11973, A	615	40.6	2.4	8353	3	US-08-611-587-1	Sequence 1, Appli
C 543	41	2.4	163	4	US-09-621-976-9608	Sequence 9608, Ap	C 615	40.6	2.4	8638	4	US-10-029-907-6	Sequence 6, Appli
C 544	41	2.4	257	2	US-08-620-678A-24	Sequence 24, Appl	C 617	40.6	2.4	8643	4	US-10-029-907-4	Sequence 4, Appli
C 545	41	2.4	257	2	US-08-897-126-24	Sequence 24, Appl	C 618	40.6	2.4	13146	2	US-08-724-354D-3	Sequence 3, Appli
C 546	41	2.4	601	4	US-09-949-016-193621	Sequence 193621, A	C 619	40.6	2.4	13146	2	US-08-724-354D-3	Sequence 3, Appli
C 547	41	2.4	985	4	US-09-322-409-25	Sequence 25, Appl	620	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 1786, A
C 548	41	2.4	985	4	US-09-322-409-27	Sequence 27, Appl	621	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 1786, A
C 549	41	2.4	985	4	US-09-451-527-25	Sequence 25, Appl	622	40.6	2.4	15661	4	US-09-949-016-117205	Sequence 17205, A
C 550	41	2.4	985	4	US-09-451-527-27	Sequence 27, Appl	623	40.6	2.4	15661	4	US-09-949-016-117205	Sequence 17205, A
C 551	41	2.4	1406	4	US-10-000-489-81	Sequence 81, Appl	624	40.6	2.4	29321	4	US-09-949-016-14257	Sequence 14257, A
C 552	41	2.4	1493	1	US-08-340-820-24	Sequence 24, Appl	625	40.6	2.4	29321	4	US-09-949-016-14257	Sequence 14257, A
C 553	41	2.4	1493	1	US-08-593-535-24	Sequence 24, Appl	626	40.6	2.4	50000	3	US-09-146-053-3	Sequence 3, Appli
C 554	41	2.4	2311	4	US-09-800-729-66	Sequence 66, Appl	627	40.6	2.4	50000	3	US-09-146-053-3	Sequence 3, Appli
C 555	41	2.4	2311	4	US-09-720-317A-19	Sequence 19, Appl	628	40.6	2.4	83708	4	US-09-949-016-13394	Sequence 13394, A
C 556	41	2.4	2320	3	US-09-202-904A-13	Sequence 13, Appl	629	40.6	2.4	83708	4	US-09-949-016-13394	Sequence 13394, A
C 557	41	2.4	2406	4	US-09-594-506-37	Sequence 37, Appl	C 629	40.6	2.4	87752	4	US-09-949-016-16807	Sequence 16807, A
C 558	41	2.4	6200	3	US-09-439-923-1	Sequence 1, Appli	C 630	40.6	2.4	175265	4	US-09-949-016-16089	Sequence 16089, A
C 559	41	2.4	6200	4	US-09-711-202A-1	Sequence 1, Appli	631	40.6	2.4	268449	4	US-09-949-016-17244	Sequence 17244, A
C 560	41	2.4	6200	4	US-09-711-202A-1	Sequence 1, Appli	632	40.6	2.4	390416	4	US-09-949-016-17244	Sequence 17244, A
C 561	41	2.4	7286	3	US-09-331-581-3	Sequence 3, Appli	C 633	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 562	41	2.4	7938	3	US-09-331-581-14	Sequence 14, Appl	C 634	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 563	41	2.4	54033	4	US-09-949-016-12091	Sequence 12091, A	635	40.4	2.4	190	4	US-09-621-976-16784	Sequence 16784, A
C 564	41	2.4	54033	4	US-09-949-016-14325	Sequence 14325, A	636	40.4	2.4	326	4	US-09-621-976-16024	Sequence 16024, A
C 565	41	2.4	68283	4	US-09-949-016-12261	Sequence 12261, A	637	40.4	2.4	334	4	US-09-621-976-16044	Sequence 16044, A
C 566	41	2.4	113701	4	US-09-949-016-13214	Sequence 13214, A	638	40.4	2.4	335	4	US-09-621-976-16061	Sequence 16061, A
C 567	41	2.4	124264	4	US-09-949-016-16396	Sequence 16396, A	639	40.4	2.4	336	4	US-09-621-976-16061	Sequence 16061, A
C 568	41	2.4	128175	4	US-09-949-016-16268	Sequence 16268, A	640	40.4	2.4	336	4	US-09-621-976-16061	Sequence 16061, A
C 569	40.8	2.4	84	4	US-09-621-976-14571	Sequence 14571, A	641	40.4	2.4	338	4	US-09-621-976-16041	Sequence 16041, A
C 570	40.8	2.4	102	4	US-09-621-976-14804	Sequence 14804, A	C 642	40.4	2.4	389	4	US-09-513-999C-420	Sequence 420, App
C 571	40.8	2.4	179	4	US-09-621-976-9575	Sequence 9575, Ap	643	40.4	2.4	593	4	US-09-904-615-59	Sequence 59, Appl
C 572	40.8	2.4	188	4	US-09-621-976-10364	Sequence 10364, A	644	40.4	2.4	601	4	US-09-949-016-189988	Sequence 189988, A
C 573	40.8	2.4	273	4	US-09-809-545A-31	Sequence 31, Appl	645	40.4	2.4	1052	4	US-09-489-847-23	Sequence 23, Appl
C 574	40.8	2.4	283	4	US-09-621-976-16989	Sequence 16989, A	646	40.4	2.4	1503	4	US-09-907-794A-220	Sequence 220, App
C 575	40.8	2.4	1129	3	US-09-227-357-40	Sequence 40, Appl	647	40.4	2.4	1503	4	US-09-905-125A-220	Sequence 220, App
C 576	40.8	2.4	1214	4	US-09-780-717-28	Sequence 28, Appl	648	40.4	2.4	1503	4	US-09-902-775A-220	Sequence 220, App
C 577	40.8	2.4	1683	3	US-09-347-803-11	Sequence 11, Appl	649	40.4	2.4	1503	4	US-09-906-700-220	Sequence 220, App
C 578	40.8	2.4	2488	4	US-09-816-093-1	Sequence 1, Appli	650	40.4	2.4	1503	4	US-09-903-603A-220	Sequence 220, App
C 579	40.8	2.4	3124	3	US-09-734-030-1	Sequence 1, Appli	651	40.4	2.4	1503	4	US-09-904-920A-220	Sequence 220, App
C 580	40.8	2.4	3124	4	US-10-153-921-1	Sequence 1, Appli	652	40.4	2.4	1503	4	US-09-909-064-220	Sequence 220, App
C 581	40.8	2.4	3124	4	US-10-669-689-1	Sequence 1, Appli	653	40.4	2.4	1503	4	US-09-905-381A-220	Sequence 220, App
C 582	40.8	2.4	15722	4	US-09-949-016-16709	Sequence 16709, A	654	40.4	2.4	1503	4	US-09-906-618-220	Sequence 220, App
C 583	40.8	2.4	61124	4	US-09-949-016-11914	Sequence 11914, A	655	40.4	2.4	1512	2	US-08-903-965C-8	Sequence 8, Appli
C 584	40.8	2.4	61140	4	US-09-949-016-15771	Sequence 15771, A	656	40.4	2.4	1542	4	US-09-205-258-123	Sequence 123, App
C 585	40.8	2.4	65744	4	US-09-949-016-12591	Sequence 12591, A	657	40.4	2.4	1685	4	US-09-907-794A-83	Sequence 83, Appl
C 586	40.8	2.4	65745	4	US-09-949-016-15871	Sequence 15871, A	658	40.4	2.4	1685	4	US-09-905-125A-83	Sequence 83, Appl
C 587	40.8	2.4	76269	4	US-09-949-016-14603	Sequence 14603, A	659	40.4	2.4	1685	4	US-09-902-775A-83	Sequence 83, Appl
C 588	40.8	2.4	100836	4	US-09-949-016-12871	Sequence 12871, A	660	40.4	2.4	1685	4	US-09-906-700-83	Sequence 83, Appl
C 589	40.8	2.4	321023	4	US-09-949-016-17063	Sequence 17063, A	661	40.4	2.4	1685	4	US-09-903-603A-83	Sequence 83, Appl
C 590	40.8	2.4	321022	4	US-09-949-016-11852	Sequence 11852, A	662	40.4	2.4	1685	4	US-09-904-920A-83	Sequence 83, Appl
C 591	40.8	2.4	321022	4	US-09-949-016-11852	Sequence 11852, A	663	40.4	2.4	1685	4	US-09-909-064-83	Sequence 83, Appl
C 592	40.8	2.4	1664976	4	US-08-916-412B-1	Sequence 1, Appli	664	40.4	2.4	1685	4	US-09-905-381A-83	Sequence 83, Appl
C 593	40.8	2.4	1664976	4	US-08-916-412B-1	Sequence 1, Appli	665	40.4	2.4	1685	4	US-09-906-618-83	Sequence 83, Appl
C 594	40.6	2.4	147	4	US-09-621-970-851	Sequence 851, Ap	666	40.4	2.4	1718	4	US-09-778-510-5	Sequence 5, Appli
C 595	40.6	2.4	189	4	US-09-621-976-14761	Sequence 14761, A	667	40.4	2.4	1820	4	US-09-778-510-5	Sequence 1, Appli
C 596	40.6	2.4	376	2	US-08-623-906A-18	Sequence 18, Appl	668	40.4	2.4	1830	4	US-09-248-796A-409	Sequence 409, App
C 597	40.6	2.4	601	4	US-09-949-016-47249	Sequence 47249, A	669	40.4	2.4	2223	1	US-08-257-073-4	Sequence 4, Appli
C 598	40.6	2.4	601	4	US-09-949-016-47327	Sequence 47327, A	670	40.4	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli
C 599	40.6	2.4	601	4	US-09-949-016-57131	Sequence 57131, A	671	40.4	2.4	3200	1	US-08-384-850-1	Sequence 1, Appli
C 600	40.6	2.4	601	4	US-09-949-016-57132	Sequence 57132, A	672	40.4	2.4	192700	4	US-09-949-016-11820	Sequence 11820, A
C 601	40.6	2.4	601	4	US-09-949-016-57133	Sequence 57133, A	673	40.4	2.4	192700	4	US-09-949-016-11820	Sequence 11820, A
C 602	40.6	2.4	601	4	US-09-949-016-57133	Sequence 57133, A	C 674	40.4	2.4	202001	4	US-09-734-674-3	Sequence 3, Appli
C 603	40.6	2.4	601	4	US-09-949-016-88560	Sequence 88560, A	C 675	40.4	2.4	422592	4	US-09-949-016-14182	Sequence 14182, A
C 604	40.6	2.4	601	4	US-09-949-016-88565	Sequence 88565, A	676	40.2	2.4	454	2	US-08-623-906A-6	Sequence 6, Appli
C 605	40.6	2.4	601	4	US-09-949-016-193622	Sequence 193622, A	677	40.2	2.4	572	3	US-09-342-653-5	Sequence 5, Appli
C 606	40.6	2.4	601	4	US-09-949-016-193623	Sequence 193623, A	678	40.2	2.4	601	4	US-09-949-016-17855	Sequence 17855, A
C 607	40.6	2.4	795	4	US-09-949-016-193624	Sequence 193624, A	679	40.2	2.4	601	4	US-09-949-016-41735	Sequence 41735, A
C 608	40.6	2.4	1147	1	US-08-665-716-1	Sequence 1, Appli	680	40.2	2.4	601	4	US-09-949-016-56224	Sequence 56224, A
C 609	40.6	2.4	1198	3	US-09-248-335-27	Sequence 27, Appl	C 681	40.2	2.4	601	4	US-09-949-016-84943	Sequence 84943, A
C 610	40.6	2.4	1878	3	US-09-465-558-39	Sequence 39, Appl	682	40.2	2.4	601	4	US-09-949-016-162251	Sequence 162251, A
C 611	40.6	2.4	2458	3	US-08-611-587-6	Sequence 6, Appli	C 683	40.2	2.4	601	4	US-09-949-016-162252	Sequence 162252, A
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685	40.2	2.4	753	4	US-09-902-331B-9	Sequence 9, Appli	758	39.8	2.4	332	4	US-09-621-976-16050	Sequence 16050, A
686	40.2	2.4	958	2	US-08-757-046A-5	Sequence 5, Appli	759	39.8	2.4	332	4	US-09-621-976-16053	Sequence 16053, A
687	40.2	2.4	958	3	US-09-447-208-5	Sequence 5, Appli	760	39.8	2.4	443	4	US-09-621-976-17631	Sequence 17631, A
688	40.2	2.4	958	3	US-09-135-988-5	Sequence 5, Appli	761	39.8	2.4	588	4	US-09-205-258-64	Sequence 64, Appli
689	40.2	2.4	958	3	US-09-277-716-5	Sequence 5, Appli	762	39.8	2.4	601	4	US-09-949-016-29142	Sequence 29142, A
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692	40.2	2.4	958	3	US-09-609-161B-5	Sequence 5, Appli	765	39.8	2.4	601	4	US-09-949-016-29145	Sequence 29145, A
693	40.2	2.4	958	3	US-08-990-103-5	Sequence 5, Appli	766	39.8	2.4	601	4	US-09-949-016-41097	Sequence 41097, A
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696	40.2	2.4	958	4	US-10-126-798-5	Sequence 5, Appli	769	39.8	2.4	601	4	US-09-949-016-41100	Sequence 41100, A
697	40.2	2.4	958	4	US-10-126-777-5	Sequence 5, Appli	770	39.8	2.4	601	4	US-09-949-016-161232	Sequence 161232, A
698	40.2	2.4	1190	4	US-09-390-207-1	Sequence 1, Appli	771	39.8	2.4	601	4	US-09-949-016-195763	Sequence 195763, A
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700	40.2	2.4	1359	3	US-09-387-574-11	Sequence 11, Appli	773	39.8	2.4	1046	1	US-08-361-467B-4	Sequence 4, Appli
701	40.2	2.4	1359	3	US-09-668-096-11	Sequence 11, Appli	774	39.8	2.4	1046	1	US-08-484-332C-4	Sequence 4, Appli
702	40.2	2.4	1606	4	US-09-820-004-1	Sequence 1, Appli	775	39.8	2.4	1172	1	US-07-945-288-9	Sequence 9, Appli
703	40.2	2.4	1895	3	US-09-444-336-7	Sequence 7, Appli	776	39.8	2.4	1172	1	US-08-462-831-9	Sequence 9, Appli
704	40.2	2.4	2065	2	US-08-968-751-1	Sequence 1, Appli	777	39.8	2.4	1172	1	US-08-461-809-9	Sequence 9, Appli
705	40.2	2.4	5006	4	US-09-976-594-530	Sequence 530, App	778	39.8	2.4	1172	1	US-08-461-441-9	Sequence 9, Appli
706	40.2	2.4	50383	4	US-09-949-016-17600	Sequence 17600, A	779	39.8	2.4	1172	5	PCT-US93-08518-9	Sequence 9, Appli
C 707	40.2	2.4	53769	4	US-09-949-016-17527	Sequence 17527, A	780	39.8	2.4	1602	1	US-08-530-950-3	Sequence 3, Appli
C 708	40.2	2.4	86639	4	US-09-949-016-17397	Sequence 17397, A	781	39.8	2.4	1602	3	US-08-888-429A-3	Sequence 3, Appli
C 709	40.2	2.4	88240	4	US-09-949-016-16279	Sequence 16279, A	782	39.8	2.4	1602	3	US-09-149-879-3	Sequence 3, Appli
710	40.2	2.4	88843	4	US-09-949-016-12346	Sequence 12346, A	783	39.8	2.4	1602	4	US-09-057-009-3	Sequence 3, Appli
711	40.2	2.4	89844	4	US-09-949-016-13656	Sequence 13656, A	784	39.8	2.4	1602	4	US-09-593-653-3	Sequence 3, Appli
C 712	40.2	2.4	93398	4	US-09-949-016-14167	Sequence 14167, A	785	39.8	2.4	1692	4	US-09-821-803A-5	Sequence 5, Appli
C 713	40.2	2.4	144158	4	US-09-949-016-11755	Sequence 11755, A	786	39.8	2.4	1725	4	US-09-668-097A-21	Sequence 21, Appli
C 714	40.2	2.4	144158	4	US-09-949-016-12936	Sequence 12936, A	C 787	39.8	2.4	2239	4	US-10-380-105-7	Sequence 7, Appli
C 715	40.2	2.4	256287	4	US-09-949-016-14608	Sequence 14608, A	788	39.8	2.4	4860	4	US-09-949-016-296	Sequence 296, App
716	40	2.4	92	4	US-09-621-976-13620	Sequence 13620, A	789	39.8	2.4	4860	1	US-08-242-677-1	Sequence 1, Appli
717	40	2.4	146	4	US-09-621-976-8850	Sequence 8850, Ap	790	39.8	2.4	10502	4	US-09-949-016-16708	Sequence 16708, A
718	40	2.4	160	4	US-09-621-976-10335	Sequence 10335, A	C 791	39.8	2.4	16073	4	US-09-949-016-12312	Sequence 12312, A
719	40	2.4	289	1	US-08-341-568-3	Sequence 3, Appli	C 792	39.8	2.4	16073	4	US-09-949-016-12905	Sequence 12905, A
720	40	2.4	289	2	US-08-911-020-3	Sequence 3, Appli	793	39.8	2.4	13557	5	PCT-US92-06300-1	Sequence 1, Appli
721	40	2.4	293	4	US-09-621-976-16965	Sequence 16965, A	794	39.8	2.4	25175	4	US-09-949-016-16247	Sequence 16247, A
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725	40	2.4	601	4	US-09-949-016-40845	Sequence 40845, A	C 798	39.8	2.4	36159	4	US-10-135-687-3	Sequence 3, Appli
726	40	2.4	601	4	US-09-949-016-40846	Sequence 40846, A	799	39.8	2.4	38772	4	US-09-949-016-12382	Sequence 12382, A
727	40	2.4	1578	3	US-09-416-050A-1	Sequence 1, Appli	800	39.8	2.4	38772	4	US-09-949-016-12729	Sequence 12729, A
728	40	2.4	1578	3	US-09-664-800-1	Sequence 1, Appli	C 801	39.8	2.4	83178	4	US-09-949-016-14606	Sequence 14606, A
729	40	2.4	1578	3	US-09-665-309-1	Sequence 1, Appli	802	39.8	2.4	93894	4	US-09-949-016-13629	Sequence 13629, A
730	40	2.4	1578	3	US-09-661-569-1	Sequence 1, Appli	C 803	39.8	2.4	153866	4	US-09-949-016-16919	Sequence 16919, A
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733	40	2.4	5225	4	US-09-949-016-16351	Sequence 16351, A	806	39.6	2.4	316	4	US-09-513-999C-838	Sequence 838, App
734	40	2.4	6243	2	US-09-056-075-1	Sequence 1, Appli	807	39.6	2.4	339	4	US-09-621-976-16015	Sequence 16015, A
735	40	2.4	7224	4	US-08-486-049-1	Sequence 1, Appli	C 808	39.6	2.4	516	3	US-09-018-584A-24	Sequence 24, Appli
736	40	2.4	8100	4	US-09-554-337-4	Sequence 4, Appli	C 809	39.6	2.4	516	4	US-09-784-423-24	Sequence 24, Appli
737	40	2.4	15538	4	US-09-554-337-1	Sequence 1, Appli	C 810	39.6	2.4	593	3	US-09-385-982-262	Sequence 262, App
C 738	40	2.4	28555	4	US-09-949-016-13046	Sequence 13046, A	811	39.6	2.4	601	4	US-09-949-016-160808	Sequence 160808, A
C 739	40	2.4	35064	4	US-09-949-016-12778	Sequence 12778, A	812	39.6	2.4	633	4	US-09-270-767-6288	Sequence 6288, Ap
C 740	40	2.4	35064	4	US-09-949-016-13196	Sequence 13196, A	813	39.6	2.4	633	4	US-09-270-767-21570	Sequence 21570, A
C 741	40	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	814	39.6	2.4	711	4	US-09-621-976-17854	Sequence 17854, A
C 742	40	2.4	62908	4	US-09-949-016-17554	Sequence 17554, A	815	39.6	2.4	796	1	US-08-104-073-2	Sequence 2, Appli
C 743	40	2.4	137048	4	US-09-949-016-12427	Sequence 12427, A	816	39.6	2.4	1210	3	US-09-443-041A-29	Sequence 29, Appli
C 744	40	2.4	137048	4	US-09-949-016-13438	Sequence 13438, A	817	39.6	2.4	1332	2	US-09-057-762-1	Sequence 1, Appli
C 745	40	2.4	462589	4	US-09-949-016-12900	Sequence 12900, A	818	39.6	2.4	1332	3	US-08-326-119A-1	Sequence 1, Appli
C 746	40	2.4	476044	4	US-09-949-016-12412	Sequence 12412, A	819	39.6	2.4	1559	4	US-09-489-847-42	Sequence 42, Appli
747	40	2.4	786431	4	US-09-751-389-3	Sequence 3, Appli	820	39.6	2.4	1740	4	US-09-709-103-45	Sequence 45, Appli
748	39.8	2.4	92	4	US-09-621-976-14689	Sequence 14689, A	821	39.6	2.4	1740	4	US-09-439-410A-45	Sequence 45, Appli
749	39.8	2.4	98	1	US-08-621-976-12430	Sequence 12430, A	822	39.6	2.4	2445	4	US-09-949-016-781	Sequence 781, App
750	39.8	2.4	97	1	US-08-088-658-42	Sequence 42, Appli	823	39.6	2.4	2539	4	US-10-144-198-21	Sequence 21, Appli
751	39.8	2.4	98	2	US-08-471-907A-42	Sequence 42, Appli	824	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
752	39.8	2.4	98	4	US-09-621-976-12160	Sequence 12160, A	825	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
753	39.8	2.4	98	4	US-09-621-976-15091	Sequence 15091, A	826	39.6	2.4	3366	4	US-09-596-141C-6	Sequence 6, Appli
754	39.8	2.4	159	4	US-09-621-976-17448	Sequence 17448, A	827	39.6	2.4	3366	4	US-09-595-526C-6	Sequence 6, Appli
755	39.8	2.4	179	4	US-09-621-976-18054	Sequence 18054, A	828	39.6	2.4	4239	4	US-09-815-048-1	Sequence 1, Appli
C 756	39.8	2.4	200	3	US-09-014-416-64	Sequence 64, Appli	829	39.6	2.4	10442	4	US-09-596-141C-1	Sequence 1, Appli
757	39.8	2.4	329	4	US-09-621-976-16012	Sequence 16012, A	830	39.6	2.4	10442	4	US-09-595-526C-1	Sequence 1, Appli

831	39.6	2.4	10474	4	US-09-596-141C-7	Sequence 7, Appli	904	39.2	2.3	3080	4	US-09-865-364-25	Sequence 25, Appl
832	39.6	2.4	10474	4	US-09-596-141C-9	Sequence 9, Appli	C 905	39.2	2.3	5852	1	US-07-867-106-2	Sequence 2, Appli
833	39.6	2.4	10474	4	US-09-595-526C-7	Sequence 7, Appli	C 906	39.2	2.3	6370	4	US-09-306-595C-2	Sequence 2, Appli
834	39.6	2.4	16595	3	US-09-595-526C-9	Sequence 9, Appli	C 907	39.2	2.3	6370	4	US-09-925-388-2	Sequence 2, Appli
835	39.6	2.4	23193	4	US-09-146-053-7	Sequence 7, Appli	C 908	39.2	2.3	15459	4	US-09-949-016-16456	Sequence 16456, A
836	39.6	2.4	23193	4	US-09-949-016-17215	Sequence 17215, A	C 909	39.2	2.3	44549	3	US-09-146-053-5	Sequence 5, Appli
837	39.6	2.4	80346	3	US-09-078-294-4	Sequence 4, Appli	C 910	39.2	2.3	44549	3	US-09-949-016-17323	Sequence 17323, A
838	39.6	2.4	80395	3	US-09-078-294-4	Sequence 4, Appli	C 911	39.2	2.3	46988	4	US-09-949-016-12139	Sequence 12139, A
839	39.6	2.4	85369	4	US-09-949-016-112171	Sequence 15684, A	C 912	39.2	2.3	61922	4	US-09-949-016-15338	Sequence 15338, A
840	39.6	2.4	117001	4	US-09-949-016-115684	Sequence 15684, A	C 913	39.2	2.3	61922	4	US-09-949-016-11772	Sequence 11772, A
841	39.6	2.4	250958	4	US-09-949-016-16061	Sequence 16061, A	C 914	39.2	2.3	68580	4	US-09-949-016-15844	Sequence 15844, A
842	39.6	2.4	312474	4	US-09-949-016-17434	Sequence 17434, A	C 915	39.2	2.3	73519	4	US-09-949-016-16344	Sequence 16344, A
843	39.4	2.3	169	4	US-09-621-978-11249	Sequence 11249, A	C 916	39.2	2.3	105919	4	US-09-949-016-11769	Sequence 11769, A
844	39.4	2.3	196	4	US-09-270-767-29394	Sequence 29394, A	C 917	39.2	2.3	112219	4	US-09-949-016-12453	Sequence 12453, A
845	39.4	2.3	601	4	US-09-949-016-120672	Sequence 120672, A	C 918	39.2	2.3	112222	4	US-09-949-016-14324	Sequence 14324, A
846	39.4	2.3	624	4	US-09-949-016-175160	Sequence 175160, A	C 919	39.2	2.3	113186	4	US-09-949-016-17572	Sequence 17572, A
847	39.4	2.3	647	4	US-09-270-767-13424	Sequence 13424, A	C 920	39.2	2.3	113701	4	US-09-949-016-13214	Sequence 13214, A
848	39.4	2.3	1509	3	US-09-495-050A-54	Sequence 54, Appli	C 921	39.2	2.3	165841	4	US-09-949-016-16192	Sequence 16192, A
849	39.4	2.3	12703	4	US-09-949-016-16685	Sequence 179, App	C 922	39.2	2.3	187595	4	US-09-949-016-15546	Sequence 15546, A
850	39.4	2.3	12703	4	US-09-949-016-15629	Sequence 15629, A	C 923	39.2	2.3	260286	4	US-09-949-016-17037	Sequence 17037, A
851	39.4	2.3	19601	4	US-09-949-016-15629	Sequence 15629, A	C 924	39.2	2.3	260286	4	US-09-949-016-12106	Sequence 12106, A
852	39.4	2.3	24645	4	US-09-949-016-14062	Sequence 14062, A	C 925	39.2	2.3	392000	4	US-10-027-983-11	Sequence 11, Appl
853	39.4	2.3	25659	4	US-09-949-016-15052	Sequence 15052, A	C 926	39	2.3	127	3	US-08-341-568-1	Sequence 51, Appl
854	39.4	2.3	29927	4	US-09-949-016-11814	Sequence 11814, A	C 927	39	2.3	176	3	US-09-014-416-63	Sequence 63, Appl
855	39.4	2.3	29927	4	US-09-949-016-17474	Sequence 17474, A	C 928	39	2.3	183	3	US-09-014-416-60	Sequence 60, Appl
856	39.4	2.3	34372	4	US-09-949-016-17475	Sequence 17475, A	C 929	39	2.3	185	4	US-09-621-976-16779	Sequence 16779, A
857	39.4	2.3	31111	4	US-09-949-016-15628	Sequence 15628, A	C 930	39	2.3	204	4	US-09-621-976-1323	Sequence 1323, Ap
858	39.4	2.3	34875	4	US-09-949-016-13098	Sequence 13098, A	C 931	39	2.3	266	4	US-09-621-976-16813	Sequence 16813, A
859	39.4	2.3	37802	4	US-09-949-016-13099	Sequence 13099, A	C 932	39	2.3	321	4	US-08-520-678A-23	Sequence 23, Appl
860	39.4	2.3	37802	4	US-09-949-016-12639	Sequence 12639, A	C 933	39	2.3	321	3	US-08-897-126-23	Sequence 23, Appl
861	39.4	2.3	44393	4	US-09-949-016-14945	Sequence 14945, A	C 934	39	2.3	332	4	US-09-621-976-16031	Sequence 16031, A
862	39.4	2.3	44393	4	US-09-949-016-14945	Sequence 14945, A	C 935	39	2.3	332	4	US-08-623-906A-14	Sequence 14, Appl
863	39.4	2.3	44393	4	US-09-949-016-14946	Sequence 14946, A	C 936	39	2.3	348	2	US-08-341-568-1	Sequence 1, Appl
864	39.4	2.3	55841	4	US-09-949-016-16911	Sequence 16911, A	C 937	39	2.3	536	2	US-08-341-568-1	Sequence 1, Appl
865	39.4	2.3	55841	4	US-09-949-016-16602	Sequence 16602, A	C 938	39	2.3	536	2	US-08-341-568-1	Sequence 1, Appl
866	39.4	2.3	67888	4	US-09-949-001-37	Sequence 37, Appl	C 939	39	2.3	599	3	US-09-328-111-147	Sequence 147, App
867	39.4	2.3	83516	4	US-09-949-016-13847	Sequence 13847, A	C 940	39	2.3	601	4	US-09-949-016-19754	Sequence 19754, A
868	39.4	2.3	86936	4	US-09-949-016-17314	Sequence 17314, A	C 941	39	2.3	601	4	US-09-949-016-43955	Sequence 43955, A
869	39.4	2.3	94877	4	US-09-949-016-16114	Sequence 16114, A	C 942	39	2.3	601	4	US-09-949-016-71483	Sequence 71483, A
870	39.4	2.3	116425	4	US-09-949-016-11809	Sequence 11809, A	C 943	39	2.3	601	4	US-09-949-016-80449	Sequence 80449, A
871	39.4	2.3	137949	4	US-09-818-512-3	Sequence 3, Appli	C 944	39	2.3	601	4	US-09-949-016-80451	Sequence 80451, A
872	39.4	2.3	137949	4	US-09-949-016-12196	Sequence 12196, A	C 945	39	2.3	601	4	US-09-949-016-81973	Sequence 81973, A
873	39.4	2.3	137956	4	US-09-949-016-13760	Sequence 13760, A	C 946	39	2.3	601	4	US-09-949-016-152093	Sequence 152093, A
874	39.4	2.3	236341	4	US-09-949-016-13978	Sequence 13978, A	C 947	39	2.3	601	4	US-09-949-016-152166	Sequence 152166, A
875	39.4	2.3	253345	4	US-09-949-016-12656	Sequence 12656, A	C 948	39	2.3	601	4	US-09-949-016-152239	Sequence 152239, A
876	39.4	2.3	253364	4	US-09-949-016-13639	Sequence 13639, A	C 949	39	2.3	601	4	US-09-949-016-152312	Sequence 152312, A
877	39.2	2.3	85	4	US-09-621-976-13395	Sequence 13395, A	C 950	39	2.3	601	4	US-09-949-016-159398	Sequence 159398, A
878	39.2	2.3	85	4	US-09-621-976-14949	Sequence 14949, A	C 951	39	2.3	601	4	US-09-949-016-159471	Sequence 159471, A
879	39.2	2.3	89	4	US-09-621-976-14749	Sequence 14749, A	C 952	39	2.3	601	4	US-09-949-016-159544	Sequence 159544, A
880	39.2	2.3	89	4	US-09-621-976-14974	Sequence 14974, A	C 953	39	2.3	601	4	US-09-949-016-159617	Sequence 159617, A
881	39.2	2.3	91	4	US-09-621-976-12161	Sequence 12161, A	C 954	39	2.3	601	4	US-09-949-016-160807	Sequence 160807, A
882	39.2	2.3	208	1	US-08-686-878A-37	Sequence 37, Appl	C 955	39	2.3	601	4	US-09-949-016-161983	Sequence 161983, A
883	39.2	2.3	208	3	US-09-175-928-37	Sequence 37, Appl	C 956	39	2.3	1069	3	US-09-372-422A-7	Sequence 7, Appli
884	39.2	2.3	271	4	US-09-621-976-10380	Sequence 10380, A	C 957	39	2.3	1133	4	US-09-916-204-1	Sequence 1, Appli
885	39.2	2.3	505	4	US-09-621-976-15639	Sequence 15639, A	C 958	39	2.3	1133	4	US-10-282-048-1	Sequence 1, Appli
886	39.2	2.3	601	4	US-09-949-016-126414	Sequence 126414, A	C 959	39	2.3	1249	4	US-09-461-325-128	Sequence 128, App
887	39.2	2.3	601	4	US-09-949-016-126417	Sequence 126417, A	C 960	39	2.3	1249	4	US-10-012-542-128	Sequence 128, App
888	39.2	2.3	601	4	US-09-949-016-145250	Sequence 145250, A	C 961	39	2.3	1249	4	US-10-115-123-128	Sequence 128, App
889	39.2	2.3	601	4	US-09-949-016-145251	Sequence 145251, A	C 962	39	2.3	1260	4	US-09-461-325-93	Sequence 93, Appl
890	39.2	2.3	756	4	US-09-949-016-159061	Sequence 159061, A	C 963	39	2.3	1260	4	US-10-012-542-93	Sequence 93, Appl
891	39.2	2.3	756	4	US-09-614-912-93	Sequence 93, Appl	C 964	39	2.3	1260	4	US-10-115-123-93	Sequence 93, Appl
892	39.2	2.3	960	3	US-09-270-767-28941	Sequence 28941, A	C 965	39	2.3	1785	4	US-09-248-796A-928	Sequence 928, App
893	39.2	2.3	960	3	US-09-248-335-57	Sequence 57, Appl	C 966	39	2.3	1798	2	US-08-557-128-12	Sequence 12, Appl
894	39.2	2.3	1476	4	US-09-248-796A-5437	Sequence 5437, Ap	C 967	39	2.3	2378	3	US-08-802-805D-20	Sequence 20, Appl
895	39.2	2.3	1700	2	US-08-897-340-4	Sequence 4, Appli	C 968	39	2.3	2378	4	US-08-860-370-1	Sequence 1, Appli
896	39.2	2.3	2045	3	US-09-252-329-4	Sequence 4, Appli	C 969	39	2.3	2485	4	US-09-889-463A-9	Sequence 9, Appli
897	39.2	2.3	2291	4	US-09-152-060-22	Sequence 22, Appl	C 970	39	2.3	2744	3	US-09-071-101-1	Sequence 1, Appli
898	39.2	2.3	2291	4	US-09-220-132-114	Sequence 114, App	C 971	39	2.3	2744	3	US-09-369-618-1	Sequence 1, Appli
899	39.2	2.3	2291	4	US-09-814-915A-95	Sequence 95, Appl	C 972	39	2.3	2744	3	US-09-369-617-1	Sequence 1, Appli
900	39.2	2.3	3080	3	US-09-099-041A-25	Sequence 25, Appl	C 973	39	2.3	3450	4	US-09-902-540-9001	Sequence 9001, Ap
901	39.2	2.3	3080	3	US-09-245-281A-25	Sequence 25, Appl	C 974	39	2.3	3527	2	US-08-909-965C-7	Sequence 7, Appli
902	39.2	2.3	3080	3	US-09-207-359B-25	Sequence 25, Appl	C 975	39	2.3	4137	3	US-09-499-964-2	Sequence 2, Appli
903	39.2	2.3	3080	4	US-09-340-620A-25	Sequence 25, Appli	C 976	39	2.3	7305	4	US-09-902-540-961	Sequence 961, App

c 977	39	2.3	7889	4	US-09-539-601-10	Sequence 10, Appl	1050	38.8	2.3	225	4	US-09-248-796A-10883	Sequence 10883, A
c 978	39	2.3	8001	4	US-09-539-601-7	Sequence 7, Appl	1051	38.8	2.3	259	4	US-09-621-976-16294	Sequence 16294, A
c 979	39	2.3	8001	4	US-09-539-601-16	Sequence 16, Appl	1052	38.8	2.3	371	4	US-09-621-976-19223	Sequence 19223, A
c 980	39	2.3	8001	4	US-09-539-601-22	Sequence 22, Appl	c1053	38.8	2.3	599	4	US-09-270-767-13708	Sequence 13708, A
c 981	39	2.3	8001	4	US-09-539-601-28	Sequence 28, Appl	1054	38.8	2.3	601	4	US-09-949-016-67114	Sequence 67114, A
c 982	39	2.3	8637	4	US-09-539-601-4	Sequence 4, Appl	1055	38.8	2.3	601	4	US-09-949-016-67115	Sequence 67115, A
c 983	39	2.3	8638	4	US-10-029-907-7	Sequence 7, Appl	1056	38.8	2.3	601	4	US-09-949-016-76961	Sequence 76961, A
c 984	39	2.3	8638	4	US-10-029-907-24	Sequence 24, Appl	1057	38.8	2.3	601	4	US-09-949-016-76962	Sequence 76962, A
c 985	39	2.3	8638	4	US-10-029-907-25	Sequence 25, Appl	1058	38.8	2.3	601	4	US-09-949-016-76963	Sequence 76963, A
c 986	39	2.3	8639	4	US-10-029-907-1	Sequence 1, Appl	1059	38.8	2.3	601	4	US-09-949-016-76964	Sequence 76964, A
c 987	39	2.3	8639	4	US-10-029-907-13	Sequence 13, Appl	1060	38.8	2.3	601	4	US-09-949-016-109665	Sequence 109665, A
c 988	39	2.3	8649	4	US-09-539-601-13	Sequence 13, Appl	1061	38.8	2.3	601	4	US-09-949-016-113694	Sequence 113694, A
c 989	39	2.3	8907	4	US-09-949-016-16261	Sequence 16261, A	1062	38.8	2.3	601	4	US-09-949-016-113695	Sequence 113695, A
c 990	39	2.3	9595	3	US-09-014-416-4	Sequence 4, Appl	c1063	38.8	2.3	601	4	US-09-949-016-126815	Sequence 126815, A
c 991	39	2.3	9599	3	US-09-014-416-6	Sequence 6, Appl	c1064	38.8	2.3	601	4	US-09-949-016-127893	Sequence 127893, A
c 992	39	2.3	9599	3	US-09-014-416-2	Sequence 6, Appl	c1065	38.8	2.3	601	4	US-09-949-016-128230	Sequence 128230, A
c 993	39	2.3	9740	4	US-09-949-016-15833	Sequence 15833, A	c1066	38.8	2.3	601	4	US-09-949-016-145252	Sequence 145252, A
c 994	39	2.3	11076	4	US-09-539-601-1	Sequence 1, Appl	1067	38.8	2.3	601	4	US-09-949-016-201489	Sequence 201489, A
c 995	39	2.3	11076	4	US-09-539-601-19	Sequence 19, Appl	1068	38.8	2.3	1492	4	US-09-369-247-23	Sequence 23, Appl
c 996	39	2.3	11076	4	US-09-539-601-25	Sequence 25, Appl	1069	38.8	2.3	1843	4	US-09-328-925-49	Sequence 49, Appl
c 997	39	2.3	11076	4	US-09-539-601-31	Sequence 31, Appl	1070	38.8	2.3	1843	4	US-09-949-016-50	Sequence 50, Appl
c 998	39	2.3	11517	1	US-07-920-281C-1	Sequence 1, Appl	1071	38.8	2.3	1844	4	US-10-003-392-7	Sequence 7, Appl
c 999	39	2.3	11517	3	US-08-466-277-1	Sequence 1, Appl	1072	38.8	2.3	4773	4	US-09-270-767-14129	Sequence 14129, A
c 1000	39	2.3	11517	4	US-09-688-842-1	Sequence 1, Appl	1073	38.8	2.3	5009	1	US-08-487-890A-3	Sequence 3, Appl
c 1001	39	2.3	11641	4	US-09-949-016-11906	Sequence 11906, A	1074	38.8	2.3	5009	2	US-08-478-435-3	Sequence 3, Appl
c 1002	39	2.3	11643	4	US-09-949-016-14931	Sequence 14931, A	1075	38.8	2.3	5009	2	US-08-337-483-3	Sequence 3, Appl
c 1003	39	2.3	17879	4	US-09-949-016-12992	Sequence 12992, A	1076	38.8	2.3	5009	3	US-08-478-373-3	Sequence 3, Appl
c 1004	39	2.3	23319	4	US-09-949-016-14407	Sequence 14407, A	1077	38.8	2.3	5009	3	US-08-474-671-3	Sequence 3, Appl
c 1005	39	2.3	25431	4	US-09-949-016-13234	Sequence 13234, A	1078	38.8	2.3	5009	3	US-08-483-577A-3	Sequence 3, Appl
c 1006	39	2.3	37215	4	US-09-949-016-15526	Sequence 15526, A	1079	38.8	2.3	5009	3	US-08-897-438-3	Sequence 3, Appl
c 1007	39	2.3	45427	4	US-09-949-016-16243	Sequence 16243, A	1080	38.8	2.3	5009	3	US-08-637-654-3	Sequence 3, Appl
c 1008	39	2.3	45446	3	US-09-146-053-6	Sequence 6, Appl	1081	38.8	2.3	5009	3	US-08-649-518-3	Sequence 3, Appl
c 1009	39	2.3	50383	4	US-09-949-016-17600	Sequence 17600, A	1082	38.8	2.3	5033	1	US-08-487-890A-2	Sequence 2, Appl
c 1010	39	2.3	51698	4	US-09-949-016-12671	Sequence 12671, A	1083	38.8	2.3	5033	2	US-08-478-435-2	Sequence 2, Appl
c 1011	39	2.3	78846	4	US-09-949-016-12396	Sequence 12396, A	1084	38.8	2.3	5033	2	US-08-337-483-2	Sequence 2, Appl
c 1012	39	2.3	78846	4	US-09-949-016-12791	Sequence 12791, A	1085	38.8	2.3	5033	2	US-08-478-373-2	Sequence 2, Appl
c 1013	39	2.3	78846	4	US-09-949-016-12792	Sequence 12792, A	1086	38.8	2.3	5033	3	US-08-474-671-2	Sequence 2, Appl
c 1014	39	2.3	78846	4	US-09-949-016-12793	Sequence 12793, A	1087	38.8	2.3	5033	3	US-08-483-577A-2	Sequence 2, Appl
c 1015	39	2.3	78850	4	US-09-949-016-16013	Sequence 16013, A	1088	38.8	2.3	5033	3	US-08-897-438-2	Sequence 2, Appl
c 1016	39	2.3	78850	4	US-09-949-016-16014	Sequence 16014, A	1089	38.8	2.3	5033	3	US-08-637-654-2	Sequence 2, Appl
c 1017	39	2.3	78850	4	US-09-949-016-16015	Sequence 16015, A	1090	38.8	2.3	5033	3	US-08-649-518-2	Sequence 2, Appl
c 1018	39	2.3	78850	4	US-09-949-016-16016	Sequence 16016, A	1091	38.8	2.3	20445	4	US-09-949-016-14875	Sequence 14875, A
c 1019	39	2.3	78850	4	US-09-949-016-16201	Sequence 16201, A	c1092	38.8	2.3	31469	4	US-09-949-016-14974	Sequence 14974, A
c 1020	39	2.3	78850	4	US-09-949-016-16202	Sequence 16202, A	c1093	38.8	2.3	31469	4	US-09-949-016-13722	Sequence 13722, A
c 1021	39	2.3	78850	4	US-09-949-016-16203	Sequence 16203, A	c1094	38.8	2.3	41454	4	US-09-949-016-17107	Sequence 17107, A
c 1022	39	2.3	78850	4	US-09-949-016-16204	Sequence 16204, A	1095	38.8	2.3	45469	4	US-09-949-016-13398	Sequence 13398, A
c 1023	39	2.3	118382	4	US-09-949-016-15996	Sequence 15996, A	c1096	38.8	2.3	55195	4	US-09-949-016-15854	Sequence 15854, A
c 1024	39	2.3	118382	4	US-09-949-016-15997	Sequence 15997, A	c1097	38.8	2.3	65990	4	US-09-949-016-11830	Sequence 11830, A
c 1025	39	2.3	134140	4	US-09-949-016-12672	Sequence 12672, A	1098	38.8	2.3	74177	4	US-09-949-016-11988	Sequence 11988, A
c 1026	39	2.3	134241	4	US-09-949-016-12424	Sequence 12424, A	1099	38.8	2.3	74177	4	US-09-949-016-17388	Sequence 17388, A
c 1027	39	2.3	134242	4	US-09-949-016-15813	Sequence 15813, A	c1100	38.8	2.3	118067	4	US-09-497-855A-32	Sequence 32, Appl
c 1028	39	2.3	134242	4	US-09-949-016-15814	Sequence 15814, A	c1101	38.8	2.3	133559	4	US-09-949-016-15845	Sequence 15845, A
c 1029	39	2.3	134242	4	US-09-949-016-15815	Sequence 15815, A	1102	38.6	2.3	83	4	US-09-621-976-12087	Sequence 12087, A
c 1030	39	2.3	177797	4	US-09-949-016-14125	Sequence 14125, A	1103	38.6	2.3	83	4	US-09-621-976-12175	Sequence 12175, A
c 1031	39	2.3	186959	4	US-09-949-016-13125	Sequence 13125, A	1104	38.6	2.3	83	4	US-09-621-976-12429	Sequence 12429, A
c 1032	39	2.3	192506	4	US-09-949-016-15830	Sequence 15830, A	1105	38.6	2.3	83	4	US-09-621-976-12450	Sequence 12450, A
c 1033	39	2.3	227979	4	US-09-949-016-15833	Sequence 15833, A	1106	38.6	2.3	84	1	US-08-664-596B-3	Sequence 3, Appl
c 1034	39	2.3	235064	4	US-09-949-016-15390	Sequence 15390, A	1107	38.6	2.3	84	1	US-08-738-367-3	Sequence 3, Appl
c 1035	39	2.3	238815	4	US-09-949-016-16274	Sequence 16274, A	1108	38.6	2.3	91	4	US-09-621-976-14925	Sequence 14925, A
c 1036	39	2.3	258775	4	US-09-949-016-16435	Sequence 16435, A	1109	38.6	2.3	102	4	US-09-621-976-11436	Sequence 11436, A
c 1037	39	2.3	421491	4	US-09-949-016-12805	Sequence 12805, A	1110	38.6	2.3	299	4	US-09-621-976-10211	Sequence 10211, A
c 1038	39	2.3	421494	4	US-09-949-016-14060	Sequence 14060, A	1111	38.6	2.3	300	4	US-09-621-976-16227	Sequence 16227, A
c 1039	38.8	2.3	84	4	US-09-621-976-14577	Sequence 14577, A	1112	38.6	2.3	327	4	US-09-621-976-16018	Sequence 16018, A
c 1040	38.8	2.3	91	3	US-09-404-879A-201	Sequence 201, App	1113	38.6	2.3	344	2	US-08-623-906A-8	Sequence 8, Appl
c 1041	38.8	2.3	91	4	US-09-338-933-201	Sequence 201, App	1114	38.6	2.3	443	4	US-09-936-885A-1	Sequence 1, Appl
c 1042	38.8	2.3	91	4	US-09-215-681-201	Sequence 201, App	c1115	38.6	2.3	500	4	US-09-270-767-3118	Sequence 3118, Ap
c 1043	38.8	2.3	91	4	US-09-216-003A-201	Sequence 201, App	c1116	38.6	2.3	500	4	US-09-767-18400	Sequence 18400, A
c 1044	38.8	2.3	91	4	US-09-667-857-201	Sequence 201, App	1117	38.6	2.3	601	4	US-09-949-016-59330	Sequence 59330, A
c 1045	38.8	2.3	101	3	US-09-404-879A-293	Sequence 293, App	1118	38.6	2.3	601	4	US-09-949-016-126899	Sequence 126899, A
c 1046	38.8	2.3	101	4	US-09-338-933-293	Sequence 293, App	1119	38.6	2.3	601	4	US-09-949-016-180024	Sequence 180024, A
c 1047	38.8	2.3	101	4	US-09-215-681-293	Sequence 293, App	1120	38.6	2.3	700	3	US-09-152-060-26	Sequence 26, Appl
c 1048	38.8	2.3	101	4	US-09-216-003A-293	Sequence 293, App	c1121	38.6	2.3	986	4	US-09-328-475C-141	Sequence 141, App
c 1049	38.8	2.3	101	4	US-09-667-857-293	Sequence 293, App	1122	38.6	2.3	1027	3	US-09-465-558-57	Sequence 57, Appl

c1123	38.6	2.3	1279	3	US-09-248-335-25	Sequence 25, Appl	1196	38.4	2.3	7119	4	US-09-949-016-13558	Sequence 15358, A
c1124	38.6	2.3	1447	4	US-09-976-594-338	Sequence 338, App	c1197	38.4	2.3	78630	4	US-09-949-016-16790	Sequence 16790, A
1125	38.6	2.3	2031	4	US-09-417-251A-9	Sequence 9, Appl	c1198	38.4	2.3	129415	4	US-09-949-016-16997	Sequence 16997, A
1126	38.6	2.3	5021	4	US-09-949-016-786	Sequence 786, App	c1199	38.4	2.3	137394	4	US-09-949-016-13872	Sequence 13872, A
c1127	38.6	2.3	23569	4	US-09-949-016-12153	Sequence 12153, A	c1200	38.4	2.3	137743	4	US-09-949-016-12178	Sequence 12178, A
c1128	38.6	2.3	23574	4	US-09-949-016-15351	Sequence 15351, A	1201	38.4	2.3	150780	4	US-09-949-016-14711	Sequence 14711, A
1129	38.6	2.3	26843	4	US-09-949-016-11208	Sequence 17208, A	c1202	38.4	2.3	176373	3	US-09-128-153-17	Sequence 17, Appl
c1130	38.6	2.3	37292	4	US-09-949-016-15382	Sequence 15382, A	c1203	38.4	2.3	181429	4	US-09-949-016-12372	Sequence 12372, A
1131	38.6	2.3	43255	4	US-09-949-016-11909	Sequence 11909, A	c1204	38.4	2.3	181430	4	US-09-949-016-15772	Sequence 15772, A
1132	38.6	2.3	43507	4	US-09-949-016-13297	Sequence 13297, A	c1205	38.4	2.3	211049	4	US-09-949-016-15770	Sequence 15770, A
c1133	38.6	2.3	46841	4	US-09-949-016-13466	Sequence 13466, A	1206	38.4	2.3	251769	4	US-09-949-016-11185	Sequence 13185, A
1134	38.6	2.3	51259	3	US-08-781-891-209	Sequence 209, App	1207	38.4	2.3	251769	4	US-09-949-016-11186	Sequence 13186, A
c1135	38.6	2.3	51259	4	US-09-618-168-209	Sequence 209, App	1208	38.4	2.3	266748	4	US-09-949-016-13187	Sequence 13187, A
c1136	38.6	2.3	56326	4	US-09-949-016-16468	Sequence 16468, A	1209	38.4	2.3	266748	4	US-09-949-016-13188	Sequence 13188, A
c1137	38.6	2.3	95648	4	US-09-949-016-13139	Sequence 13139, A	c1210	38.4	2.3	784019	4	US-09-949-016-14033	Sequence 14033, A
1138	38.6	2.3	152331	3	US-09-128-155-16	Sequence 16, Appl	c1211	38.4	2.3	828152	4	US-09-949-016-12777	Sequence 12777, A
c1139	38.6	2.3	173992	4	US-09-949-016-13379	Sequence 13379, A	1212	38.2	2.3	83	4	US-09-621-976-12195	Sequence 12195, A
1140	38.4	2.3	80	1	US-07-920-281C-25	Sequence 25, Appl	1213	38.2	2.3	83	4	US-09-621-976-14751	Sequence 14751, A
1141	38.4	2.3	80	3	US-08-466-277-25	Sequence 25, App	1214	38.2	2.3	83	4	US-09-621-976-14959	Sequence 14959, A
1142	38.4	2.3	80	4	US-09-688-842-25	Sequence 25, Appl	1215	38.2	2.3	138	4	US-09-621-976-9595	Sequence 9595, Ap
c1143	38.4	2.3	106	4	US-09-621-976-12079	Sequence 12079, A	1216	38.2	2.3	232	4	US-09-621-976-11701	Sequence 17701, A
c1144	38.4	2.3	141	3	US-08-737-078A-1	Sequence 1, Appl	1217	38.2	2.3	253	4	US-09-621-976-13799	Sequence 12799, A
c1145	38.4	2.3	141	5	PCT-US94-04706-1	Sequence 1, Appl	c1218	38.2	2.3	271	2	US-08-731-272A-29	Sequence 29, Appl
1146	38.4	2.3	234	4	US-09-621-976-16557	Sequence 16557, A	1219	38.2	2.3	333	4	US-09-248-796A-11241	Sequence 11241, A
1147	38.4	2.3	250	4	US-09-621-976-18363	Sequence 18363, A	c1220	38.2	2.3	333	4	US-08-623-906A-13	Sequence 13, Appl
1148	38.4	2.3	366	4	US-09-252-991A-620	Sequence 620, App	c1221	38.2	2.3	601	4	US-09-949-016-32559	Sequence 32559, A
1149	38.4	2.3	366	4	US-09-134-000C-13	Sequence 13, Appl	c1222	38.2	2.3	601	4	US-09-949-016-32561	Sequence 32561, A
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c1151	38.4	2.3	601	4	US-09-949-016-48846	Sequence 48846, A	c1224	38.2	2.3	601	4	US-09-949-016-80104	Sequence 80104, A
1152	38.4	2.3	601	4	US-09-949-016-49018	Sequence 49018, A	1225	38.2	2.3	601	4	US-09-949-016-94321	Sequence 94321, A
c1153	38.4	2.3	601	4	US-09-949-016-49190	Sequence 49190, A	1226	38.2	2.3	601	4	US-09-949-016-126059	Sequence 126059, A
1154	38.4	2.3	601	4	US-09-949-016-49366	Sequence 49366, A	c1227	38.2	2.3	601	4	US-09-949-016-132201	Sequence 132201, A
c1155	38.4	2.3	601	4	US-09-949-016-127053	Sequence 127053, A	c1228	38.2	2.3	601	4	US-09-949-016-133406	Sequence 133406, A
1156	38.4	2.3	601	4	US-09-949-016-127054	Sequence 127054, A	1229	38.2	2.3	601	4	US-09-949-016-140018	Sequence 140018, A
c1157	38.4	2.3	601	4	US-09-949-016-127055	Sequence 127055, A	1230	38.2	2.3	601	4	US-09-949-016-155055	Sequence 155055, A
c1158	38.4	2.3	601	4	US-09-949-016-127056	Sequence 127056, A	c1231	38.2	2.3	601	4	US-09-949-016-155362	Sequence 155362, A
c1159	38.4	2.3	601	4	US-09-949-016-127058	Sequence 127058, A	c1232	38.2	2.3	601	4	US-09-949-016-155364	Sequence 155364, A
c1160	38.4	2.3	601	4	US-09-949-016-127059	Sequence 127059, A	c1233	38.2	2.3	601	4	US-09-949-016-173108	Sequence 173108, A
c1161	38.4	2.3	601	4	US-09-949-016-127060	Sequence 127060, A	c1234	38.2	2.3	601	4	US-09-949-016-173109	Sequence 173109, A
c1162	38.4	2.3	601	4	US-09-949-016-127061	Sequence 127061, A	1235	38.2	2.3	601	4	US-09-949-016-179952	Sequence 179952, A
1163	38.4	2.3	601	4	US-09-949-016-161233	Sequence 161233, A	c1236	38.2	2.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
1164	38.4	2.3	601	4	US-09-949-016-205887	Sequence 205887, A	1237	38.2	2.3	1074	3	US-09-248-335-67	Sequence 67, Appl
c1165	38.4	2.3	730	4	US-09-270-767-14600	Sequence 14600, A	1238	38.2	2.3	1100	3	US-07-861-458C-4	Sequence 4, Appl
c1166	38.4	2.3	912	4	US-09-252-991A-774	Sequence 774, App	1239	38.2	2.3	1325	1	US-08-306-691B-51	Sequence 51, Appl
1167	38.4	2.3	948	4	US-09-252-991A-643	Sequence 643, App	c1240	38.2	2.3	1325	2	US-08-464-517-1	Sequence 1, Appl
c1168	38.4	2.3	997	4	US-09-907-794A-376	Sequence 376, App	1241	38.2	2.3	1325	2	US-08-246-361A-1	Sequence 1, Appl
1169	38.4	2.3	997	4	US-09-905-125A-376	Sequence 376, App	1242	38.2	2.3	1325	3	US-08-463-772-1	Sequence 1, Appl
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1171	38.4	2.3	997	4	US-09-906-700-376	Sequence 376, App	1244	38.2	2.3	1663	4	US-09-464-535-43	Sequence 43, Appl
c1172	38.4	2.3	997	4	US-09-903-603A-376	Sequence 376, App	1245	38.2	2.3	1872	3	US-09-291-922-27	Sequence 27, Appl
1173	38.4	2.3	997	4	US-09-904-920A-376	Sequence 376, App	1246	38.2	2.3	2445	6	5215909-9	Patent No. 5215909
1174	38.4	2.3	997	4	US-09-909-064-376	Sequence 376, App	1247	38.2	2.3	2445	6	5215909-9	Patent No. 5215909
c1175	38.4	2.3	997	4	US-09-905-381A-376	Sequence 376, App	1248	38.2	2.3	2460	4	US-09-270-767-12063	Sequence 12063, A
1176	38.4	2.3	997	4	US-09-906-618-376	Sequence 376, App	1249	38.2	2.3	3157	4	US-09-949-016-16185	Sequence 16185, A
c1177	38.4	2.3	1518	4	US-09-614-913-191	Sequence 191, App	c1250	38.2	2.3	3958	4	US-09-949-016-13026	Sequence 13026, A
1178	38.4	2.3	1810	4	US-09-800-729-73	Sequence 73, App	c1251	38.2	2.3	10451	4	US-09-949-016-13192	Sequence 12192, A
c1179	38.4	2.3	1811	4	US-09-800-729-77	Sequence 77, Appl	c1252	38.2	2.3	12047	2	US-09-022-461-1	Sequence 1, Appl
c1180	38.4	2.3	1972	4	US-09-403-861A-1	Sequence 1, Appl	c1253	38.2	2.3	12047	3	US-09-033-556-3	Sequence 3, Appl
1181	38.4	2.3	3243	4	US-09-949-016-11186	Sequence 12186, A	c1254	38.2	2.3	12047	4	US-09-474-699-11	Sequence 11, Appl
c1182	38.4	2.3	4890	4	US-09-677-046A-3	Sequence 3, Appl	c1255	38.2	2.3	12047	4	US-09-151-376-3	Sequence 3, Appl
1183	38.4	2.3	4943	4	US-09-677-046A-7	Sequence 7, Appl	c1256	38.2	2.3	12047	4	US-09-814-351-11	Sequence 11, Appl
1184	38.4	2.3	5170	4	US-08-677-046A-5	Sequence 5, Appl	1257	38.2	2.3	15575	4	US-09-949-016-12634	Sequence 12634, A
1185	38.4	2.3	6124	3	US-08-213-419B-3	Sequence 3, Appl	1258	38.2	2.3	1325	4	US-09-949-016-16568	Sequence 16568, A
c1186	38.4	2.3	8642	4	US-10-029-907-2	Sequence 2, Appl	1259	38.2	2.3	20229	4	US-09-949-016-16649	Sequence 16649, A
1187	38.4	2.3	17656	3	US-09-433-579-3	Sequence 3, Appl	1260	38.2	2.3	20805	4	US-09-949-016-13772	Sequence 13772, A
c1188	38.4	2.3	36371	4	US-09-949-016-13876	Sequence 13876, A	1261	38.2	2.3	23907	4	US-09-949-016-13329	Sequence 15329, A
c1189	38.4	2.3	36274	4	US-09-949-016-13289	Sequence 13289, A	c1262	38.2	2.3	33237	4	US-09-949-016-14108	Sequence 14108, A
c1190	38.4	2.3	38099	4	US-09-949-016-13617	Sequence 13617, A	1263	38.2	2.3	33099	4	US-09-949-016-16094	Sequence 16094, A
1191	38.4	2.3	41708	3	US-09-470-512A-3	Sequence 3, Appl	c1264	38.2	2.3	33983	4	US-09-949-016-15700	Sequence 15700, A
c1192	38.4	2.3	41708	4	US-09-676-519-18	Sequence 18, Appl	1265	38.2	2.3	31639	4	US-09-949-016-15471	Sequence 15471, A
1193	38.4	2.3	41798	4	US-09-949-016-16058	Sequence 16058, A	1266	38.2	2.3	53336	4	US-09-949-016-12500	Sequence 12500, A
c1194	38.4	2.3	42348	4	US-09-949-016-17157	Sequence 17157, A	1267	38.2	2.3	53337	4	US-09-949-016-16092	Sequence 16092, A
1195	38.4	2.3	67479	4	US-09-949-016-11804	Sequence 11804, A	c1268	38.2	2.3	58397	4	US-09-949-016-14469	Sequence 14469, A

c1269	38.2	2.3	53076	4	US-09-949-016-15097	Sequence 15097, A	c1342	38	2.3	84587	4	US-09-949-016-15733	Sequence 15733, A
1270	38.2	2.3	62072	4	US-09-949-016-16076	Sequence 16076, A	c1343	38	2.3	117838	4	US-09-949-016-17595	Sequence 17595, A
c1271	38.2	2.3	82000	4	US-09-949-016-15595	Sequence 15595, A	c1344	38	2.3	124110	4	US-09-949-016-17533	Sequence 17533, A
1272	38.2	2.3	89689	4	US-09-949-016-13089	Sequence 13089, A	c1345	38	2.3	145812	4	US-09-949-016-15698	Sequence 15698, A
c1273	38.2	2.3	101356	4	US-09-949-016-12364	Sequence 12364, A	c1346	38	2.3	152070	4	US-09-949-016-15402	Sequence 15402, A
c1274	38.2	2.3	101357	4	US-09-949-016-16924	Sequence 16924, A	c1347	38	2.3	152486	4	US-09-949-016-12869	Sequence 12869, A
1275	38.2	2.3	106746	4	US-09-326-402C-1	Sequence 1, Appli	c1348	38	2.3	192700	4	US-09-949-016-11820	Sequence 11820, A
1276	38.2	2.3	106746	4	US-09-326-402C-12	Sequence 12, Appli	c1349	38	2.3	192704	4	US-09-949-016-17182	Sequence 17182, A
1277	38.2	2.3	107980	4	US-09-949-016-14370	Sequence 14370, A	c1350	38	2.3	205044	4	US-09-949-016-15851	Sequence 15851, A
1278	38.2	2.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c1351	38	2.3	205044	4	US-09-949-016-15852	Sequence 15852, A
1279	38.2	2.3	113876	4	US-09-949-016-14829	Sequence 14829, A	c1352	38	2.3	205044	4	US-09-949-016-15853	Sequence 15853, A
1280	38.2	2.3	115508	4	US-09-949-016-11800	Sequence 11800, A	c1353	38	2.3	223471	4	US-09-949-016-12387	Sequence 12387, A
1281	38.2	2.3	115508	4	US-09-949-016-14826	Sequence 14826, A	c1354	38	2.3	223471	4	US-09-949-016-12724	Sequence 12724, A
1282	38.2	2.3	115508	4	US-09-949-016-14827	Sequence 14827, A	c1355	38	2.3	223471	4	US-09-949-016-12725	Sequence 12725, A
1283	38.2	2.3	142504	4	US-09-949-016-13693	Sequence 13693, A	c1356	38	2.3	300598	4	US-09-949-016-11868	Sequence 11868, A
1284	38.2	2.3	142504	4	US-09-949-016-12474	Sequence 12474, A	c1357	38	2.3	302604	4	US-09-949-016-14589	Sequence 14589, A
c1285	38.2	2.3	149971	4	US-09-949-016-13590	Sequence 13590, A	c1358	38	2.3	302604	4	US-09-949-016-14589	Sequence 14589, A
c1286	38.2	2.3	157822	4	US-09-949-016-16723	Sequence 16723, A	c1359	38	2.3	308362	4	US-09-949-016-17119	Sequence 17119, A
1287	38.2	2.3	161124	4	US-09-949-016-11760	Sequence 11760, A	c1360	38	2.3	389504	4	US-09-949-016-11774	Sequence 11774, A
c1288	38.2	2.3	183770	4	US-09-949-016-15494	Sequence 15494, A	c1361	37.8	2.3	165	4	US-09-621-976-8127	Sequence 8127, Ap
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ALIGNMENTS

RESULT 1

US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
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Query Match 99.0%; Score 1661.4; DB 4; Length 1693;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1265 CAATGAAATTAGAAGAAACACAGCCTCATGCGGACAGAAATTTGAGGAGGGGGAACAAAG 1324
Db |||||
QY 1261 CAATGAAATTAGAAGAAACACAGCCTCATGCGGACAGAAATTTGAGGAGGGGGAACAAAG 1320
Db |||||
QY 1325 AATACTTTGGGGGAAAAGAGTTTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATATTTA 1384
Db |||||
QY 1321 AATACTTTGGGGGAAAAGAGTTTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATATTTA 1380
Db |||||
QY 1385 GGTACAAATGGAGTTTTTCTTTTCCCAACCGGGAAGAAACACAGCACACCCGGGCTTGGACCCA 1444

Db |||||
QY 1381 GGTACAAATGGAGTTTTTCTTTTCCCAACCGGGAAGAACACAGACACACCCGGCTTGGACCCA 1440
Db |||||
QY 1445 CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTG 1504
Db |||||
QY 1441 CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTG 1500
Db |||||
QY 1505 CCCACAGAGTGCCCCACGTCGGAACATTTCTGGAGCTGGCCATCCCAATTCAAATCAGTCC 1564
Db |||||
QY 1501 CCCACAGAGTGCCCCACGTCGGAACATTTCTGGAGCTGGCCATCCCAATTCAAATCAGTCC 1560
Db |||||
QY 1565 ATAGAGACGAACAGATGAGACCTTCCGGGCCAAAGCGTGGCGCTCGCGGCACCTTTGGTAG 1624
Db |||||
QY 1561 ATAGAGACGAACAGATGAGACCTTCCGGGCCAAAGCGTGGCGCTCGCGGCACCTTTGGTAG 1620
Db |||||
QY 1625 ACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATAAAAAAGACAAAAAAA 1679
Db |||||
QY 1621 ACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATAAAAAAGACAAAAAAA 1675
Db |||||

RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700.397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1

Query Match 61.5%; Score 1032; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 4.3e-273;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ATGAAAAACCATCCAGCCAAAAAATGCACAAATTTCTATCTTTGGGCAATCTTTCACGGGGCTG 193
Db 1 ATGAAAAACCATCCAGCCAAAAAATGCACAAATTTCTATCTTTGGGCAATCTTTCACGGGGCTG 60

QY 194 GCTGCTCTGTGTCTTTCCAGAGGATGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 253
Db 61 GCTGCTCTGTGTCTTTCCAGAGGATGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 120

QY 254 GCTATGGAACAACGTGACCGTCCGGCAGGGGAGAGCGCACCTCAGGTGCATCTATTTCAC 313
Db 121 GCTATGGAACAACGTGACCGTCCGGCAGGGGAGAGCGCACCTCAGGTGCATCTATTTCAC 180

QY 314 AACCGGGTTCACCCGGGTGGCTTAAACCGCAGCACCCTCTATCTATCTGTTGGGAATGAC 373
Db 181 AACCGGGTTCACCCGGGTGGCTTAAACCGCAGCACCCTCTATCTATCTGTTGGGAATGAC 240

QY 374 AAGTGGTCTCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 433
Db 241 AAGTGGTCTCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 300

QY 434 GAGATCCAGAAACGTGGATGTGTATGACCGAGGGCCCTTACACCTGCTCGTGCAGACAGAC 493
Db 301 GAGATCCAGAAACGTGGATGTGTATGACCGAGGGCCCTTACACCTGCTCGTGCAGACAGAC 360

QY 494 AACCAACCAAGAGACTCTAGGGTCCACTCTATTTGTGCAAGTATCTCCCAAAAATTTAGAG 553
Db 361 AACCAACCAAGAGACTCTAGGGTCCACTCTATTTGTGCAAGTATCTCCCAAAAATTTAGAG 420

554 ATTCTTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCTCACCCTGCAATAGCAACT 613
421 ATTCTTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCTCACCCTGCAATAGCAACT 480
614 GTGAGACAGAGCCTACGGTTACTTGGAGACACATCTCCCAAGCGGTTGGCTTTGGT 673
481 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCCCAAGCGGTTGGCTTTGGT 540
674 AGTGAAGACGAATATCTTGAATAATCAGGGCATCACCCGGGAGCAGTCAAGGACTACGAG 733
541 AGTGAAGACGAATATCTTGAATAATCAGGGCATCACCCGGGAGCAGTCAAGGACTACGAG 600
734 TGCAGTGCCTCAATGAAGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACGTTGAAC 793
601 TGCAGTGCCTCAATGAAGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACGTTGAAC 660
794 TATCACCACATATCTTGAAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
661 TATCACCACATATCTTGAAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
854 CTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGATGACAAA 913
721 CTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGATGACAAA 780
914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGGAAACAGACCTTTCTCTCAAAACTC 973
781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGGAAACAGACCTTTCTCTCAAAACTC 840
974 ATCTTCTCAATGTCTTGAACATGACTATGGAAGTGAAGTGGGAACTACACTTGGTGGCCTCCAAACAG 1033
841 ATCTTCTCAATGTCTTGAACATGACTATGGAAGTGAAGTGGGAACTACACTTGGTGGCCTCCAAACAG 900
1034 CTGGGCCACACCAATGCCAGCATCATGTTATTTGGTCCAGGGCGCGTCAAGCAGGTGAGC 1093
901 CTGGGCCACACCAATGCCAGCATCATGTTATTTGGTCCAGGGCGCGTCAAGCAGGTGAGC 960
1094 AACGCGAGTCAAGAGGCGCAGGCTGCGTTCGGCTGCTGCTTCTTGGTCTTGGCACCTG 1153
961 AACGCGAGTCAAGAGGCGCAGGCTGCGTTCGGCTGCTGCTTCTTGGTCTTGGCACCTG 1020
1154 CTCTCAAAATTT 1165
1021 CTCTCAAAATTT 1032

RESULT 3

US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: G61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-5

Query Match 55.9%; Score 939; DB 4; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.4e-247;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
227 GCGAGCGGAGATGCCACCTTCCCAAGCTATGGACAAAGTGAACGCTGCGGACGGTCCGGCAGGGGAG 286

1 CGCAGCGGAGATGCCACCTTCCCAAGCTATATGGAACAGCTGACGGTCCCGGAGGGGAG 60
287 AGCGCCACCCCTCAGGTGCACTATTGCAACACCGGTCACCCGGGTGGCTTAAACCCG 346
61 AGCGCCACCCCTCAGGTGCACTATTGCAACACCGGTCACCCGGGTGGCTTAAACCCG 120
347 AGCAACATCTCTATGCTGGGAATGCAAGTGGTGCCTGGATCCTCGCGTGTCTTCTG 406
121 AGCAACATCTCTATGCTGGGAATGCAAGTGGTGCCTGGATCCTCGCGTGTCTTCTG 180
407 AGCAACACCCCAACCGCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACGAGG 466
181 AGCAACACCCCAACCGCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACGAGG 240
467 CTTTACACCTGCTCGGTGCAGACAGCAACACCAAGACCTCTAGGGTCCACCTCATTT 526
241 CTTTACACCTGCTCGGTGCAGACAGCAACACCAAGACCTCTAGGGTCCACCTCATTT 300
527 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCCAATTAATGAAGGAA 586
301 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCCAATTAATGAAGGAA 360
587 AATATTAGCCTCAGCTGCACTAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGAC 646
361 AATATTAGCCTCAGCTGCACTAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGAC 420
647 ATCTCTCCCAAGCGGTTGGCTTTGCTGAGTGAAGACGAATCTTGGAAATTCAGGGCATC 706
421 ATCTCTCCCAAGCGGTTGGCTTTGCTGAGTGAAGACGAATCTTGGAAATTCAGGGCATC 480
707 ACCGGGAGCAGTCAAGGAGCTACAGTGCAGTGCCTCCAATGACGTGCGCGCCGCGTG 766
481 ACCGGGAGCAGTCAAGGAGCTACAGTGCAGTGCCTCCAATGACGTGCGCGCCGCGTG 540
767 GTACGGAGATTAAGGTCAACGTGAACTATCCACCATACATTTCAAGAGCCAAAGGTACA 826
541 GTACGGAGATTAAGGTCAACGTGAACTATCCACCATACATTTCAAGAGCCAAAGGTACA 600
827 GGTGTCCTCCGCTGGGACAAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCA 886
601 GGTGTCCTCCGCTGGGACAAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660
887 GAATTCAGTGGTACAAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTG 946
661 GAATTCAGTGGTACAAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTG 720
947 GAAAACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGG 1006
721 GAAAACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGG 780
1007 AACTACACTTGGTGGCTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTT 1066
781 AACTACACTTGGTGGCTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTT 840
1067 GGTCCAGCGCGCTCAGCAGAGTGAAGCAACCGCAGCTCGAGGAGGCGGCTCGCTGCG 1126
841 GGTCCAGCGCGCTCAGCAGAGTGAAGCAACCGCAGCTCGAGGAGGCGGCTCGCTGCG 900
1127 CTGCTGCCTCTTCTGGTCTTGGACCTGCTCTCAAAATTT 1165
901 CTGCTGCCTCTTCTGGTCTTGGACCTGCTCTCAAAATTT 939

RESULT 4

US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria

;; TITLE OF INVENTION: Limbic System-Associated Membrane
;; TITLE OF INVENTION: Protein and DNA
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 31743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1238 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 56...1069
;; OTHER INFORMATION:
US-08-414-657D-3

Query Match 20.4%; Score 343; DB 2; Length 1238;
Best Local Similarity 62.0%; Pred. No. 9.5e-84;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;
QY 205 TCTCTTCCAAAGAGTGCCCGTGCAGCGGAGATGCCACCTTCCCAAGAGCTATGACAA 264
DB 121 TCTTCCACAGGACTGCCCGTTCGCGAGCGTGGAT-----TTTAAACCGAGGCACGACAA 174
QY 285 CQTGACGTCGGCAGGGGGAGAGCGCCACCTCAGGTGCACATTTGACAAACCGGCTCAC 324
DB 175 CATCACCGTGAGCGAGGGGGACACGGCCATCTCAGGTGTGTGGTGAAGACAAAGACTC 234
QY 325 CGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAGTGTGGCT 384
DB 235 GAAAGTGGCCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGACACAGTGTCTCT 294
QY 385 GGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
DB 295 GGACCTCGGGTTGAGCTGGAGAAACGCGCATCTCTGGAATACAGCCTCCGAATCCAGAA 354
QY 445 CQTGATGTGTATGACGAGGGGCCCTTACACCTGCTGGTGGAGACAGACAAACCCAA 504
DB 355 GGTGGATGTCTATGATGAAGGATCTTACACATGCTCAGTTTCAGACACAGCATGAGCCAA 414
QY 505 GACCTTAGGGTCCACCTCATTTGTCAGTATCTCCAAAATTTGAGAGATTTCTTCAGA 564
DB 415 GACCTCTCAAGTTTACTTGAATGTGAAGTTCCAAAGATCTTCAACATCTCTCTCGA 474
QY 565 TATCTCCATTAATGAAGGAAACAATATTAGCCCTACCTGATGACAACTGGTAGACAGA 624
DB 475 TGTCTACTGTGAATGAGGGCAGCAATGTAAACCTTGTCTGATGGCCAAATGGCGCCCTGA 534

QY 625 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACA 684
DB 535 ACCTGTTATACCTGGAGACACCTTACACCACTTGGAGAGAAATTTGAAGAGAGAGA 594
QY 685 ATACTTGGAAATTCAGGGCATCACCCGGAGAGTACAGGGAGTACAGAGTCAAGTGCCTC 744
DB 595 ATATCTGGAGATCTAGGCATCACAGGAAACAGTCAAGGCAAAATATGATGCAAGGCTGC 654
QY 745 CAATGACGTGGCCCGCGCGTGGTACGAGAGTAAAGTCAACCGTCACTATCCACCA 804
DB 655 CAACGAGGTCTCTCCCGCGGATGTCAAAACAAGTCAAGTCACTGTGAATATCACCAC 714
QY 805 CATTTCAAGACCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACACCTGCAAGTGA 864
DB 715 CATCACAGAGTCTAAGAGCAATGAAGCACACAGGAGCAAGCTTCCCTCAATGTGA 774
QY 865 AGCCTCAGCAGTCCCCTCAGCAGAAATTCAGTGTACAAAGGATGACAAAGACTGATGA 924
DB 775 AGCCTCAGCGGTGCTGCACCTGACTTGTAGTGTGACCGGATGACACAG---GATAAA 831
QY 925 AGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAAACTCATCTTCTCAA 984
DB 832 CAGTGCRAAACGSCCTTGAGATTAAAGAGCACTGAGGGCCAGTCTCTCCCTGAACGGTGA 891
QY 985 TGTCTCTGAACATGACTATATGGAATACACTTGGTGGCTTCCAAAGCTGGGGCCACAC 1044
DB 892 CGTCACTGAGGAACTACGCAACTATACCTGTGTGGTCCCAACAGCTCGGGCTCAC 951
QY 1045 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGCAACGGCACGTC 1104
DB 952 CAATGCCAGCTAGTCTCTTTTTCAGACCCGGGTGGTGA---AGGAATCAACGGATCCAT 1008
QY 1105 GAGGAGGGCAGGCTGCTGCTGGCTGCTGCTCTTCTGCTGACCTGCTTCTCAAAAT 1164
DB 1009 CAGTCTGGCGGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCTTCTCAGCAATG 1069
QY 1165 TTGAT 1169
DB 1069 TTAAT 1073
RESULT 5
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1238 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 56...1069

OTHER INFORMATION:

US-09-135-080-3

Query Match 20.4%; Score 343; DB 3; Length 1238;
Best Local Similarity 62.0%; Pred. No. 9.5e-84;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

QY 205 TCTCTCCAGAGTCCCGTGGCGAGCGGAGTCCACCTTCCCAAGCTATGACAA 264
DB 121 TCTTCCACAGGACTGCCCGTTCCGACGTGGAT-----TTTAAACCGAGGACGACAA 174
QY 265 CGTGACGCTCGCGAGGGGAGCGCCACCTCAGGTGCACACTATTGACACGGGTAC 324
DB 175 CATCACCGTGGAGGGGAGCACGGCCATCTCTAGGTGTGGTAGAACAAGAACATC 234
QY 325 CGGGTGGCTGGCTAAACCGCAGCACCACTCTCTATGCTGGGAATGACAACTGGTGCCT 384
DB 235 GAAAGTGGCTGGTGAACCGCTCTGCATCATCTTCGCTGCACGACAACTGGTCTCT 294
QY 385 GAACTCTCGCGTGGCTTCTTCTGAGCAACACCCAAACGACGATCAGATCAGATCAGAA 444
DB 295 GGACCTCGGGTGGAGTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354
QY 445 CGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACAGCAACACCCCAA 504
DB 355 GGTGATGTCTATGAAGGATCTTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414
QY 505 GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCAGA 564
DB 415 GACCTCTCAAGTTTACTTGATTGTACAGTTCCACCAAGATCTCCAACTCTCTCGA 474
QY 565 TATCTCCATTAATGAGGAAACAATATAGCTCTACCTGATGACATGAGTGTAGACCGA 624
DB 475 TGTCACTGTGAATGAGGGCAGCAATGTAAACCTGTGTCTGATGGGCAATGGGCGCCTGA 534
QY 625 GCCTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTAGTGAAGACGA 684
DB 535 ACCTGTTATCACTGGAGACACTTACACCACTTGGAGAGAAATTTGAAGGAGAGAGAA 594
QY 685 ATACTTGGAAATTCAGGGGATCACCGGGAGCAGTACGGGGACTACGAGTGCAGTGCCTC 744
DB 595 ATATCTGGAGATCTTAGGCATCACCAAGGAAACAGTCAGGCAATATAGTGCAGGCTGC 654
QY 745 CAATGACGTGGCGGCCCGCTGGTACGGAGAGTAAGGTTCACCGTGAATATCCACCATTA 804
DB 655 CAACGAGGTCTCTCCGCGGATGTCAACAAGTCAAGGTCACTGTGAATATATCCACCCAC 714
QY 805 CATTTTCAGAGCCAGGGTACAGGTGTCTCCCGTGGGACAAAGGGGACACTGCACTGTGA 864
DB 715 CATCACAGAGTCTAAGAGCAATGAAGGCCACCAAGGACGACAAAGTCTCCCTCAATGTGA 774
QY 865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAAGACTGATTGA 924
DB 775 AGCCTCAGCGGTGCTTGACCTGACTTTGAGTGGTACCGGGATGACACAG---GATAAA 831
QY 925 AGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCTCAAAACTCATCTTCTTCAA 984

DB 832 CAGTGCAAACCGCCTTGAGATTAAAGGACACTGAGGCGCAGTCTCCTGACGGTGACCAA 891
QY 985 TGTCTCTGAACATGACTATGGGAACCTACACTTTCGTGGCTCCAAACAGCTGGGCCACAC 1044
DB 892 CGTCACTGAGGAACACTACGGCACTTATACCTGTGTGGCTGCCAACAGCTGGCGTCA 951
QY 1045 CAATGCCAGCAATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
DB 952 CAATGCCAGCTAGTCCCTTTTTCAGACCCCGGTGGTGGAG---AGGAATCAACGGATCCAT 1008
QY 1105 GAGGAGGCGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
DB 1009 CAGTCTGGCGGTACCACACTGTGGCTGCTGCGACGCTCCCTGTTCTGCTTCTCAGCAAATG 1068
QY 1165 TTGAT 1169
DB 1069 TTAAT 1073

RESULT 6

US-09-976-594-403

Sequence 403, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO 403

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 1640555CBI

US-09-976-594-403

Query Match 20.3%; Score 341.6; DB 4; Length 1195;
Best Local Similarity 60.1%; Pred. No. 2.3e-83;
Matches 626; Conservative 0; Mismatches 404; Indels 12; Gaps 3;

QY 205 TCTCTTCCAGGAGTGCCCGTGGCGAGCGGAGATGCCACCTTCCCCAAAGCTATGACAA 264
DB 66 TCTTCCACAGGACTGCTGCTGTCGCGAGCTGGAT-----TTTAAACCGAGGACGACAA 119
QY 265 CGTGACGCTCGCGAGGGGAGAGCGCCACCTCAGTGCACATTTGACAAACGGGTGAC 324
DB 120 CATCACCGTGGAGCGAGGGGACACAGCCATCTCTAGGTGCGTCTAGAAAGACAAGATCTC 179
QY 325 CGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAACTGGTGCCT 384
DB 180 AAGGTGGCTGGTGTGAACCGCTTCTGGCATCATTTTGTGTCGACATGACAAGTGGTCTCT 239
QY 385 GGAATCTCGGTGGTCTTCTGAGCAACACCCAAACGCGATACAGATCAGATCAGATCAGAA 444
DB 240 GGAACCGGGTGGAGCTGGAGAAACGCCATTTCTCTGGAATACAGCCTCCGAATCCAGAA 299
QY 445 CGTGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGACAGACAGCAACACCCCAA 504
DB 300 GGTGGATGTCTATGATGAGGGTTCCTACATTTGCTCAGTTCAGTTCAGACACAGCATGAGCCCAA 359
QY 505 GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGA 564
DB 360 GACCTCCCAAGTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
QY 565 TATCTCCATTAATGAAGGAAACAATATTAGCCTCACTGATGCAACTGGTAGACAGCA 624

[illegible]

RESULT. T 7

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US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;
; GENERAL INFORMATION:
;
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
;
; TITLE OF INVENTION: Limbic System-Associated Membrane
;
; TITLE OF INVENTION: Limbic System-Associated Membrane
;
; NUMBER OF SEQUENCES: 60
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
;
; ZIP: 08543
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;

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QY 865 AGCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGGATGACAAAGACTGATTGA 924
 DB 699 GGCCTCGGAGTGGCTCGACCTGACTTTGAGTGGTACCGGATGACACTAG---GATAAA 755
 QY 925 AGGAAGAAAGGGGTGAGAGTGGAAACAGACCTTCTCTCAAACTCATCTTCTCAA 984
 DB 756 TAGTGCCATGCGCTTGAGATTAAAGAGCAGGAGGCGCAGTCTTCCTGACGGTACCAA 815
 QY 985 TGTCTCTGAACATGACTATGGGAATCTACACTTGGCGTGGCTCCAAAGCTGGGCGACAC 1044
 DB 816 CGTCACTGAGGAGCACTACGCACTACACTGTGTGGTGGTGCACACAGCTGGGGTCCAC 875
 QY 1045 CAATGCCAGCATCATCTATTGGTCCAGGCGCGCTCAGCG 1085
 DB 876 CAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGGGTGAGAG 916

RESULT 8

US-08-414-657D-1
 ; Sequence 1, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-Seq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 977 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 2...976
 OTHER INFORMATION:
 US-08-414-657D-1

Query Match 20.3%; Score 340.6; DB 2; Length 977;
 Best Local Similarity 63.3%; Pred. No. 3.8e-83;
 Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 205 TCTCTTCAAGAGTGGCCGTCGCGAGGGAGATGCCACCTTTCCCAAGCTATGACAA 264
 DB 46 TCTTCCCAAGACTGCTCTGTTGCGAGCGTGTGAT-----TTTAAACCGAGGACGACAA 99
 QY 265 CGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTCCAC 324
 DB 100 CATCACCGTGGAGCGAGGGGACACAGCCATCTCTAGGTGCGTCTTAGAAGACAAAGACTC 159
 QY 325 CCGGCTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGGTGCCT 384
 DB 160 AAAGTGGCTGGTTGAACCGTTCTGGCATCATTTTGTGTCGACATGACAAAGTGGTCTCT 219
 QY 385 GATCTCTCGGTGGTCTCTTCTGAGCAACACCAACGAGTACAGCATCGAGATCGAGAA 444
 DB 220 GGACCCACGGGTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCTCCGAATCCAGAA 279
 QY 445 CGTGATGTATGACAGGGGCGCTTACACCTGCTCGGTGCGAGACAGACCAACCCCAA 504
 DB 280 GGTGATGTCTATGATGAGGGTTCCTACATTGCTGCTAGTTCAGACACAGCATGAGGCCAA 339
 QY 505 GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCA 564
 DB 340 GACCTCCCAAGTTTACTTGTATCGTACAAAGTCCCAACCAAGATCTCCAATATCTCTCGA 399
 QY 565 TATCTCCATTAATGAAGGAAACAATATTAGCTCTACCTGCTAGCACTGCTGAGACCA 624
 DB 400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGCTGCTGCTGCTGCTGCTGCTGCT 459
 QY 625 GCCTACGGTGTCTGAGAGACATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACCA 684
 DB 460 ACCTGTTATCCTGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAGAGAA 519
 QY 685 ATACTTGGAAATTCAGGGGATCACCCGGGAGCAGTCAGGGGACTACAGTGCAGTGCCTC 744
 DB 520 ATATCTGAGATCTCTTGGCATCACCCAGGGAGCAGTCAGGCAATATGAGTGCAGAGCTG 579
 QY 745 CAATGACGTGGCGCGCGCTGCTGAGAGAGTAAAGTCAAGTCAAGTCAAGTCAAGTCAAG 804
 DB 580 CAAAGAGGTCTCTCGCGGATGTCAAAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 639
 QY 805 CATTTCAAGAGCAGGTGACAGGTGTCCTCGTGGGAGCAAAAGGGGACACTGACGTGGA 864
 DB 640 TATCAGAAATCCAAAGCAATGAAGCCACCAAGCAGACAGCAAGCTTCACTCAAAATGTA 699
 QY 865 AGCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGGATGACAAAGACTGATTGA 924
 DB 700 GGCCTCGGAGTGGCTGCACTGCTTGTGAGTGGTACCGGGATGACACTAG---GATAAA 756
 QY 925 AGGAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAA 984
 DB 757 TAGTGCCATGCGCTTGAGATTAAAGAGCAGGAGGCGCAGTCTTCCCTGACCGTACCAA 816
 QY 985 TGTCTCTGAACATGACTATGGAACTACACTGCTGGCGCTCCAAAGCTGGGCGACAC 1044
 DB 817 CGTCACTGAGGAGCACTACGGCAACTACCTGTGTGGTGGTGGTGGTGGTGGTGGTGGT 876
 QY 1045 CAATGCCAGCATCATCTATTGGTCCAGGCGCGCTCAGCG 1085
 DB 877 CAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGGGTGAGAG 917

RESULT 9

US-09-135-080-1
 ; Sequence 1, Application US/09135080
 ; Patent No. 6423827
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat R.
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 29


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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
US-08-414-657D-5

Query Match      20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

QY 205 TCTCTTCCAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGACAA 264
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCACAGGACTGCCCGTTCGACGCTGGAT-----TTTAACCGAGGACGACAA 119
QY 265 CGTGAGGTCGGCAGCGGAGGAGCGCCACCTCAGGTGCACTATTGACAAACCGGTAC 324
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGGAGGAGGACACGGCCATCTCTCAGGTGTGGTAGAAGACAGAACTC 179
QY 325 CCGGTGGCTGGCTAAACCGCAGCACCCTCTATGCTGGAAATGACAAGTGTGCT 384
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
180 GAAAGTGGCTGGTGAACCGCTCTGGCAATCATCTTCGCTGGACGACGAACTGTCT 239
QY 385 GGATCCTCGCGTGTCTTCTGAGCAACACCCAAAGCAGTACAGCATCGAGATCCAGAA 444
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 GCACCTCGGTGGTGGAGGAGGAGGAGCGCCATCTCTGGAATACAGCTCCGAATCCAGAA 299
QY 445 CGTGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 504
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 GGTGATGTATGATGAGGAGTCTTACACATGCTCAGTTCAGACACAGCATGAGGCCAA 359
QY 505 GACCTTAGGTCACCTCATTTGTCAGTATCTCCAAATTTAGAGATTTCTTCAGA 564
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
360 GACCTCTCAAGTTTACTTGAATGTACAGTTCACCAAGATCTCCAAATCTCTTCGA 419
QY 565 TATCTCCATTAATGAAGGAAACAATATTAGCCTCAGTATGCAAGCACTGGTAGACAGA 624
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
420 TGTCACTGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
QY 625 GCCTAGGTTACTTGGAGACATCTCTCCAAAGGAGTGTGCTTGTGAGTGAAGAGA 684
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
480 ACCTGTATACCTGAGACACCTTACACCTTGGAGAGAAATTTGAAGAGAGAGAGAGA 539
QY 685 ATACTTGAAATTCAGGAGCATCACCGGAGGAGTACAGGAGTACAGTGCAGTGCCTC 744
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
540 ATATCTGGAGATCTTAGGATCACCAGGGAACAGTACAGGCAATATGAGTGAAGGCTGC 599
QY 745 CAATGACGTGGCGCGCGTGTAGGAGAGTAAAGGTCAACGTAATCCACCATTA 804
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
600 CAACGAGGTCTCTCGCGGATGTCAAAACAAGTCAAGGTCACTGTGAATATCCACCCAC 659
QY 805 CATTTAGAGCAAGGAGTACAGGTGTCCCGTGGGACAAAGGGGACACTCGAGTGTGA 864
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 CATCACAGTCTAAGAGCAATGAAGCAACCAACAGGACGACAAAGCTTCCCTCAAAATGTA 719
QY 865 AGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTACAGGATGACAAAGACTGATTGA 924
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
720 AGCCTCAGCGGTGCGCTCAGCAGTCTTGAAGTGTACCGGATGACACAG---GATAAA 776
QY 925 AGGAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAACTCATCTTCTCAA 984
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
777 CAGTGCMAACGGCTTGAGTTAAGGACACTGAGGAGGAGTCTCTCCCTGACGGTGACCA 836
QY 985 TGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTTCAACAGCTGGGACAC 1044
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
837 CGTCACTAGAGGAACACTACGGCAACTATACCTGTGTGGCTGCGCAACAGCTCGGGCTC 896
QY 1045 CAATGCCAGCATCATCTATTGTTCCAGGCGGCTCAGCAGGAGTGAAGCAACGGCAGCTC 1104
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
897 CAATGCCAGCTAGTCTCTTTTTCAGACCCCGGTCGGGTGAG---AGGAATCAACGGATCCAT 953

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QY 1105 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1164
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
954 CAGTCTGGCCGTACCACACTGTGGCTGTGGCAGCGTCCCTGTCTGCTTCTCAGCAATG 1013
QY 1165 T 1165
Db      1014 T 1014

RESULT 11
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
US-09-135-080-7

Query Match      20.3%; Score 340.6; DB 3; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

QY 205 TCTCTTCCAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGACAA 264
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCACAGGACTGCCCGTTCGACGCTGGAT-----TTTAACCGAGGACGACAA 119
QY 265 CGTGAGGTCGGCAGCGGAGGAGCGCCACCTCAGGTGCACTATTGACAAACCGGTAC 324
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 179
QY 325 CCGGTGGCTGGCTTAAACCGCAGCACCCTCTATGCTGGAAATGACAAGTGTGCT 384

```

```

;
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
; US-08-414-657D-9
;
; Query Match 20.2%; Score 338.6; DB 2; Length 861;
; Best Local Similarity 63.7%; Pred. No. 1.2e-82;
; Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
;
; QY 253 AGCTATGACAAACGTCGCGTCCGGCAGGGGAGAGGCGCCACCTTCAGGTGCACATTATGA 312
; DB 24 AGGCACGACAAACATCACCGTGAGCAGGGGAGACAGCCATCTCAGTGGTCTTAGA 83
; QY 313 CAACGGGTGTCACCGGGTGGCTTAAACCGCAGACACCATCTCTATGCTGGGAATGA 372
; DB 84 AGACAAGAACTCAAAGGTGGCTGTTGAAACCGTCTGGCATCATTTTGTGGACATGA 143
; QY 373 CAAGTGGTGGCTGGATCTTCGGTGGTCTTCTGAGCAACACCCAAACGCGAGTACAGCAT 432
; DB 144 CAAGTGGTCTCTGACCCACCGGTTGAGCTGGAGAAACGCCATTCTCTGGAAATACAGCT 203
; QY 433 CGAGATCCAGAAACCTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
; DB 204 CCGAATCCAGAGGTGGATGTCTATGATGAGGGTCTCTACACTTCTCAGTTCAGACACA 263
; QY 493 CAACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTAGA 552
; DB 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGTAGTGGGAGCAACCGTACTCTGGTCTGATGGCCAA 323
; QY 553 GATTCTTCAGATATCTCCATTATGAGGGAACAAATATTAGCTCACCCTGCATAGCAAC 612
; DB 324 TATCTCTCGGATGTCTACTGTGAATGAGGGCAGCAACCGTACTCTGGTCTGATGGCCAA 383
; QY 613 TGGTAGACGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGTGGTTGT 672
; DB 384 TGGCCGCTCTGAACCTGTTATCACCTGGAGACACCTTACACCACTGGAAGGAATTTGA 443
; QY 673 GAGTGAAGCAATATCTTGGAAATTCAGGGGATATACCCGGGAGCAGTCAAGGGGACTAGA 732
; DB 444 AGGAGAAGAAATATCTGGAGATCTTGGGATCTTGGGATCACCAGGGGAGCAGTCAAGCAATATGA 503

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```

;
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
; US-08-414-657D-9
;
; Query Match 20.2%; Score 338.6; DB 2; Length 861;
; Best Local Similarity 63.7%; Pred. No. 1.2e-82;
; Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
;
; QY 253 AGCTATGACAAACGTCGCGTCCGGCAGGGGAGAGGCGCCACCTTCAGGTGCACATTATGA 312
; DB 24 AGGCACGACAAACATCACCGTGAGCAGGGGAGACAGCCATCTCAGTGGTCTTAGA 83
; QY 313 CAACGGGTGTCACCGGGTGGCTTAAACCGCAGACACCATCTCTATGCTGGGAATGA 372
; DB 84 AGACAAGAACTCAAAGGTGGCTGTTGAAACCGTCTGGCATCATTTTGTGGACATGA 143
; QY 373 CAAGTGGTGGCTGGATCTTCGGTGGTCTTCTGAGCAACACCCAAACGCGAGTACAGCAT 432
; DB 144 CAAGTGGTCTCTGACCCACCGGTTGAGCTGGAGAAACGCCATTCTCTGGAAATACAGCT 203
; QY 433 CGAGATCCAGAAACCTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
; DB 204 CCGAATCCAGAGGTGGATGTCTATGATGAGGGTCTCTACACTTCTCAGTTCAGACACA 263
; QY 493 CAACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTAGA 552
; DB 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGTAGTGGGAGCAACCGTACTCTGGTCTGATGGCCAA 323
; QY 553 GATTCTTCAGATATCTCCATTATGAGGGAACAAATATTAGCTCACCCTGCATAGCAAC 612
; DB 324 TATCTCTCGGATGTCTACTGTGAATGAGGGCAGCAACCGTACTCTGGTCTGATGGCCAA 383
; QY 613 TGGTAGACGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGTGGTTGT 672
; DB 384 TGGCCGCTCTGAACCTGTTATCACCTGGAGACACCTTACACCACTGGAAGGAATTTGA 443
; QY 673 GAGTGAAGCAATATCTTGGAAATTCAGGGGATATACCCGGGAGCAGTCAAGGGGACTAGA 732
; DB 444 AGGAGAAGAAATATCTGGAGATCTTGGGATCTTGGGATCACCAGGGGAGCAGTCAAGCAATATGA 503

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RESULT 12
 US-08-414-657D-9
 ; Sequence 9, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:

```

QY 733 GTGAGTGTGCTCAATGAGTGGCGCGCGCGTGGTACGAGAGTAAAGGTCAACGGTGA 792
Db 504 GTGCAAGCTGCAACGAGGTCTCTCGCGGATGTCAAAAGTCAAGGTCACTGTGA 563
QY 793 CTATCCACCATATTTGAGAGCAAGGTACAGGTGTCCTCGGTGGGACAAAGGGAC 852
Db 564 CTATCTCTCCCACTATCAAGAGCAATCAAGAGCAATGAAGCCACCAAGAGGCTTC 623
QY 853 ACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 912
Db 624 ACTCAATGTGAGGCTTGGGAGTCCCTGACCTGACTTGTAGTGGTACCGGATGAC 683
QY 913 AAGACTGATGAAGAAAGAGGGTGAAGTGGAAACAGACCTTCTCTCAAAACT 972
Db 684 TAG---GATAAATAGTGGCTTGAAGATTAAGAGCAGGAGGCGGAGTCTTCCT 740
QY 973 CATCTTCTCAATGTCTGACATGACTATGGGAACTACACTTGGTGGCTCCAA 1032
Db 741 GACGGTGACCAACGTCACCTGAGGAGCACTACGGCAACTACACCTGTGGTGGC 800
QY 1033 GCTGGGCGACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGTCAGCG 1085
Db 801 GCTGGGGTCCCAATGCGAGCTAGTCTCTTTTCAAGCTGGGTGGTGAGAG 853

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RESULT 13

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US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence

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; LOCATION: 1...912
; OTHER INFORMATION:
US-08-414-657D-6

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Query Match 20.2%; Score 338.6; DB 2; Length 912;
Best Local Similarity 63.7%; Pred. No. 1.3e-82;
Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

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QY 253 AGCTATGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTTCAGGTGACTATTGA 312
Db 24 AGGCACGCAACATCACCCTGAGCGAGGGGACACAGCCATCTCAGGTGGTCTAGA 83
QY 313 CAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGA 372
Db 84 AGACAAGAACTCAAAAGGTGGCTGGCTGAAACCGTTCTGGCATCATTTTGTGGCATGA 143
QY 373 CAAGTGGTGGCTGGATCCTCGGGTGGTCTTCTGAGCAACACCCAAACGCGAGTACAGCAT 432
Db 144 CAAGTGGTCTCTGGACCCACCGGTTGAGCTGGAGAAACGCCAATCTCTGGAAATACAGCCT 203
QY 433 CGAGATCCAGAACCGTGGATGTATGACGAGGGGCCCTTTACACCTGCTCGGTGACACAGA 492
Db 204 CCGAATCCAGAAAGTGGATGTCTATGATGAGGTTCTTACACTTGTCTCAGTTTACACACA 263
QY 493 CAACCCCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAATTTGTAGA 552
Db 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATGCTACAAAGTCCCAACAAAGATCTCCAA 323
QY 553 GATTTCTTCAGATATCTCCATTATGAGGAAACAAATATTAGCTCACCCTGCATAGCAAC 612
Db 324 TATCTCTCGGATGTCTGTAATGAGGGCAGCAACGTGACTCTGGTCTGATGGCCAA 383
QY 613 TGGTAGACCAAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGTGGTGT 672
Db 384 TGGCGCTCTGAACTGTATACCTGATGAGACACCTTACACCAACTGGAAGGAATTTGA 443
QY 673 GAGTGAAGACGAATATCTTGGAAATTTAGGGCATCACCGGGAGCAGTCAAGGGACTAGA 732
Db 444 AGGAGAAGAAAGATATCTGGAGATCTCTGGCATCACACAGGGAGCAGTCAAGGCAAAATGA 503
QY 733 GTGCAAGTCCCTCAATGACGTGGCGCGCGCTGGTACGGAGAGTAAAGGTCAACCGTGA 792
Db 504 GTGCAAAAGCTGCCAAACGAGGTCTCTCTGGCGGATGTCAAAACAAAGTCAAGGTCACTGTGAA 563
QY 793 CTATCCACCATATATTTCAAGAGCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGAC 852
Db 564 CTATCTCTCCCACTATCACAGATCCAGAGCAATGAAGCCACCAAGAGCAGCAAGCTTC 623
QY 853 ACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 912
Db 624 ACTCAATGTGAGGCTCGGCGAGTCCCTGACCTGACTTTGAGTGGTACCGGGATGACAC 683
QY 913 AAGACTGATGAAGAAAGGGTCAAGTGGAAACAGACCTTCTCTCAAAACT 972
Db 684 TAG---GATAAATAGTGGCTTGAAGATTAAGAGCAGGAGGCGGAGTCTTCCT 740
QY 973 CATCTTCTCAATGTCTTGAACATGACTATGGGAACTTACACTTGGTGGCTCCAA 1032
Db 741 GACGGTGACCAACGCTCACTGAGGAGCACTACGGCAACTTACACTTGTGGTGGC 800
QY 1033 GCTGGGCGACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGTCAGCG 1085
Db 801 GCTGGGGTCCCAATGCGAGCTAGTCTCTTTTCAAGCTGGGTGGTGAGAG 853

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RESULT 14

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US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak

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; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...945
; OTHER INFORMATION:
; US-08-414-657D-8
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; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
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TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
US-08-414-657D-10

Search completed: June 16, 2005, 10:28:02
Job time : 382.373 secs

Query Match 19.9%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 2.6e-81;
Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

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c1221	49.6	3.0	543	20	US-10-425-115-117433	Sequence 117433, A	c1294	49.2	2.9	11394	15	US-10-240-453-96	Sequence 96, Appl
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c1298	49	2.9	256	9	US-09-732-560-89	Sequence 89, Appl	1371	48.8	2.9	588	19	US-10-437-963-55397	Sequence 55397, A
c1299	49	2.9	342	19	US-10-021-323-9783	Sequence 9783, Ap	1372	48.8	2.9	608	20	US-10-425-115-150409	Sequence 150409, A
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c1304	49	2.9	416	20	US-10-021-323-8207	Sequence 8207, Ap	1377	48.8	2.9	836	21	US-10-485-231-47	Sequence 47, Appl
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98	342.2	20.4	425	7	H87092	H87092 y874g04.r1	C 171	234.6	14.0	425	4	BG054945	BG054945 nac92f04.
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100	340.6	20.3	1017	9	A406971	A406971 Homo sapi	C 173	234	13.9	934	7	CN015939	CN015939 AGENCOURT
101	340.6	20.3	1017	9	A406973	A406973 Mus muscu	C 174	233.2	13.9	599	7	CN229507	CN229507 RJB072D02
102	339.4	20.2	2768	3	AK030681	AK030681 Mus muscu	C 175	232	13.8	245	7	R88615	R88615 ym93f06.r1
103	338	20.1	1015	9	A406972	A406972 Pan trogl	C 176	231.8	13.8	277	4	BI011319	BI011319 QV2-EN009
104	337.2	20.1	596	4	BM726313	BM726313 UI-R-EJ0-	C 177	235.8	13.4	564	7	C0602836	C0602836 DG8-24911
105	336.6	20.0	579	2	B9644523	B9644523 BB644523	C 178	225.8	13.4	639	7	CV030684	CV030684 9878 Full
106	336	20.0	336	1	A1262562	A1262562 qk42f01.x	C 179	225	13.4	660	7	CR543517	CR543517 DKF7p459N
107	333	19.7	467	3	AK044845	AK044845 Mus muscu	C 180	221.8	13.2	415	5	BY263876	BY263876 BY263876
108	330.2	19.8	478	7	H05429	H05429 Y180h09.r1	C 181	220	13.1	444	1	AA682970	AA682970 ae99a04.s
109	325	19.4	329	7	F06205	F06205 HSC10F041.n	C 182	218	13.0	229	1	AA450172	AA450172 zx42d09.x
110	323.4	19.3	478	5	BY245406	BY245406 BY245406	C 183	216	12.9	563	5	B0637244	B0637244 he07e09.y
111	323.2	19.2	859	6	CK232578	CK232578 AGENCOURT	C 184	215.4	12.8	697	5	BQ021243	BQ021243 UI-H-DH1-
112	322	19.2	772	7	CK776016	CK776016 967158 MA	C 185	213.8	12.7	640	7	CR545244	CR545244 DKF7p459F
113	320	19.1	896	5	RQ890272	RQ890272 AGENCOURT	C 186	213	12.7	672	6	CA444805	CA444805 UI-H-DH1-
114	310.2	18.5	602	2	BB611718	BB611718 BB611718	C 187	212.4	12.7	867	6	CD300857	CD300857 AGENCOURT
115	310	18.5	2798	3	AK028345	AK028345 Mus muscu	C 188	211.2	12.6	456	5	BY249027	BY249027 AGENCOURT
116	306	18.2	780	7	CK313831	CK313831 SB0203882	C 189	210.6	12.5	656	7	CK619540	CK619540 mk25d06.y
117	305.8	18.2	445	5	BY269882	BY269882 BY269882	C 190	209	12.4	257	2	AK327110	AK327110 20640.MAR
118	302.4	18.0	513	5	BX279850	BX279850 BX279850	C 191	208.4	12.4	678	5	B0624639	B0624639 UI-H-FG1-
119	302.4	18.0	690	7	CN233126	CN233126 WLB057E10	C 192	208.4	12.4	1148	5	BM466102	BM466102 AGENCOURT
120	302.2	18.0	759	7	CN094277	CN094277 EC2BBA9CA	C 193	207.6	12.4	226	2	AM374585	AM374585 MRI-CT005
121	301.4	18.0	643	5	B0390882	B0390882 RJB067132	C 194	204.2	12.2	636	7	CK843444	CK843444 UI-R-BJ2-
122	299.2	17.8	704	7	CN228803	CN228803 RJB061B04	C 195	204.2	12.2	726	5	BX912600	BX912600 BX912600
123	297.4	17.7	764	4	BY752729	BY752729 603028343	C 196	204	12.2	357	5	BY303236	BY303236 UI-H-FP1-
124	292.4	17.4	764	5	BM945665	BM945665 UI-M-EMO-	C 197	203.6	12.1	625	6	CA307492	CA307492 UI-H-FP1-
125	291.6	17.4	415	7	R18841	R18841 Y922g06.r1	C 198	203.4	12.1	656	2	BB643056	BB643056 BB643056
126	290.4	17.3	778	7	CN078143	CN078143 EC2BBA14C	C 199	203.4	12.1	771	7	CN528825	CN528825 UI-M-HQ0-
127	290.2	17.3	457	5	BY249728	BY249728 BY249728	C 200	202.6	12.1	1084	6	CD255729	CD255729 AGENCOURT
128	290	17.3	290	7	F05894	F05894 HSC0PH101.n	C 201	202.2	12.0	538	7	CK842319	CK842319 UI-R-AD0-
129	288.8	17.2	567	2	BF078551	BF078551 228917.MA	C 202	200.2	11.9	719	7	CK465166	CK465166 936244.MA
130	287.6	17.1	481	5	BY256150	BY256150 BY256150	C 203	200	11.9	786	7	CO811192	CO811192 AGENCOURT
131	286.2	17.0	497	2	BB854833	BB854833 BB854833	C 204	199.8	11.9	858	7	CO914076	CO914076 AGENCOURT
132	284.8	17.0	684	5	B0625289	B0625289 UI-H-FG1-	C 205	199.8	11.9	468	2	BF110673	BF110673 7n55h10.x
133	284.2	16.9	528	2	B8856778	B8856778 BB856778	C 206	198.6	11.8	663	2	BB633037	BB633037 BB633037
134	280	16.7	677	5	B0444788	B0444788 UI-M-ER0-	C 207	198	11.8	519	7	CV038761	CV038761 4136000.B
135	279.8	16.7	677	6	CD217649	CD217649 P9rln.Pk0	C 208	198	11.8	525	4	BG373976	BG373976 UI-R-CV1-
136	277.6	16.5	590	7	CR545391	CR545391 DKF7p459M	C 209	197.6	11.8	537	2	BB770360	BB770360 BB770360
137	276.2	16.5	297	1	AA037351	AA037351 zc03b06.s	C 210	195.6	11.6	347	7	CN094278	CN094278 EC2BBA9CA
138	273.6	16.3	815	5	B0230452	B0230452 603320607	C 211	194.4	11.6	670	7	CN083622	CN083622 EC2BBA22D
139	272.6	16.2	827	6	CA306798	CA306798 UI-H-FP1-	C 212	194.4	11.6	708	7	CN083621	CN083621 EC2BBA22D
140	271.8	16.2	2096	3	AK035218	AK035218 Mus muscu	C 213	193	11.5	559	5	BY476545	BY476545 BY476545
141	270.2	16.1	1953	3	AK030503	AK030503 Mus muscu	C 214	192.8	11.5	825	5	BP166655	BP166655 BP166655
142	267.6	15.9	858	6	CD325821	CD325821 AGENCOURT	C 215	192	11.4	659	2	AW149545	AW149545 xfi39c10.x
143	267.2	15.9	284	7	CR543721	CR543721 DKF7p459H	C 216	191.4	11.4	294	7	W15256	W15256 zc16r017.s1
144	264.8	15.8	695	7	CN228731	CN228731 RJB060E12	C 217	189.4	11.3	764	6	CA350929	CA350929 621861.NC
145	263.2	15.7	683	2	BB318882	BB318882 BB318882	C 218	188	11.2	611	6	CA355517	CA355517 627428.NC
146	263.6	15.7	2534	3	AK039193	AK039193 Mus muscu	C 219	187.6	11.2	593	7	CK845949	CK845949 968393.MA
147	263	15.7	2330	3	BC080168	BC080168 Xenopus.l	C 220	186.8	11.1	565	2	BB663866	BB663866 147903.MA
148	256.8	15.3	754	7	CO043662	CO043662 UI-M-ER0-	C 221	186.8	11.1	880	6	CD303536	CD303536 AGENCOURT
149	256	15.2	257	7	Z39203	Z39203 HSC13G042.n	C 222	186.6	11.1	509	2	BB771080	BB771080 BB771080
150	255.2	15.2	587	7	CN088583	CN088583 EC2BBA30B	C 223	186.2	11.1	572	6	CB265380	CB265380 1004285.H
151	253	15.1	410	5	BY276506	BY276506 BY276506	C 224	186	11.1	640	7	CO351229	CO351229 DR.AOV.FL
152	247	14.7	796	7	CO399311	CO399311 AGENCOURT	C 225	186	11.1	753	1	AI1589824	AI1589824 tm74g09.x
153	246.8	14.7	442	5	BX112198	BX112198 BX112198	C 226	185.2	11.0	905	5	BUI186468	BUI186468 AGENCOURT
154	246.8	14.7	523	2	BE550993	BE550993 7b67a03.x	C 227	184.4	11.0	392	2	BE651010	BE651010 UI-M-BH3-
155	246.4	14.7	849	6	CA472810	CA472810 AGENCOURT	C 228	183	10.9	835	5	EX881962	EX881962 BY243052
156	243.8	14.5	652	7	CN078144	CN078144 EC2BBA14C	C 229	182.8	10.9	527	5	BY243052	BY243052 BX243052
157	241.8	14.4	653	7	CF180026	CF180026 815076.MA	C 230	181	10.8	755	5	BX913106	BX913106 BX913106
158	241.6	14.4	434	1	AI360870	AI360870 qy01b10.x	C 231	180.6	10.8	647	7	CV030870	CV030870 10123.Fu1
159	240.8	14.3	621	5	BX312928	BX312928 BX312928	C 232	179.8	10.7	220	7	H16176	H16176 ym21909.r1
160	240.6	14.3	496	5	BP201259	BP201259 BP201259	C 233	179.2	10.7	578	2	BE121132	BE121132 UI-R-CA0-
161	240.6	14.3	926	6	CD325412	CD325412 AGENCOURT	C 234	179.2	10.7	836	4	BI733097	BI733097 603554684
162	240.2	14.3	456	6	CD080385	CD080385 UI-M-GV0-	C 235	178	10.6	178	6	CB118055	CB118055 K-EST0164
163	239.8	14.3	502	1	AI796834	AI796834 we22h06.x	C 236	178	10.6	909	5	BUI12565	BUI12565 603120307
164	239	14.2	511	5	BX493152	BX493152 DKF7p781G	C 237	176.4	10.5	448	4	BG375509	BG375509 UI-R-CV1-
165	238.8	14.2	611	7	R75391	R75391 MB00556R.MO	C 238	176.4	10.5	496	2	BF523086	BF523086 UI-R-C2p-
166	238	14.2	282	7	R75391	R75391 MB00556R.MO	C 239	176	10.5	666	5	BM951674	BM951674 UI-M-EG0-
167	235.6	14.0	482	4	BI767217	BI767217 603057906	C 240	175.6	10.5	2296	3	CK592222	CK592222 full-1en9
168	235.4	14.0	798	2	AW967001	AW967001 EST379075	C 241	175.2	10.4	795	1	AU080106	AU080106 AU080106
169	235	14.0	674	6	CD767791	CD767791 AGENCOURT	C 242	174.6	10.4	867	7	CO543917	CO543917 LY-EST116
170	234.8	14.0	258	7	R42884	R42884 yg06h12.s1	C 243	174.4	10.4	572	2	BF407747	BF407747 UI-R-BJ2-

390	106	6.3	276	2	BB304840	BB304840	463	80.4	4.8	529	6	CD284927	CD284927
391	106	6.3	705	7	CN108877	EC2CAA32D	464	79.8	4.8	272	2	BB255894	BB255894
c 392	105.8	6.3	598	1	A1815935	aua3902.x	465	79.6	4.7	221	2	BB306421	BB306421
393	105.6	6.3	394	9	AY400233	Homo sapi	466	79.4	4.7	583	6	CA353359	CA353359
394	105.6	6.3	394	9	AY400234	Pan trogl	467	79.2	4.7	562	5	BX952176	BX952176
395	105.4	6.3	525	6	CB720159	AMGNNUC:N	c 468	78.8	4.7	560	4	BG065676	BG065676
c 396	105.2	6.3	314	7	CN075611	EC2BBA10C	469	78.6	4.7	375	5	BY292584	BY292584
397	105	6.3	288	2	BB262900	BB262900	470	78.6	4.7	442	7	CN081576	CN081576
398	104.6	6.2	651	6	CB557691	AMGNNUC:N	471	78.6	4.7	513	3	AK080669	AK080669
399	104.2	6.2	284	2	BB054624	BB054624	472	78.6	4.7	522	2	BB271167	BB271167
400	104.2	6.2	473	5	BY261511	BY261511	473	78.6	4.7	916	5	BQ672140	BQ672140
401	103.8	6.2	761	6	CD755145	AGENCOURT	474	78.4	4.7	206	2	BB589469	BB589469
402	103.4	6.2	262	1	AV030145	AV030145	475	78.2	4.7	336	4	BG1199531	BG1199531
403	103.4	6.2	279	2	BB362555	BB362555	476	78	4.6	457	7	W39242	W39242
404	103.4	6.2	327	2	BB320625	BB320625	c 477	78	4.6	660	5	BN337636	BN337636
405	102.2	6.1	291	2	BB248659	BB248659	c 478	77.6	4.6	368	7	CN086072	CN086072
406	101.2	6.0	412	5	BY274659	BY274659	479	77	4.6	297	6	BY724443	BY724443
c 407	101	6.0	298	1	AA906739	ok78h08.s	c 480	77	4.6	538	6	C76456	C76456
408	100.8	6.0	283	2	BB265542	BB265542	c 481	76.8	4.6	467	4	BI1134406	BI1134406
409	100.8	6.0	483	8	A2457316	BM0260A07	c 482	76.8	4.6	581	8	BH269028	BH269028
410	100.6	6.0	260	2	BF455798	UI-M-CG0P	c 483	76.8	4.6	779	8	BH292378	BH292378
411	100.6	6.0	359	2	AW491830	UI-M-BH3-	c 484	76.8	4.6	1127	9	GA2000118	GA2000118
c 412	100.2	6.0	260	2	BE156390	QV0-HT036	c 485	76.6	4.6	281	1	AV227016	AV227016
c 413	100	6.0	402	2	AW522667	UI-R-B00-	486	76.6	4.6	492	4	BI359722	BI359722
414	99.4	5.9	292	2	BB375591	BB375591	487	76.2	4.5	960	5	BQ933325	BQ933325
415	98.2	5.9	489	6	CB726015	AMGNNUC:N	c 488	75.6	4.5	433	1	AL921475	AL921475
c 416	98.6	5.9	207	2	BF469799	UI-M-BH3-	c 489	75.2	4.5	652	8	BH269030	BH269030
417	98.6	5.9	694	7	CK699353	ZF101-P00	c 490	74.4	4.4	526	2	BB380085	BB380085
418	98.4	5.9	392	5	BY267956	BY267956	c 491	74.2	4.4	526	7	CO634943	CO634943
419	97.2	5.8	421	5	BY275639	BY275639	492	73.2	4.4	284	3	AK020745	AK020745
420	97.2	5.8	656	2	BB617916	BB617916	493	73.2	4.4	293	2	BB284230	BB284230
421	95.8	5.7	763	1	A1427225	nc70a03.y	494	72.8	4.3	687	5	BP461989	BP461989
422	95.6	5.7	385	5	BY275013	BY275013	495	72.8	4.3	893	9	CNS02MVY	CNS02MVY
423	94.8	5.6	240	2	BB047231	BB047231	496	72.6	4.3	339	2	BE826667	BE826667
424	94.4	5.6	646	4	BI393264	p9pin.pk0	497	72.6	4.3	816	5	BU385923	BU385923
c 425	94.2	5.6	354	2	BB282697	BB282697	c 498	72.4	4.3	378	8	AZ089779	AZ089779
c 426	94.2	5.6	740	7	CO884202	CO884202	c 499	72	4.3	334	1	A1422503	A1422503
427	93.6	5.6	401	5	BY266910	BY266910	500	71.8	4.3	264	1	AV325817	AV325817
c 428	93	5.5	375	2	BB053997	BB053997	501	71.8	4.3	274	1	AV338287	AV338287
c 429	92.8	5.5	287	2	BF358688	QV1-ET000	502	71.8	4.3	474	2	BB682022	BB682022
430	92.6	5.5	229	1	AV350601	AV350601	503	71.4	4.3	196	1	AV344490	AV344490
431	92.4	5.5	302	2	BB389565	BB389565	504	71.4	4.3	202	1	AV031929	AV031929
432	92	5.5	304	2	BB282896	BB282896	505	71.4	4.3	255	2	BB563869	BB563869
433	92	5.5	640	9	CS573801	CH240.450	506	70.8	4.2	198	1	AV030665	AV030665
434	91.4	5.4	374	5	BY294857	BY294857	507	70.8	4.2	216	1	AV341533	AV341533
c 435	91.4	5.4	452	1	A1262821	qk35h10.x	508	70.6	4.2	199	2	BB127593	BB127593
436	91	5.4	318	2	BB321476	BB321476	509	70.2	4.2	214	1	AV345671	AV345671
c 437	91	5.4	656	2	BB645027	BB645027	510	69.6	4.1	742	7	CO395507	CO395507
c 438	90.4	5.4	233	2	AW047822	UI-M-BH1-	511	69.4	4.1	261	2	BB278160	BB278160
c 439	90.2	5.4	267	2	BB480567	BB480567	512	69	4.1	191	2	BB301025	BB301025
440	90	5.4	194	4	BI337742	BI337742	513	68.6	4.1	581	7	CO879831	CO879831
c 441	90	5.4	317	2	BF056760	7k08c03.x	514	68.4	4.1	221	2	BB048644	BB048644
442	88.6	5.3	700	2	BB652926	BB652926	515	68.4	4.1	292	2	BB198259	BB198259
c 443	88.4	5.3	733	9	BX190380	Danio rer	516	68.2	4.1	313	2	AW430704	AW430704
444	88.2	5.3	374	2	BB826640	QV1-EN004	517	68	4.1	223	2	BB380518	BB380518
445	86	5.1	304	2	BB265140	BB265140	c 518	67.6	4.0	514	7	CK769283	CK769283
c 446	85.8	5.1	285	7	CN209637	4115576.B	519	67.2	4.0	821	5	BU389844	BU389844
c 447	84.6	5.1	332	2	BB826737	QV1-EN004	520	67	4.0	417	1	AV589904	AV589904
448	84.8	5.1	625	6	BY729404	BY729404	521	66	3.9	226	2	BB048138	BB048138
449	84.6	5.0	526	2	BB641806	BB641806	522	66	3.9	433	4	BG515406	BG515406
450	84.4	5.0	320	2	BB312195	BB312195	523	65.8	3.9	296	2	BB193169	BB193169
c 451	84.4	5.0	479	2	AW524531	UI-R-B00-	524	65.8	3.9	726	5	BU395513	BU395513
c 452	84	5.0	657	2	BB618284	BB618284	525	65.6	3.9	502	4	BG078950	BG078950
c 453	84	5.0	723	9	AG035406	AG035406	526	65	3.9	259	2	BB607028	BB607028
454	83.8	5.0	2594	3	AK047122	Mus muscu	c 527	64.8	3.9	702	9	CNS02PTU	CNS02PTU
455	83.4	5.0	550	2	BE012499	BE012499	c 528	64.4	3.8	527	1	AA741334	AA741334
456	83.2	5.0	233	1	AV335954	AV335954	529	64.4	3.8	558	7	CK875240	CK875240
457	82.8	4.9	262	2	BB078578	BB078578	530	63.8	3.8	217	2	BB197705	BB197705
458	82.4	4.9	728	7	CN530285	UI-M-H00-	531	62.6	3.7	226	1	AA776056	AA776056
459	82	4.9	272	2	BB596160	BB596160	c 532	62.6	3.7	539	1	AL918370	AL918370
460	81.8	4.9	392	2	AW291014	UI-H-B12-	533	61.8	3.7	201	1	AV227064	AV227064
461	81.6	4.9	586	4	BM696801	UI-E-DW0-	c 534	61.8	3.7	247	7	CR474371	CR474371
c 462	80.6	4.8	1463	8	CC288776	CH261-170	535	61.8	3.7	550	7	CR544600	CR544600

536	61	200	1	AV028623	AV028623	AV028623	609	54.2	3.2	806	4	BI762516	BI762516	603048638
537	60.8	189	1	AV029446	AV029446	AV029446	610	54.2	3.2	859	6	CB319037	CB319037	AGENCOURT
538	60.8	255	2	BB577810	BB577810	BB577810	C 611	54	3.2	212	4	BG981747	BG981747	MR3-CN014
539	60.4	222	2	BB053503	BB053503	BB053503	C 612	54	3.2	241	4	BG980534	BG980534	MR3-CN014
540	60.4	484	5	BX099260	BX099260	BX099260	613	54	3.2	365	6	CB573833	CB573833	AGENCOURT
541	60.2	1008	9	CL093894	CL093894	CL093894	614	54	3.2	774	1	AJ786997	AJ786997	AJ786997
542	60	702	4	BG695650	BG695650	BG695650	615	54	3.2	1176	5	BM927266	BM927266	AGENCOURT
543	59.6	420	6	CB798880	CB798880	CB798880	C 616	53.8	3.2	244	2	BF362751	BF362751	RC1-NN007
544	59.6	845	4	BM042630	BM042630	BM042630	617	53.8	3.2	276	7	CO181006	CO181006	EC13331.5
545	59	303	1	AI422504	AI422504	AI422504	618	53.8	3.2	276	7	CO195427	CO195427	EC40320.5
546	58.6	276	6	BB268580	BB268580	BB268580	619	53.8	3.2	286	7	CO182679	CO182679	EC23645.5
547	58.6	426	7	CK776772	CK776772	CK776772	620	53.8	3.2	303	7	CO181557	CO181557	EC14539.5
548	58.6	736	8	AG989621	AG989621	AG989621	621	53.8	3.2	350	7	CO191915	CO191915	EC32401.5
549	58.4	242	4	BG980478	BG980478	BG980478	622	53.8	3.2	361	5	BUS89906	BUS89906	AGENCOURT
550	58.4	565	7	CO590783	CO590783	CO590783	623	53.8	3.2	382	7	CO181851	CO181851	EC15101.5
551	58.2	376	7	CO182357	CO182357	CO182357	624	53.8	3.2	385	7	CO180258	CO180258	EC1313.5
552	58.2	369	7	CO181363	CO181363	CO181363	625	53.8	3.2	395	7	CO182619	CO182619	EC23422.5
553	58.2	421	7	CO181992	CO181992	CO181992	626	53.8	3.2	398	7	CO193679	CO193679	EC36616.5
554	58.2	504	7	CO193442	CO193442	CO193442	627	53.8	3.2	450	7	CO194401	CO194401	EC38508.5
555	58.2	531	7	CO193920	CO193920	CO193920	628	53.8	3.2	452	7	CO193143	CO193143	EC35202.5
556	57.8	831	9	CNS011FZ	CNS011FZ	CNS011FZ	629	53.8	3.2	464	7	CO183541	CO183541	EC25934.5
557	57.4	559	7	CF123525	CF123525	CF123525	630	53.8	3.2	487	7	CO195262	CO195262	EC39947.5
558	57	643	8	AQ327238	AQ327238	AQ327238	631	53.8	3.2	490	7	CO180558	CO180558	EC02047.5
559	57	841	5	BUS30009	BUS30009	BUS30009	632	53.8	3.2	523	7	CO183076	CO183076	EC24521.5
560	56.8	569	5	BF377634	BF377634	BF377634	633	53.8	3.2	524	7	CO182642	CO182642	EC23489.5
561	56.8	574	5	BP321522	BP321522	BP321522	634	53.8	3.2	547	7	CO185170	CO185170	EC29789.5
562	56.8	582	5	BP208357	BP208357	BP208357	635	53.8	3.2	552	7	CO194609	CO194609	EC39890.5
563	56.6	324	7	CO192533	CO192533	CO192533	C 636	53.8	3.2	569	8	AQ394216	AQ394216	CITR1-R1-
564	56.6	502	7	CO691339	CO691339	CO691339	637	53.8	3.2	582	4	BQ219746	BQ219746	RST39511
565	56.6	574	7	CO184164	CO184164	CO184164	638	53.8	3.2	759	9	CNS05QXV	CNS05QXV	AL411257
566	56.6	964	9	CNS05CLJ	CNS05CLJ	CNS05CLJ	639	53.8	3.2	880	6	CD522648	CD522648	AGENCOURT
567	56.4	1389	4	BI911314	BI911314	BI911314	640	53.8	3.2	913	7	CK157193	CK157193	FGAS03828
568	56.2	481	7	CO180995	CO180995	CO180995	641	53.8	3.2	1511	3	BC030320	BC030320	Mus muscu
569	56.2	1019	5	BO723771	BO723771	BO723771	642	53.6	3.2	271	2	BB432888	BB432888	BB432888
570	56.2	1119	6	CD050433	CD050433	CD050433	643	53.6	3.2	532	6	CA354283	CA354283	625969 NC
571	56	497	7	CO180052	CO180052	CO180052	644	53.6	3.2	551	1	AL036240	AL036240	DKP2564J
572	56	710	7	CO961229	CO961229	CO961229	645	53.6	3.2	692	7	CK654124	CK654124	AGENCOURT
573	56	771	5	BUS56340	BUS56340	BUS56340	C 646	53.6	3.2	754	9	AG483752	AG483752	Mus muscu
574	56	1472	9	CL490510	CL490510	CL490510	647	53.6	3.2	772	5	BUS37238	BUS37238	AGENCOURT
575	55.8	929	9	CNS050X	CNS050X	CNS050X	648	53.6	3.2	778	4	BI859188	BI859188	60385268
576	55.8	1376	9	AG320971	AG320971	AG320971	C 649	53.6	3.2	893	7	CK196964	CK196964	AGENCOURT
577	55.6	861	7	CK017071	CK017071	CK017071	650	53.6	3.2	949	6	CD387866	CD387866	AGENCOURT
578	55.4	311	4	BG193769	BG193769	BG193769	651	53.4	3.2	226	6	CD765502	CD765502	EST00188
579	55.4	355	7	CO878692	CO878692	CO878692	652	53.4	3.2	230	4	BF968205	BF968205	602268946
580	55.4	626	8	AZ385580	AZ385580	AZ385580	653	53.4	3.2	363	2	BF076420	BF076420	225985 MA
581	55.4	835	5	BUS54638	BUS54638	BUS54638	654	53.4	3.2	422	7	CV525233	CV525233	MD1V4010h
582	55.2	285	6	CB986322	CB986322	CB986322	655	53.4	3.2	582	5	BP283085	BP283085	BP283085
583	55.2	518	7	CB974991	CB974991	CB974991	656	53.4	3.2	584	5	BP327099	BP327099	BP327099
584	55.2	991	4	BG435647	BG435647	BG435647	657	53.4	3.2	661	7	CF358754	CF358754	RV150d08.Y
585	55.2	1175	6	CD504945	CD504945	CD504945	658	53.4	3.2	698	1	AV682763	AV682763	AV682763
586	55	230	7	CO885649	CO885649	CO885649	659	53.4	3.2	816	5	BUS43005	BUS43005	AGENCOURT
587	55	647	9	AG044222	AG044222	AG044222	660	53.4	3.2	880	7	CB963135	CB963135	AGENCOURT
588	55	1043	6	CD385012	CD385012	CD385012	661	53.4	3.2	884	5	BUS66030	BUS66030	Mus muscu
589	55	1123	5	BUS02918	BUS02918	BUS02918	C 662	53.4	3.2	885	9	AG566030	AG566030	AGENCOURT
590	54.8	262	6	CB337385	CB337385	CB337385	663	53.4	3.2	935	5	BUS60555	BUS60555	AGENCOURT
591	54.8	400	7	CF578533	CF578533	CF578533	664	53.4	3.2	1101	9	CNS00HAV	CNS00HAV	Drosophil
592	54.8	684	7	CV274449	CV274449	CV274449	665	53.4	3.2	195	7	CF546382	CF546382	lae72e03
593	54.6	204	4	BG980696	BG980696	BG980696	666	53.2	3.2	422	2	AW778899	AW778899	ho1608.X
594	54.6	246	1	AL040243	AL040243	AL040243	667	53.2	3.2	560	6	CB339387	CB339387	CA23E103I
595	54.6	348	6	CB829769	CB829769	CB829769	C 668	53.2	3.2	609	6	CA367906	CA367906	934919 NC
596	54.6	390	1	AA490022	AA490022	AA490022	669	53.2	3.2	693	7	CK463316	CK463316	934211 MA
597	54.6	434	6	CA399771	CA399771	CA399771	670	53.2	3.2	712	9	CNS04AL2	CNS04AL2	Tetraodon
598	54.6	478	6	CB179629	CB179629	CB179629	671	53.2	3.2	808	7	CF150373	CF150373	AGENCOURT
599	54.6	842	7	CK128791	CK128791	CK128791	672	53.2	3.2	818	5	BUS64240	BUS64240	AGENCOURT
600	54.6	844	9	CNS0052P	CNS0052P	CNS0052P	673	53.2	3.2	864	7	CK395877	CK395877	AGENCOURT
601	54.6	847	7	CK400611	CK400611	CK400611	674	53.2	3.2	869	5	BUS38204	BUS38204	AGENCOURT
602	54.6	1049	4	BG623609	BG623609	BG623609	675	53.2	3.2	871	5	BUS40167	BUS40167	AGENCOURT
603	54.6	1056	4	BG032994	BG032994	BG032994	676	53.2	3.2	895	5	BUS588665	BUS588665	AGENCOURT
604	54.4	625	7	CF921039	CF921039	CF921039	677	53.2	3.2	906	5	BUS31084	BUS31084	AGENCOURT
605	54.4	637	7	CO541834	CO541834	CO541834	678	53.2	3.2	1101	9	CNS00KFT	CNS00KFT	Drosophil
606	54.2	573	7	CF977921	CF977921	CF977921	C 679	53.2	3.2	1379	4	BM548276	BM548276	AGENCOURT
607	54.2	736	9	CNS03MTV	CNS03MTV	CNS03MTV	680	53.2	3.2	286	6	CD773252	CD773252	
608	54.2	749	5	BUS34260	BUS34260	BUS34260	681	53	3.2					

682 53 3.2 296 6 CB076532
683 53 3.2 335 7 CF381770
684 53 3.2 432 1 AV665533
685 53 3.2 659 9 AG083939
686 53 3.2 837 9 CNS011F1
687 53 3.2 864 7 CN177352
688 53 3.2 938 5 BU960786
689 53 3.2 941 7 CK420653
690 53 3.2 999 5 BU426211
691 53 3.2 1015 9 CL135318
692 53 3.2 1293 9 AG346949
693 52.8 3.1 196 5 BQ786696
694 52.8 3.1 234 1 AV349585
695 52.8 3.1 250 7 CO191457
696 52.8 3.1 279 7 CR659257
697 52.8 3.1 295 7 CR630157
698 52.8 3.1 302 2 BF362739
699 52.8 3.1 315 7 CF804740
700 52.8 3.1 317 7 CN537157
701 52.8 3.1 323 7 CK379820
702 52.8 3.1 399 4 BG113662
703 52.8 3.1 650 6 CD773004
704 52.8 3.1 720 7 CV066275
705 52.8 3.1 813 5 BU850671
706 52.8 3.1 840 5 BM985947
707 52.8 3.1 849 9 AG044091
708 52.8 3.1 862 6 CA463085
709 52.8 3.1 866 5 BU587173
710 52.8 3.1 914 5 BU563375
711 52.8 3.1 945 5 BU851541
712 52.8 3.1 947 6 CB205316
713 52.8 3.1 1131 4 BM542918
714 52.8 3.1 2186 3 CR749590
715 52.6 3.1 274 7 CV072032
716 52.6 3.1 304 7 CN927725
717 52.6 3.1 350 5 BX553079
718 52.6 3.1 427 6 CA778567
719 52.6 3.1 493 7 CK377070
720 52.6 3.1 504 6 CB678747
721 52.6 3.1 560 4 BG924474
722 52.6 3.1 659 6 CD771540
723 52.6 3.1 731 7 CF924696
724 52.6 3.1 778 5 BU534338
725 52.6 3.1 811 6 CB951950
726 52.6 3.1 812 9 AG031898
727 52.6 3.1 825 5 BU850748
728 52.6 3.1 829 7 CK794790
729 52.6 3.1 856 5 BU934849
730 52.6 3.1 1002 6 CB206065
731 52.6 3.1 1380 9 AG311242
732 52.6 3.1 1920 3 BC047319
733 52.4 3.1 160 2 AW318295
734 52.4 3.1 172 7 CF983728
735 52.4 3.1 199 4 BF699239
736 52.4 3.1 243 7 CK430436
737 52.4 3.1 293 4 BM155090
738 52.4 3.1 374 4 BM154585
739 52.4 3.1 432 2 AW773386
740 52.4 3.1 490 7 CO874828
741 52.4 3.1 562 2 AW636413
742 52.4 3.1 579 7 CF752690
743 52.4 3.1 603 7 CN004672
744 52.4 3.1 619 7 CO535894
745 52.4 3.1 648 8 AZ379719
746 52.4 3.1 803 6 CB318690
747 52.4 3.1 826 4 BM041903
748 52.4 3.1 870 5 BU843763
749 52.4 3.1 873 6 CB844849
750 52.4 3.1 880 7 CK159114
751 52.4 3.1 887 5 BU850963
752 52.4 3.1 949 9 CNS002P1
753 52.4 3.1 1010 6 CD171719
754 52.4 3.1 1148 6 CD500545

CB076532 hf44g04.9
CF381770 lab84b07.
AV665533 AV665533
AG083939 Pan trogl
AL100200 Drocephil
CN177352 AGENCOURT
BU960786 AGENCOURT
CK420653 AUF Iptrk
BU426211 603232486
CL135318 ISB1-106F
AG346949 Mus muscu
BQ786696 saq72a12.
AV349585 AV349585
CO191457 EC30893.5
CR659257 DKFZp468M
CR630157 DKFZp468M
BF362739 RCL1-NN007
CF804740 lad78h10.
CN537157 UI-M-HS0-
CK379820 lai59a11.
BG113662 602284164
CD773004 AGENCOURT
CV066275 WNEI32E4
BU850671 AGENCOURT
BM985947 7_C05_T3
AG044091 Pan trogl
CA463085 AGENCOURT
BU587173 AGENCOURT
BU563375 AGENCOURT
BU851541 AGENCOURT
CB205316 AGENCOURT
BM542918 AGENCOURT
CR749590 Homo sapi
CV072032 EST4193_Z
CN927725 000530AEP
BX553079 BX553079
CA778567 MPL3384_9
CK377070 lab97h03-
CB678747 OSJnef01F
BG924474 HNC271-D
CD771540 AGENCOURT
CF924696 DD005C04.
BU534338 AGENCOURT
CB951950 AGENCOURT
AG031898 Pan trogl
BU850748 AGENCOURT
CK794790 AGENCOURT
BU934849 AGENCOURT
CB206065 AGENCOURT
AG311242 Mus muscu
BC047319 Homo sapi
AW318295 sg63d05.Y
CF983728 IG02 grap
BF699239 BJ699239
CK430436 oJ49d02.Y
BM155090 fv93d10.Y
BM154585 fv86h02.Y
AW773386 tp06c01.Y
CO874828 Bovgen_03
AW636413 b146d05.w
CF752690 om_A001.0
CN004672 ip21e12.g
CO535894 tah10e04
AZ379719 IM0135K02
CB318690 AGENCOURT
BM041903 603615963
BU843763 AGENCOURT
CB844849 M2PN-0411
CK159114 FGAS04050
BU850963 AGENCOURT
AL097968 Drocephil
CD171719 AGENCOURT
CD500545 CDA45-F05

BO2777164 AGENCOURT
CL080800 CH216-159
AG350187 Mus muscu
AL133640 Homo sapi
CU513862 SAIL_880
B1524436 603051712
CF890463 TCTR-1266
BG981484 MR3-CN014
CA689180 wln96_pk0
BM529684 fy14h03.Y
COL93387 EC35693.5
BU764209 sa854a02.
CF6240732 he32e05.Y
CF622338 laf02ff12.
CK375298 lai48a03.
CL081785 EC14973.5
AL252730 Tetraodon
AZ878524 RPCI-23-1
CK384950 lah56e09.
CF968846 lag73f11.
AV681953 AG681953
CB524077 UI-M-GK0-
CK632450 AM1-AP000
CK421958 AUF_IpSpn
BG622466 602647179
CK983417 re24g03.Y
CV223060 tai56f08.
BU519721 BJ519721
CD251677 AGENCOURT
BG107420 602277525
CV522032 0089P0069
CN590804 TTE000144
BU532300 BJ532300
CK451264 904423_MA
AV757929 AV757929
BU534439 AGENCOURT
BU564052 AGENCOURT
CK159239 FGAS04064
BG572421 602593463
BU703874 BJ703874
BX504780 DKFZp686F
AA276487 vc32e10.r
CO883666 BovGen_11
CK381405 lag38a01.
BM187410 fw17d12.Y
AA616347 vnt5b12.r
CA366868 642552_NC
CF424254 lad27b04.
CB348689 CAB2SG000
CF779197 tad24e10.
CK406831 AUF_Iflvr
BX240864 DanLo_ter
BG435835 602508457
BU108854 603112530
BU946451 AGENCOURT
CK160127 FGAS04167
CD384935 AGENCOURT
CN310359 170005999
AL107211 Drocephal
BM904910 AGENCOURT
BU530627 AGENCOURT
CO727269 UMC-bend
BG736457 rk57d03.Y
BM531343 fx86a07.Y
BG980699 MR3-CN014
BM154701 fv88c10.Y
BM154695 fv88c02.Y
BM574233 fx60g11.Y
BU709836 fv44b03.Y
BM154709 fv88d07.Y

755 52.4 3.1 1298 5 BO2777164
c 756 52.4 3.1 1357 9 CL080800
c 757 52.4 3.1 1381 9 AG350187
758 52.4 3.1 1699 3 RSM801509
759 52.4 3.1 1775 9 CL513862
c 760 52.4 3.1 1924 4 B1524436
761 52.2 3.1 207 7 CF890463
c 762 52.2 3.1 211 4 BG981484
763 52.2 3.1 214 6 CA689180
764 52.2 3.1 231 4 BM529684
765 52.2 3.1 234 7 COL93387
766 52.2 3.1 276 7 CK379421
767 52.2 3.1 289 5 BU764209
768 52.2 3.1 290 5 BQ640732
769 52.2 3.1 301 7 CF622338
770 52.2 3.1 308 7 CK375298
771 52.2 3.1 352 7 COL81785
c 772 52.2 3.1 381 9 CNS03001
773 52.2 3.1 387 8 AZ878524
774 52.2 3.1 400 7 CK384950
775 52.2 3.1 405 7 CF968846
776 52.2 3.1 428 1 AV681953
777 52.2 3.1 431 6 CB524077
778 52.2 3.1 445 7 CK632450
779 52.2 3.1 466 7 CK421958
780 52.2 3.1 473 4 BG622466
781 52.2 3.1 548 7 CK983417
782 52.2 3.1 573 7 CV223060
783 52.2 3.1 584 4 BU519721
784 52.2 3.1 614 6 CD251677
785 52.2 3.1 635 4 BG107420
786 52.2 3.1 688 7 CV522032
787 52.2 3.1 710 7 CN590804
788 52.2 3.1 712 4 BU532300
789 52.2 3.1 723 7 CK451264
790 52.2 3.1 743 1 AV757929
791 52.2 3.1 819 5 BU534439
792 52.2 3.1 846 5 BU564052
793 52.2 3.1 906 7 CK159239
794 52.2 3.1 1000 4 BG572421
795 52 3.1 169 4 BU703874
796 52 3.1 172 5 BX504780
797 52 3.1 192 1 AA276487
798 52 3.1 202 7 CO883666
799 52 3.1 228 7 CK381405
800 52 3.1 243 4 BM187410
801 52 3.1 266 1 AA616347
802 52 3.1 403 6 CA366868
803 52 3.1 425 7 CF424254
c 804 52 3.1 461 6 CB348689
805 52 3.1 478 7 CF779197
806 52 3.1 500 7 CK406831
807 52 3.1 590 9 BX240864
808 52 3.1 615 4 BG435835
809 52 3.1 743 5 BU108854
810 52 3.1 852 5 BU946451
811 52 3.1 882 7 CK160127
812 52 3.1 935 6 CD384935
813 52 3.1 939 7 CN310359
814 52 3.1 1016 9 CNS01609
815 52 3.1 1331 5 BM904910
816 51.8 3.1 194 5 BU530627
817 51.8 3.1 218 7 CO727269
818 51.8 3.1 225 4 BG736457
819 51.8 3.1 236 2 AW657557
820 51.8 3.1 252 4 BM531343
821 51.8 3.1 269 4 BG980699
822 51.8 3.1 278 4 BG983803
823 51.8 3.1 310 4 BM154701
824 51.8 3.1 311 4 BM154695
825 51.8 3.1 320 4 BM574233
826 51.8 3.1 320 5 BU709836
827 51.8 3.1 321 4 BM154709

828	51.8	3.1	323	4	BM155040	BM155040 fv92g05.y	901	51.6	3.1	963	7	CF780924	CF780924 AGENCOURT
829	51.8	3.1	336	5	BQ783539	BQ783539 fab30h11.	c 902	51.6	3.1	968	5	BX381631	BX381631 BX381631
830	51.8	3.1	340	4	BM155408	BM155408 fw04e06.y	c 903	51.6	3.1	969	7	CK426147	CK426147 AUF Iptes
831	51.8	3.1	345	4	BM534831	BM534831 fx71h06.y	904	51.6	3.1	1002	5	BUS50111	BUS50111 AGENCOURT
832	51.8	3.1	351	1	AL724883	AL724883 AL724883	905	51.6	3.1	1006	5	BUS30175	BUS30175 AGENCOURT
833	51.8	3.1	354	4	BM154696	BM154696 fv86c03.y	906	51.6	3.1	1035	6	CD246704	CD246704 AGENCOURT
834	51.8	3.1	356	6	BM155084	BM155084 fv93c11.y	907	51.6	3.1	1093	9	CNS04C0C	AL283845 Tetraodon
835	51.8	3.1	358	6	CB721263	CB721263 jmm603C06	908	51.6	3.1	1122	4	B1259611	B1259611 602968384
836	51.8	3.1	439	1	AV682218	AV682218 AV682218	c 909	51.6	3.1	1333	9	AG390651	AG390651 Mus muscu
837	51.8	3.1	463	1	AV682001	AV682001 AV682001	910	51.6	3.1	1426	4	BG388238	BG388238 602413232
838	51.8	3.1	503	8	B08074	B08074 T7G24-Sp6.1	911	51.4	3.1	201	2	AM102260	AM102260 g885d10.y
839	51.8	3.1	540	6	CA320990	CA320990 UI-M-FV0-	912	51.4	3.1	232	4	BM280863	BM280863 ki06b01.y
840	51.8	3.1	557	9	CE135710	CE135710 tiGr-g8s-	913	51.4	3.1	252	4	BM574901	BM574901 fx37e09.y
841	51.8	3.1	563	7	CF805126	CF805126 lad62f08.	914	51.4	3.1	277	6	CD722233	CD722233 CJ07b05.y
842	51.8	3.1	599	8	B16188	B16188 347E7-TV CI	915	51.4	3.1	334	7	CO194571	CO194571 EC38826.5
843	51.8	3.1	606	6	CD239409	CD239409 FNPUB12	c 916	51.4	3.1	361	1	A1819970	A1819970 WJ88h03.x
844	51.8	3.1	610	8	B17639	B17639 347E7-TV B	917	51.4	3.1	366	7	CO722305	CO722305 WJfz30190
845	51.8	3.1	632	7	CV199140	CV199140 km36h05.y	918	51.4	3.1	371	1	AV689111	AV689111 AV689111
846	51.8	3.1	674	6	CD638408	CD638408 AGENCOURT	919	51.4	3.1	372	7	CF331850	CF331850 NACL--08-
847	51.8	3.1	700	6	CD640967	CD640967 AGENCOURT	920	51.4	3.1	401	4	BG108147	BG108147 602280213
848	51.8	3.1	747	9	CNS011RQ	AL100640 Drosophila	c 921	51.4	3.1	440	4	BG944106	BG944106 ax46e08.x
849	51.8	3.1	748	9	AG031854	AG031854 Pan trogl	922	51.4	3.1	441	4	BM285111	BM285111 kh94h02.y
850	51.8	3.1	780	7	CN2323584	CN2323584 AGENCOURT	923	51.4	3.1	464	5	BQ639526	BQ639526 he16g12.y
851	51.8	3.1	797	5	BUS55131	BUS55131 AGENCOURT	924	51.4	3.1	475	5	BQ093142	BQ093142 fy94c12.y
852	51.8	3.1	804	5	BUS30964	BUS30964 AGENCOURT	925	51.4	3.1	476	6	CB721269	CB721269 jmm603D03
853	51.8	3.1	814	5	BUS566469	BUS566469 AGENCOURT	926	51.4	3.1	487	5	BQ196890	BQ196890 NXLV106.F
854	51.8	3.1	820	6	CA464889	CA464889 AGENCOURT	927	51.4	3.1	557	6	CA779552	CA779552 MPL384.12
855	51.8	3.1	872	7	CK157539	CK157539 FGAS03867	928	51.4	3.1	557	7	CF123296	CF123296 UI-HF-GHO
856	51.8	3.1	877	3	BC040855	BC040855 Homo sapi	929	51.4	3.1	578	5	BP265719	BP265719 BP265719
857	51.8	3.1	920	5	BUS63586	BUS63586 AGENCOURT	930	51.4	3.1	583	6	CB073419	CB073419 taa32f07.
858	51.8	3.1	973	5	BQ721625	BQ721625 AGENCOURT	931	51.4	3.1	591	4	B1378442	B1378442 BFLGI.000
859	51.8	3.1	982	4	BG288697	BG288697 602385510	932	51.4	3.1	620	6	CA321372	CA321372 UI-M-FV0-
860	51.8	3.1	1084	5	BUI189453	BUI189453 AGENCOURT	933	51.4	3.1	624	4	BG622353	BG622353 602647035
861	51.8	3.1	1126	6	CD523341	CD523341 AGENCOURT	c 934	51.4	3.1	702	8	AQ256508	AQ256508 nbxb0016M
862	51.8	3.1	1452	9	CL125503	CL125503 ISBI-87B2	935	51.4	3.1	720	6	CD641235	CD641235 AGENCOURT
863	51.6	3.1	191	7	CK895966	CK895966 SGP158500	936	51.4	3.1	762	7	CK655134	CK655134 AGENCOURT
864	51.6	3.1	216	4	BJ699031	BJ699031 BJ699031	937	51.4	3.1	783	7	CN385817	CN385817 LE2TR04J2
865	51.6	3.1	220	2	BE014996	BE014996 1269311.MA	938	51.4	3.1	789	6	CB571699	CB571699 AGENCOURT
866	51.6	3.1	254	4	BG981471	BG981471 MR3-CN014	939	51.4	3.1	800	5	B0843107	B0843107 AGENCOURT
867	51.6	3.1	300	7	CK428349	CK428349 laj14g03.	940	51.4	3.1	859	7	CN839423	CN839423 AGENCOURT
868	51.6	3.1	309	4	BM186118	BM186118 fv98b09.y	941	51.4	3.1	867	5	B0843011	B0843011 AGENCOURT
869	51.6	3.1	335	7	CF211902	CF211902 CGF100066	942	51.4	3.1	883	7	CB204789	CB204789 AGENCOURT
870	51.6	3.1	347	4	BM130321	BM130321 pb29e10.y	943	51.4	3.1	883	7	CK865669	CK865669 AGENCOURT
871	51.6	3.1	348	7	CK379136	CK379136 lai31b08.	944	51.4	3.1	935	5	BQ958308	BQ958308 AGENCOURT
872	51.6	3.1	375	1	AL713177	AL713177 DKE2p686L	945	51.4	3.1	939	7	CN014330	CN014330 AGENCOURT
873	51.6	3.1	432	7	CF337277	CF337277 JMT--07-K	946	51.4	3.1	941	6	CB195504	CB195504 AGENCOURT
874	51.6	3.1	438	4	B679676	B679676 BJ679676	947	51.4	3.1	973	5	B0845046	B0845046 AGENCOURT
875	51.6	3.1	484	4	BM342763	BM342763 fw47g02.y	948	51.4	3.1	975	5	B0963322	B0963322 AGENCOURT
876	51.6	3.1	495	5	BM903137	BM903137 NXLV.080	949	51.4	3.1	1011	6	CD388840	CD388840 AGENCOURT
877	51.6	3.1	577	4	BG927541	BG927541 HNC10-1-B	950	51.4	3.1	1014	5	BUS65689	BUS65689 AGENCOURT
878	51.6	3.1	602	5	BUS89676	BUS89676 AGENCOURT	c 951	51.4	3.1	1074	8	BZ696936	BZ696936 SP_Ba009
879	51.6	3.1	604	4	BG927528	BG927528 HNC10-1-C	952	51.4	3.1	1101	9	CNS00ED1	AL068937 Drogoph11
880	51.6	3.1	607	1	AS522011	AS522011 vh78c09.r	953	51.4	3.1	1112	5	BM920193	BM920193 AGENCOURT
881	51.6	3.1	617	4	BI829090	BI829090 603079182	954	51.4	3.1	1112	5	BM920193	BM920193 AGENCOURT
882	51.6	3.1	627	6	CA330151	CA330151 haa92b01.	c 955	51.2	3.0	151	7	CF203260	CF203260 RR890915N
883	51.6	3.1	643	4	BI870743	BI870743 603392853	c 956	51.2	3.0	185	4	BG980530	BG980530 MR3-CN014
884	51.6	3.1	693	6	CD770749	CD770749 AGENCOURT	c 957	51.2	3.0	193	7	CK615915	CK615915 ou07c12.y
885	51.6	3.1	697	5	CB319237	CB319237 AGENCOURT	c 958	51.2	3.0	199	4	BG981500	BG981500 MR3-CN014
886	51.6	3.1	761	5	BUS55158	BUS55158 AGENCOURT	c 959	51.2	3.0	201	4	BM265810	BM265810 fw36b10.y
887	51.6	3.1	771	7	CN831817	CN831817 Tetraodon	c 960	51.2	3.0	202	4	BG983780	BG983780 MR4-CN014
888	51.6	3.1	780	9	CNS04142	AL291788 Tetraodon	c 961	51.2	3.0	210	4	BM573150	BM573150 fx98h10.y
889	51.6	3.1	787	9	AG364646	AG364646 Mus muscu	c 962	51.2	3.0	213	4	BM155328	BM155328 fw02b03.y
890	51.6	3.1	818	5	BUS050474	BUS050474 AGENCOURT	c 963	51.2	3.0	217	4	BG981736	BG981736 MR3-CN014
891	51.6	3.1	833	5	BUS50474	BUS50474 AGENCOURT	c 964	51.2	3.0	218	4	BM154944	BM154944 fv91e06.y
892	51.6	3.1	853	1	AV758844	AV758844 AV758844	c 965	51.2	3.0	219	1	AL714277	AL714277 AL714277
893	51.6	3.1	855	7	CN330709	CN330709 AGENCOURT	c 966	51.2	3.0	219	1	AL714277	AL714277 AL714277
894	51.6	3.1	856	2	BE309150	BE309150 601501758	967	51.2	3.0	219	4	BM154546	BM154546 fv86d07.y
895	51.6	3.1	866	7	CF765154	CF765154 CES002716	968	51.2	3.0	220	4	BM573836	BM573836 fy04f07.y
896	51.6	3.1	868	5	BUS30888	BUS30888 AGENCOURT	969	51.2	3.0	225	4	BM154392	BM154392 fv84e06.y
897	51.6	3.1	869	5	BUS566247	BUS566247 AGENCOURT	970	51.2	3.0	225	4	BM186096	BM186096 fv97h07.y
898	51.6	3.1	902	2	BF575271	BF575271 602133679	971	51.2	3.0	230	4	BM186042	BM186042 fv97h12.y
899	51.6	3.1	926	5	BUS54921	BUS54921 AGENCOURT	972	51.2	3.0	231	7	CO181733	CO181733 EC14891.5
900	51.6	3.1	932	3	CR648408	CR648408 Tetraodon	973	51.2	3.0	233	5	BQ786705	BQ786705 saq72b12.

1120	50.8	3.0	499	7	C0726605	C0726605 ILLUMIGEN	1193	50.6	3.0	397	7	CF546355	CF546355 lae71h04.
1121	50.8	3.0	514	7	CN833696	CN833696 AGENCOURT	c1194	50.6	3.0	402	2	AW190286	AW190286 x113004.x
1122	50.8	3.0	546	7	CF123716	CF123716 UI-HF-CH0	1195	50.6	3.0	408	7	CN048707	CN048707 V2_P1_O13
1123	50.8	3.0	556	7	CV199827	CV199827 km20h10.y	1196	50.6	3.0	409	4	BI899036	BI899036 480885 MA
1124	50.8	3.0	571	5	B0747579	B0747579 UI-M-FA0-	1197	50.6	3.0	409	7	CK384344	CK384344 lah22c05.
1125	50.8	3.0	577	4	CB524184	CB524184 UI-M-GK0-	1198	50.6	3.0	412	6	CB075778	CB075778 hz51b09.b
1126	50.8	3.0	642	4	BI870877	BI870877 603394773	1199	50.6	3.0	414	5	EX504814	EX504814 DKFp686J
c1127	50.8	3.0	651	8	AQ510797	AQ510797 rdx50048J	1200	50.6	3.0	431	7	CF123177	CF123177 UI-HF-CH0
1128	50.8	3.0	659	6	CD642013	CD642013 AGENCOURT	1201	50.6	3.0	432	1	AL725854	AL725854 AJ725854
1129	50.8	3.0	660	1	AV704928	AV704928 AV704928	1202	50.6	3.0	434	1	AJ791630	AJ791630 AJ791630
1130	50.8	3.0	702	7	CV520959	CV520959 0089P0052	1203	50.6	3.0	434	1	AL719646	AL719646 AL719646
1131	50.8	3.0	717	7	CF981073	CF981073 re02e06.y	1204	50.6	3.0	436	1	AL729450	AL729450 AL729450
1132	50.8	3.0	723	1	AV733682	AV733682 AV733682	1205	50.6	3.0	437	1	AV682737	AV682737 AV682737
1133	50.8	3.0	741	7	CV491293	CV491293 AGENCOURT	1206	50.6	3.0	444	6	CD239166	CD239166 FNPBUC12
1134	50.8	3.0	781	6	CB318685	CB318685 AGENCOURT	1207	50.6	3.0	446	4	BM319186	BM319186 kJ180d11.y
c1135	50.8	3.0	815	8	BI9681	BI9681 F4H19-T7.1	1208	50.6	3.0	450	7	C0888261	C0888261 BovGen.16
c1136	50.8	3.0	817	8	BH156712	BH156712 ENTSM497F	1209	50.6	3.0	451	1	AL721247	AL721247 AL721247
1137	50.8	3.0	820	4	BF968558	BF968558 602271159	1210	50.6	3.0	451	2	BE883021	BE883021 601510028
1138	50.8	3.0	822	5	B0843356	B0843356 AGENCOURT	1211	50.6	3.0	459	7	CF980375	CF980375 re04b03.y
1139	50.8	3.0	822	9	CNS00911	AL052989 Drosophila	1212	50.6	3.0	462	4	BM569326	BM569326 kJ59F02.y
1140	50.8	3.0	830	7	CK395910	CK395910 AGENCOURT	1213	50.6	3.0	463	6	CB445238	CB445238 696490 MA
1141	50.8	3.0	832	5	B0842545	B0842545 AGENCOURT	1214	50.6	3.0	464	4	BM517997	BM517997 kI86e09.y
1142	50.8	3.0	835	5	B0529221	B0529221 AGENCOURT	1215	50.6	3.0	465	4	BM517871	BM517871 kI83f02.y
c1143	50.8	3.0	836	5	B0565750	B0565750 AGENCOURT	c1216	50.6	3.0	468	6	CF047285	CF047285 QCK6904.y
1144	50.8	3.0	847	7	C0847224	C0847224 ILLUMIGEN	1217	50.6	3.0	471	4	BI702656	BI702656 ffs5h03.y
c1145	50.8	3.0	881	7	CK151831	CK151831 FGAS03458	1218	50.6	3.0	475	4	BM567111	BM567111 kJ110c09.y
c1146	50.8	3.0	886	7	CK157081	CK157081 FGAS03815	1219	50.6	3.0	482	7	CF124659	CF124659 UI-HF-CH0
c1147	50.8	3.0	886	7	CK161161	CK161161 FGAS04285	1220	50.6	3.0	501	1	AJ798819	AJ798819 AJ798819
c1148	50.8	3.0	891	9	CNS0092U	AL053767 Drosophila	1221	50.6	3.0	509	6	CB080062	CB080062 hp80f10.b
1149	50.8	3.0	905	7	CH322888	CH322888 AGENCOURT	1222	50.6	3.0	571	5	BP256021	BP256021 BP256021
c1150	50.8	3.0	908	7	CV066886	CV066886 WNE19e5 W	1223	50.6	3.0	581	5	BP375614	BP375614 ENEL10099
1151	50.8	3.0	909	7	CK407058	CK407058 AUF_Iflvr	1224	50.6	3.0	584	7	CV053519	CV053519 ENEL10099
1152	50.8	3.0	926	4	BG575702	BG575702 602598774	1225	50.6	3.0	585	7	CO403863	CO403863 AGENCOURT
1153	50.8	3.0	940	6	CK386618	CK386618 AGENCOURT	c1226	50.6	3.0	597	4	BG572394	BG572394 602593434
1154	50.8	3.0	955	2	BE890041	BE890041 601512310	1227	50.6	3.0	606	5	BUL14551	BUL14551 603131443
1155	50.8	3.0	956	6	CD512769	CD512769 AGENCOURT	1228	50.6	3.0	614	6	CB980039	CB980039 CAB70001
c1156	50.8	3.0	975	3	CR733776	CR733776 Tetraodon	1229	50.6	3.0	617	7	CF370504	CF370504 f950b02.y
c1157	50.8	3.0	996	9	CNS04XL6	AL311811 Tetraodon	1230	50.6	3.0	624	5	BP382214	BP382214 BP382214
c1158	50.8	3.0	1009	9	AG392861	AG392861 Mus muscu	1231	50.6	3.0	634	7	CK320427	CK320427 L3P07d09
1159	50.8	3.0	1023	5	B0506457	B0506457 AGENCOURT	1232	50.6	3.0	638	4	BG218217	BG218217 RST37944
1160	50.8	3.0	1031	9	CNS016VY	B0506457 Drosophila	1233	50.6	3.0	642	7	CK456995	CK456995 921256 MA
1161	50.8	3.0	1098	6	CD049441	CD049441 AGENCOURT	1234	50.6	3.0	717	8	AZ849900	AZ849900 2M0151103
1162	50.8	3.0	1101	9	CNS016TQ	AL107192 Drosophila	1235	50.6	3.0	722	7	CV064765	CV064765 WNE1445
c1163	50.8	3.0	1151	9	AG324438	AG324438 Mus muscu	1236	50.6	3.0	752	6	CD521791	CD521791 AGENCOURT
c1164	50.8	3.0	1227	9	AG361182	AG361182 Mus muscu	c1237	50.6	3.0	771	9	AG517090	AG517090 Mus muscu
c1165	50.8	3.0	1274	9	AG341312	AG341312 Mus muscu	1238	50.6	3.0	772	5	B0598222	B0598222 AGENCOURT
1166	50.8	3.0	1690	9	CL078351	CL078351 CH216-149	1239	50.6	3.0	801	7	CF289632	CF289632 AGENCOURT
1167	50.8	3.0	4796	3	CR749476	CR749476 Homo sapi	1240	50.6	3.0	803	5	BU565241	BU565241 AGENCOURT
1168	50.6	3.0	157	4	BM513623	BM513623 Kx97b03.y	1241	50.6	3.0	806	7	CK128745	CK128745 AGENCOURT
1169	50.6	3.0	169	1	AL697897	AL697897 DKFp686A	1242	50.6	3.0	809	5	BU843613	BU843613 AGENCOURT
1170	50.6	3.0	191	4	BI705400	BI705400 fr58g02.y	1243	50.6	3.0	813	5	BU842611	BU842611 AGENCOURT
1171	50.6	3.0	193	4	BM530850	BM530850 fy17e12.y	c1244	50.6	3.0	814	7	CK200263	CK200263 FGAS00877
1172	50.6	3.0	194	4	BM154531	BM154531 fy86c02.y	1245	50.6	3.0	816	5	BU564811	BU564811 AGENCOURT
1173	50.6	3.0	196	4	BI705266	BI705266 fr55f03.y	1246	50.6	3.0	826	9	CL043364	CL043364 CH216-560
1174	50.6	3.0	210	4	BM154362	BM154362 fv84b10.y	1247	50.6	3.0	827	9	BH182445	BH182445 021_O13-
1175	50.6	3.0	220	5	B0785757	B0785757 saq87c03	1248	50.6	3.0	827	9	CL619394	CL619394 T7 end of
1176	50.6	3.0	222	7	CF926234	CF926234 laf86e09	1249	50.6	3.0	829	5	BU531959	BU531959 AGENCOURT
1177	50.6	3.0	236	4	BI681181	BI681181 460497 MA	1250	50.6	3.0	832	9	CNS00818	AL051195 Drosophila
1178	50.6	3.0	236	7	CP754919	CP754919 lae09c01	1251	50.6	3.0	833	5	BU588052	BU588052 AGENCOURT
c1179	50.6	3.0	252	6	CB0433981	CB0433981 NISC GC01	1252	50.6	3.0	833	5	BU588052	BU588052 AGENCOURT
c1180	50.6	3.0	287	6	CB343712	CB343712 CA3ZEN000	1253	50.6	3.0	844	9	AG058605	AG058605 Fan trogl
1181	50.6	3.0	291	7	CO195274	CO195274 EC39963.5	1254	50.6	3.0	845	5	BU537023	BU537023 AGENCOURT
1182	50.6	3.0	318	6	CB984581	CB984581 AGENCOURT	1255	50.6	3.0	853	5	BU537023	BU537023 AGENCOURT
c1183	50.6	3.0	337	5	B0780082	B0780082 UI-R-FF0-	1256	50.6	3.0	854	5	BU603992	BU603992 AGENCOURT
1184	50.6	3.0	345	2	BE878725	BE878725 601492990	1257	50.6	3.0	859	7	CO808031	CO808031 AGENCOURT
1185	50.6	3.0	346	5	BK476056	BK476056 DKFp686B	c1258	50.6	3.0	868	7	CK200194	CK200194 FGAS00870
1186	50.6	3.0	348	6	CB704554	CB704554 AMGNNUC:S	1259	50.6	3.0	874	6	CB844981	CB844981 MZPN-0547
1187	50.6	3.0	375	3	AY068947	AY068947 Schmidtea	1260	50.6	3.0	876	7	CN323414	CN323414 AGENCOURT
1188	50.6	3.0	377	1	AL722378	AL722378 AL722378	1261	50.6	3.0	881	8	AZ200698	AZ200698 SP 1026 A
c1189	50.6	3.0	386	6	CB044394	CB044394 NISC GC04	1262	50.6	3.0	883	9	CL067381	CL067381 CH216-110
1190	50.6	3.0	387	1	AA204368	AA204368 mu31c08.r	1263	50.6	3.0	886	9	CNS011SM	AL100672 Drosophila
1191	50.6	3.0	391	4	BQ688931	BQ688931 BUC	c1264	50.6	3.0	888	4	BM415362	BM415362 OP20436 M
c1192	50.6	3.0	391	5	BQ395470	BQ395470 NISC ng15	c1265	50.6	3.0	888	7	CK160993	CK160993 FGAS004266

1266	50.6	3.0	889	5	BU851997	BU851997	AGENCOURT	1339	50.4	3.0	762	7	CK397238	CK397238	AGENCOURT
1267	50.6	3.0	904	4	BI859386	603388113		1340	50.4	3.0	771	5	BU560352	AGENCOURT	
1268	50.6	3.0	915	4	BU518636	602578491		1341	50.4	3.0	777	2	BE875022	BE875022	601487588
1269	50.6	3.0	915	5	BQ718652	AGENCOURT		c1342	50.4	3.0	778	9	AG586300	Mus muscu	
1270	50.6	3.0	916	5	BU588527	AGENCOURT		1343	50.4	3.0	787	5	BU536254	AGENCOURT	
1271	50.6	3.0	936	5	BQ233428	AGENCOURT		1344	50.4	3.0	802	6	CD000230	AGENCOURT	
1272	50.6	3.0	937	9	CNS00120	Drosophil		c1345	50.4	3.0	803	4	BG335466	602403936	
1273	50.6	3.0	941	5	BU534769	AGENCOURT		1346	50.4	3.0	818	5	BU529789	AGENCOURT	
1274	50.6	3.0	944	5	BQ431642	AGENCOURT		c1347	50.4	3.0	828	8	AZ194425	SP_1026_A	
1275	50.6	3.0	955	5	BU533926	AGENCOURT		1348	50.4	3.0	844	9	AG129984	Pan trogl	
1276	50.6	3.0	955	5	BU566880	AGENCOURT		1349	50.4	3.0	858	9	CNS0127J	Drosophil	
1277	50.6	3.0	956	7	CK423987	AUF IpSto		1350	50.4	3.0	873	7	CF455006	AGENCOURT	
1278	50.6	3.0	960	6	CB597408	AGENCOURT		c1351	50.4	3.0	877	7	CK159921	FGAS04144	
c1279	50.6	3.0	962	8	AZ680445	ENTM50TR		1352	50.4	3.0	892	5	BU960887	AGENCOURT	
1280	50.6	3.0	978	4	BF969662	602272040		1353	50.4	3.0	895	6	CB229191	AGENCOURT	
c1281	50.6	3.0	1005	8	BH164025	ENTQU60TF		1354	50.4	3.0	908	6	CD513633	AGENCOURT	
1282	50.6	3.0	1054	3	AF130104	Homo sapi		1355	50.4	3.0	912	5	BU529547	AGENCOURT	
1283	50.6	3.0	1063	5	BU840218	AGENCOURT		1356	50.4	3.0	916	5	CNS06VOC	T3 end of	
1284	50.6	3.0	1101	9	CNS00FJ7	AGENCOURT		1357	50.4	3.0	923	5	BU533956	AGENCOURT	
1285	50.6	3.0	1122	4	BU501454	602548028		1358	50.4	3.0	892	5	BU960887	AGENCOURT	
c1286	50.6	3.0	1124	9	AG288406	Mus muscu		1359	50.4	3.0	998	6	CD049247	AGENCOURT	
1287	50.6	3.0	1150	6	CD249726	AGENCOURT		1360	50.4	3.0	1011	5	BU934341	AGENCOURT	
1288	50.6	3.0	1165	9	CL051682	CH216-74F		1361	50.4	3.0	1038	6	CD249177	AGENCOURT	
c1289	50.6	3.0	1178	9	AG430313	Mus muscu		1362	50.4	3.0	1081	5	BU510236	AGENCOURT	
c1290	50.6	3.0	1260	3	AY108843	Zea mays		c1363	50.4	3.0	1095	9	CNS016E8	Drosophil	
1291	50.6	3.0	1380	6	CD248372	AGENCOURT		1364	50.4	3.0	1114	4	BM452203	AGENCOURT	
1292	50.6	3.0	1908	8	CC230203	CH261-62P		c1365	50.4	3.0	1161	9	AG365964	Mus muscu	
1293	50.6	3.0	3517	3	BC030264	Homo sapi		1366	50.4	3.0	1205	4	BM544190	AGENCOURT	
1294	50.6	3.0	3543	3	HSMB03534	AGENCOURT		1367	50.4	3.0	1291	5	BQ231056	AGENCOURT	
1295	50.4	3.0	141	7	CK467264	938548 MA		1368	50.4	3.0	1504	3	BC023270	Homo sapi	
1296	50.4	3.0	164	7	CS548135	CR548135	DKFZp4591	1369	50.4	3.0	1651	9	CL079030	CH216-154	
1297	50.4	3.0	213	7	CF118240	FB351.21		c1370	50.2	3.0	199	5	BQ326520	MR4-CN014	
1298	50.4	3.0	261	7	CR763363	DKFZp4701		c1371	50.2	3.0	201	4	BG981501	MR3-CN014	
1299	50.4	3.0	270	4	BM281117	K109f12.Y		c1372	50.2	3.0	203	6	CA667413	w1eul.pk0	
1300	50.4	3.0	273	4	BI089262	602853209		1373	50.2	3.0	207	7	CN276442	170006001	
1301	50.4	3.0	278	5	BQ289264	PJ27g05.Y		1374	50.2	3.0	208	6	CA802715	sau41a12.	
1302	50.4	3.0	278	6	CD641261	AGENCOURT		1375	50.2	3.0	209	7	CO182797	EC24037.5	
1303	50.4	3.0	293	4	BI855783	603382721		1376	50.2	3.0	211	2	BE013113	122910 MA	
1304	50.4	3.0	296	1	AI856737	sb41e07.Y		1377	50.2	3.0	214	4	BM265899	fw37b09.Y	
1305	50.4	3.0	306	1	AA789781	Yt99c07.Y		1378	50.2	3.0	216	4	BM155135	fw09b04.Y	
1306	50.4	3.0	307	6	CD722153	AGENCOURT		1379	50.2	3.0	220	7	CF383299	lac39c02.	
1307	50.4	3.0	378	1	AV760102	AGENCOURT		1380	50.2	3.0	223	5	BQ276953	AGENCOURT	
1308	50.4	3.0	382	6	CA987506	AGENCOURT		1381	50.2	3.0	239	4	BM532471	fy08e08.Y	
1309	50.4	3.0	408	6	CB9770419	AMGNNUC:S		1382	50.2	3.0	241	4	BM186126	fv98c06.Y	
1310	50.4	3.0	419	5	BU530428	AGENCOURT		1383	50.2	3.0	243	7	CO193787	EC36808.5	
1311	50.4	3.0	419	6	CS934821	laa44h01.		c1384	50.2	3.0	252	7	CF212181	CGF100066	
1312	50.4	3.0	430	6	CS075623	h249c09.b		1385	50.2	3.0	270	7	CK625724	mjl3e12.Y	
1313	50.4	3.0	435	4	BM283047	ki44d10.Y		1386	50.2	3.0	271	6	CA802092	sau30a04.	
1314	50.4	3.0	466	4	BM567650	sak77a05.		1387	50.2	3.0	296	2	BE059362	sn31g07.Y	
1315	50.4	3.0	471	5	BU851050	AGENCOURT		1388	50.2	3.0	301	7	CF123294	UI-HF-CHO	
c1316	50.4	3.0	480	5	BQ398528	NISC_mc08		1389	50.2	3.0	301	7	CF123294	UI-HF-CHO	
1317	50.4	3.0	493	7	CF314113	HD--02-10		1390	50.2	3.0	317	1	AI349964	ta97h04.x	
1318	50.4	3.0	500	2	BF882334	IL3-ET011		1391	50.2	3.0	346	6	CF546293	AMGNNUC:S	
1319	50.4	3.0	500	4	BG571546	602592845		1392	50.2	3.0	346	7	CF546293	lae70e12.	
1320	50.4	3.0	501	6	CA336663	NISC_LV03		1393	50.2	3.0	347	6	CB705238	AGNNNUC:Y	
1321	50.4	3.0	518	7	CK431061	oj57d12.Y		1394	50.2	3.0	365	4	BI941631	sc80f10.Y	
1322	50.4	3.0	531	1	AL712171	DKFZp686D		1395	50.2	3.0	374	7	CO878391	BoyGen.06	
1323	50.4	3.0	538	1	AV757416	AV757416		1396	50.2	3.0	377	7	CO195922	EC43542.5	
1324	50.4	3.0	568	7	CV285468	tak47h02.		1397	50.2	3.0	378	7	CF124412	UI-HF-CHO	
c1325	50.4	3.0	571	5	BQ522127	NISC nl14		1398	50.2	3.0	386	2	BF037097	601456863	
c1326	50.4	3.0	579	6	CB607201	AMGNNUC:S		1399	50.2	3.0	417	7	CK384549	lah26f05.	
1327	50.4	3.0	582	5	BP249933	BP249933		1400	50.2	3.0	420	1	AL711793	DKFZp686B	
1328	50.4	3.0	595	8	BH189680	001_K_11-		1401	50.2	3.0	426	7	CK421093	AUF IpSpn	
1329	50.4	3.0	607	1	AL729731	T3_end of		1402	50.2	3.0	427	2	BF793360	602254790	
1330	50.4	3.0	641	1	AV735039	AV735039		1403	50.2	3.0	442	1	AV763658	AV763658	
1331	50.4	3.0	643	5	BQ747828	UI-M-FA0-		1404	50.2	3.0	444	7	CF612777	laf06b12.	
1332	50.4	3.0	662	7	CF350633	r153c08.Y		1405	50.2	3.0	449	4	BI380861	BFGL1_002	
1333	50.4	3.0	682	4	BM734248	kj12e12.Y		1406	50.2	3.0	457	8	AQ752942	HS 5231_A	
1334	50.4	3.0	693	7	CO581501	ILLUMIGEN		c1407	50.2	3.0	471	7	CF307986	ABF--01-J	
1335	50.4	3.0	732	9	AG546088	Mus muscu		1408	50.2	3.0	483	1	CF315792	HD--04-NL	
c1336	50.4	3.0	741	7	CN842216	AGENCOURT		1409	50.2	3.0	490	1	AV756619	AV756619	
1337	50.4	3.0	743	9	AG285987	Mus muscu		1410	50.2	3.0	525	5	BP683189	BP683189	
c1338	50.4	3.0					1411	50.2	3.0	525	7	CV066363	WNEL3a1 W		

1412	50.2	3.0	538	1	AL727686	AL727686	AL727686	1485	50	3.0	346	2	BF751308	BF751308	RC3-BN042
1413	50.2	3.0	601	6	CD239085	FNPBK001	AD732976	1486	50	3.0	350	2	BF806065	BF806065	MR1-C1018
1414	50.2	3.0	603	1	AV732976	AV732976	AD732976	1487	50	3.0	354	7	CK428760	CK428760	la16b02
1415	50.2	3.0	604	5	BP271854	BP271854	CD239279	1488	50	3.0	361	7	CK004628	CK004628	AGENCOURT
1416	50.2	3.0	609	6	CD239279	FNPBMF09	CD239279	1489	50	3.0	363	7	CV194197	CV194197	SnESTbaa9
1417	50.2	3.0	609	6	CD239341	FNPBND08	CD239341	1490	50	3.0	372	7	CF801074	CF801074	xj71d08.Y
1418	50.2	3.0	653	9	CNS02MID	AL203530	Tetraodon	1491	50	3.0	375	2	AW827214	AW827214	xn09f12.Y
1419	50.2	3.0	693	1	AV734099	AV734099	BUS37749	1492	50	3.0	390	7	CF425690	CF425690	lad3a05
1420	50.2	3.0	750	5	BUS37749	AGENCOURT	BUS37749	1493	50	3.0	392	5	BQ290505	BQ290505	NXR045.B
1421	50.2	3.0	754	6	CD523365	CD523365	AGENCOURT	1494	50	3.0	402	7	CO192753	CO192753	EC34419.5
1422	50.2	3.0	759	8	B12963	T23D1-T7.1	B12963	1495	50	3.0	405	5	BU055967	BU055967	UI-M-FP0-
1423	50.2	3.0	781	9	AG592717	Mus muscu	AG592717	1496	50	3.0	406	6	CB975383	CB975383	CAB30006
1424	50.2	3.0	782	5	EX422198	EX422198	AV757528	1497	50	3.0	408	5	BQ126842	BQ126842	ii19h05.Y
1425	50.2	3.0	802	1	AV757528	AV757528	Mus muscu	1498	50	3.0	408	7	CK565162	CK565162	vor12a2.D
1426	50.2	3.0	802	9	AG452709	AG452709	Mus muscu	1499	50	3.0	408	7	AA597163	AA597163	do35h02.r
1427	50.2	3.0	840	7	CV486146	CV486146	AGENCOURT	1500	50	3.0	424	1	CK233937	CK233937	re21f12.Y
1428	50.2	3.0	847	6	CD250700	CD250700	AGENCOURT								
1429	50.2	3.0	864	5	BU850507	BU850507	AGENCOURT								
1430	50.2	3.0	868	7	CK158040	CK158040	FGAS03924								
1431	50.2	3.0	875	7	CK159714	CK159714	FGAS04120								
1432	50.2	3.0	880	9	AG439347	AG439347	Mus muscu								
1433	50.2	3.0	883	5	BU181547	BU181547	AGENCOURT								
1434	50.2	3.0	891	7	CK169028	CK169028	FGAS04363								
1435	50.2	3.0	899	7	CK157998	CK157998	FGAS03920								
1436	50.2	3.0	915	7	CK160067	CK160067	FGAS04160								
1437	50.2	3.0	927	5	BQ920326	BQ920326	AGENCOURT								
1438	50.2	3.0	927	7	CK403949	CK403949	AUF IfhdK								
1439	50.2	3.0	930	7	CK406519	CK406519	AUF Iflvr								
1440	50.2	3.0	940	5	BU536064	BU536064	AGENCOURT								
1441	50.2	3.0	974	5	BQ277100	BQ277100	AGENCOURT								
1442	50.2	3.0	978	6	CD248362	CD248362	AGENCOURT								
1443	50.2	3.0	991	9	CNS0012D	AL074343	Drosophil								
1444	50.2	3.0	993	5	BUS65978	BUS65978	AGENCOURT								
1445	50.2	3.0	996	5	CNS06HDI	AL398872	T7 end of								
1446	50.2	3.0	999	5	BU513295	BU513295	AGENCOURT								
1447	50.2	3.0	999	6	CD107489	CD107489	AGENCOURT								
1448	50.2	3.0	1022	9	AJ591981	AJ591981	Arabidops								
1449	50.2	3.0	1030	2	BF339600	BF339600	602039073								
1450	50.2	3.0	1065	4	BG119329	BG119329	602349008								
1451	50.2	3.0	1101	9	CNS012TP	AL102007	Drosophil								
1452	50.2	3.0	1101	9	CNS012TP	AL108548	Drosophil								
1453	50.2	3.0	1190	4	B1872043	B1872043	603396339								
1454	50.2	3.0	1208	4	BM548834	BM548834	AGENCOURT								
1455	50.2	3.0	1284	9	AG324289	AG324289	Mus muscu								
1456	50.2	3.0	1372	9	CL647622	CL647622	CH213-143								
1457	50.2	3.0	1372	9	CL114085	CL114085	ISB1-591								
1458	50.2	3.0	1730	9	CL078531	CL078531	CH216-151								
1459	50.2	3.0	2677	3	BC040828	BC040828	Mus muscu								
1460	50.2	3.0	3191	3	HSN804649	AL833336	Homo sapi								
1461	50.2	3.0	148	7	CO726601	CO726601	ILLUMIGEN								
1462	50.2	3.0	149	7	CF124930	CF124930	UI-HF-CHO								
1463	50.2	3.0	157	2	AW268072	AW268072	xr92d05.x								
1464	50.2	3.0	170	7	CO417512	CO417512	Mdf33012P								
1465	50.2	3.0	172	7	COL65849	COL65849	FLD1-57_B								
1466	50.2	3.0	179	5	BQ077081	BQ077081	fz12d12.Y								
1467	50.2	3.0	180	7	CF3377194	CF3377194	lah99e05								
1468	50.2	3.0	192	7	CF315538	CF315538	HD--04-H2								
1469	50.2	3.0	217	6	CA673076	CA673076	wlsu2.pk0								
1470	50.2	3.0	222	4	B1671666	B1671666	f851c07.Y								
1471	50.2	3.0	239	5	BQ934222	BQ934222	fy97f10.Y								
1472	50.2	3.0	241	7	CF123101	CF123101	UI-HF-CHO								
1473	50.2	3.0	248	7	CF969088	CF969088	lag05b05								
1474	50.2	3.0	249	2	B8666137	B8666137	149188.MA								
1475	50.2	3.0	256	4	BG651431	BG651431	sad46f04								
1476	50.2	3.0	264	4	BM155516	BM155516	fw06h05.Y								
1477	50.2	3.0	281	6	CA934992	CA934992	saue2c06								
1478	50.2	3.0	284	7	CF804419	CF804419	lad72e02								
1479	50.2	3.0	289	6	CA668025	CA668025	wlsu1.pk0								
1480	50.2	3.0	301	5	BUS63515	BUS63515	AGENCOURT								
1481	50.2	3.0	303	4	BG514981	BG514981	dad27a10								
1482	50.2	3.0	309	9	CE319405	CE319405	tigr-g8a								
1483	50.2	3.0	321	7	CF331988	CF331988	NACL--08								
1484	50.2	3.0	324	2	AW306965	AW306965	sf51a09.Y								

ALIGNMENTS

RESULT 1	AK045973	1808 bp	mus musculus adult male corpora quadrigemina cDNA, RIKEN	linear	HTC 03-APR-2004
LOCUS	AK045973				
DEFINITION	AK045973				
ACCESSION	AK045973				
VERSION	AK045973.1	GI:26337738			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
JOURNAL	High-efficiency full-length cDNA cloning				
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	99279253				
REFERENCE	10349636				
AUTHORS	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
PUBMED	11076861				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6 (bases 1 to 1808)				

AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submision
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 1808 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:B230328N06" /clone="B230328N06" /sex="male" /tissue type="corpora quadrigemina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stages="adult" 204. .1238 /note="unnamed protein product; NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT 062718, evidence: FASTV, 99.4%ID, 92.1%length, match=951) putative" /codon_start=1 /protein_id="BAC32555.1" /db_xref="GI:26337739" /translation="MKTQAKMNSISWAIFTGLAALCLFGVPRVSGDATFPKAMDN VTRQGSATLRCTIDNRVTRVWLNSTILYAGNDKWLDPRLVLLSNTQYSIEI QNVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINSGNNISLCIAT GRPPTVTRHHSFPAKGVFSEBYLEIQITREOSGEYECNSANDVAAPVVRKVT VNPYPYISEAKGTGPVQKGLQCEASAVSFQWPKDKRLVEGKGVKVENRPF LSKLTFNVSSHDYGNVTCVASNKLGHNTASIMLFGPQAVSEVNNGTSRRAGCIWLLP LLLVLLLLKPF"
FEATURES	
source	
CDS	
ORIGIN	
Query Match	66.7%; Score 1119.4; DB 3; Length 1808;
Best Local Similarity	83.1%; Pred. No. 1.8e-278;
Matches 1417; Conservative	0; Mismatches 251; Indels 37; Gaps 11;
Qy	1 GTTGTGCTTCAGCAACACAGTGGATTAAATCTCCTTGACACAGCTTGAGACAC 60
Db	59 GTTGTGCTTCAGCAACACAGTGGATTAAATCTCCTTGACACAGCTTGAGACAC 118
Qy	61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 108
Db	119 AATCTATCAGGAGGAAAGAAAGAAAGAGAGACAGAGGAAAGAAAGAAAGAAAG 178
Qy	109 AAGAAAAG 168
Db	179 AAAAAAG 238
Qy	169 CTCTTGGGCAATCTTACGGGGCTGGCTGTCTGTCTCTTCTTCCAGAGAGTGCCTGCG 228
Db	239 CTCTGTTGGCAATCTTACGGGGCTGGGGCTCTGTGCTCTTCTTCCAGAGAGTGCCTGCG 298
Qy	229 CAGCGAGATGCCACCTTCTCCCAAAGCTATAGGACAAAGTGAAGCTGCGGACAGGGGAGAG 288
Db	299 TAGCGGAGATGCCACCTTCTCCCAAAGCTATAGGACAAAGTGAAGCTGCGGACAGGGGAGAG 358
Qy	289 CGCCACCTCAGGTGCACTATTGACACCGGGTCAACCGGGTGCCTGGCTTAAACCCGAG 348
Db	359 CGCCACCTCAGGTGCACTATTGACACCGGGTCAACCGGGTGCCTGGCTTAAACCCGAG 418
Qy	349 CACCATCTCTATCTCGGAATGACAAAGTGTGCTGTGATCTCTCGGTGGTCTTCTTGAG 408
Db	419 TACCATCTCTATCTCGGAATGACAAAGTGTGCTGTGATCTCTGTGTGCTCTCTTGAG 478
Qy	409 CAACACCAAAAGCAGTACAGCATCGAGATCCAGAAAGTGTGATGTATGACGAGGGCCC 468
Db	479 TAACACCCAGACCCAGTACAGCATTTGAGATCCAGAAATGTGGATGTGATACGATGAGGGCCC 538
Qy	469 TTACACCTGTCTCGGTGACAGACAGACCAACCAACCAACCTCTAGGGTCCACCTCATTTGT 528
Db	539 TTATACCTGTCTCGGTGACAGACAGACCAACCAACCTCTAGGGTCCACCTCATTTGT 598
Qy	529 GCAAGTATCTCCCAAATTTGTAGAGATTTCTTTCAGATATCTCCATTAAATGAAGGAAACAA 588
Db	599 ACAAGTATCTCCCAAATTTGTAGAGATTTCTTTCAGATATCTCCATTAAATGAAGGAAACAA 658
Qy	589 TATTAGCTCATCTGTCATAGCAACTGTGTAGACAGACCTTACCGTTACTTGTGAGACACAT 648
Db	659 CATCAGCTCTCACTTGATAGCCACAGGTAGACCGGAGCTTACAGTAACCTGTGAGACATAT 718
Qy	649 CTCTCCCAAAGCGGTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGGCATCAC 708
Db	719 TTCTCCCAAAGCGGTGGCTTTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 778
Qy	709 CCGGAGCAGTACAGGAGTACAGAGTGCAGTGCCTCCAAATGACGTGGCGCGCGCGCTGGT 768
Db	779 TCGGGAACAGTACAGGAGTACAGAGTGCAGGCTCCCAACGACCTGGCGGACCAAGTGT 838
Qy	769 ACGGAGATGAAGTCAACCGTGAACCTATCCACCATCATTTTCAGAGCAAGGTACAGG 828
Db	839 ACGAAGAGTGAAGTCAACCGTGAACCTATCCACCATCATCTTCAGAAAGTGAAGGACAGG 898
Qy	829 TGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGGACGA 888
Db	899 TGTCCCGTGGGACAAAGGGGACCTCTGCACTGTGAAGCTTCCGAGTCCCTTCAGACGA 958
Qy	889 ATTCAGTGTGTACAAAGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGA 948
Db	959 ATTTCAATGGTTCAAGGATGACAAAGACTGGTTCGAAGGAAAGAAAGGGAGTCAAGTGA 1018
Qy	949 AAAAGACCTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAAACATGACTATGGGAA 1008
Db	1019 AAAAGACCTTTCTCTTCAAAACTCAGCTTTTTCAGCTCTCTGAAACATGACTATGGGAA 1078
Qy	1009 CTACACTTGGTGGCTTCCACAGCTGGGCGCACCAATGCGCCAGCATCATGCTATTGTTGG 1068
Db	1079 CTACACTTGGTGGCTTCCACAGCTGGGTCACCAACACGCCAGCATCATGCTATTGTTGG 1138
Qy	1069 TCCAGGCGCGCTCAGCAGAGTGAACAAACGGCACTGTCGAGGAGGGCAGGCTCGCTTGCT 1128
Db	1139 TCCCGTGTCTCAGTGAAGTCAACATGGGACATCAAGGAGGGCAGGCTGCAATTTGGCT 1198
Qy	1129 GCTGCTCTTCTGTGTGCACTGCTTCTCAAAATTTTGTATGTGAGTGCCACTTCCCGAC 1188
Db	1199 CCTCCCTCTTCTGTGTGCACTGCTTCTCAAAATTTTGTATGTGAGTGCCCTTCCCTGTC 1258
Qy	1189 CCGGGAAGGCTCGCGCCACCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1248
Db	1259 TGGGGAGA-GCTGCTGCCCGCATC---TCAATACACAGCAGCTG-----CAAAATGA 1308
Qy	1249 ACCAATCAGATATATACAAATTAAGAAATTAAGAAACACAGCCTCATGGGACAGAAATTTG 1308

Db	1309	AGCAACAGGTCAGAAATCAAAATGAAATTCGAGATCAAGCC-AATGAGACAGAAATTCG	1367
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Db	1368	AGGGAGGAGGACAAAGCATACTGTGCTAAAGGGGAAAAAAGGTTTAAGAAAGGAAATT	1427
Qy	1361	TGAAAAATTGCTTGCAGATATTTAGGTACAAATGGAGTTTCTTT-TCCCAACGGGAAGA	1419
Db	1428	TGGAATTTGCTTGCAGATATTTCCGTACCGCTGAGTTTCTTTCTTTTCCCAAGTGGGA	1487
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Db	1488	AGAAGGCACACCTAGCTTGGACCCACCCACCAAGCTGCACCTGTGTGCACCTCTCTGTGTGCCA	1547
Qy	1479	GTGTGGGCAAGGGCTCAGCCTCTCTGCCAC-AGAGTGCCCCCAGCTGGAAACATTCCTGGA	1537
Db	1548	GGGTGGGCAAGGGCTCAGCCACTCTGCCACTTAAGTGCCCCACCATGAAACATTCCTGGA	1607
Qy	1538	GCTGGCCATCCCAATTCATCAATCAGTCCATAGACAGCAAGAATG---AGACCTTCCGGC	1594
Db	1608	GTGTGGCCATCCCAATTTTCATCGTCCATAGACACAGCAGCAGCAAGAAACAAGGGCC	1667
Qy	1595	CCAGCGTGGCGCTCGGGCACTTTGTGTAGACTGTGCCACACGCGCTGTGTGTGAAC	1654
Db	1668	TTAGATGTGCCAGGAAGGGCCCTTTGGTGGGCTGTGTGACAGTCGCGTGTGCATGAAGT	1727
Qy	1655	GTGAATAAAGAGCAAAAAA	1679
Db	1728	GTGAATCTCGGAGGAAGAAAAA	1752
RESULT 2			
AK046377			
LOCUS	AK046377	1808 bp	mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male corpora quadrigenina cDNA, RIKEN full-length enriched library, clone:B230377K17 product:NEUOTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK046377		
VERSION	AK046377.1 GI:26338018		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunsi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		

AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6		
AUTHORS	(baes 1 to 1808)		
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,		
JOURNAL	Fukuda, S., Furuno, M., Hanegaki, T., Hara, A., Hahizume, W.,		
REFERENCE	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,		
AUTHORS	Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,		
TITLE	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,		
JOURNAL	Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,		
REFERENCE	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,		
AUTHORS	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,		
TITLE	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,		
JOURNAL	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,		
REFERENCE	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,		
AUTHORS	Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of		
REFERENCE	Physical and Chemical Research (RIKEN), Laboratory for Genome		
AUTHORS	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),		
TITLE	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,		
JOURNAL	Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,		
REFERENCE	URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,		
AUTHORS	Fax: 81-45-503-9216)		
TITLE	CDNA library was prepared and sequenced in Mouse Genome		
JOURNAL	Encyclopedia Project of Genome Exploration Research Group in Riken		
REFERENCE	Genomic Sciences Center and Genome Science Laboratory in Riken.		
AUTHORS	Division of Experimental Animal Research in Riken contributed to		
TITLE	prepare mouse tissues.		
JOURNAL	Please visit our web site for further details.		
REFERENCE	URL: http://genome.gsc.riken.jp/		
AUTHORS	URL: http://fantom.gsc.riken.jp/		
TITLE	Location/Qualifiers		
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AUTHORS	/mol_type="mRNA"		
TITLE	/strain="C57BL/6J"		
JOURNAL	/db_xref="PANTOM.DB:B230377K17"		
MEDLINE	/db_xref="taxon:10090"		
PUBMED	/clone="B230377K17"		
REFERENCE	/sex="male"		
AUTHORS	/tissue_type="corpora quadrigenina"		
TITLE	/clone_lib="RIKEN full-length enriched mouse cDNA library"		
JOURNAL	/dev_stage="adult"		
MEDLINE	204. -1238		
PUBMED	/note="unnamed protein product; NEUOTRIMIN PRECURSOR		
REFERENCE	(GP5) homolog [Rattus norvegicus] (SWISSPROT Q02718,		
AUTHORS	evidence: FASTA, 99.4%ID, 92.1%length, match=951)		
TITLE	putative"		
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MEDLINE	/protein_id="BAC32695.1"		
PUBMED	/db_xref="GI:26338019"		
REFERENCE	/translation="MKTIOAKMNSISWAIFTGLAALCLFQGVPRVSGDATFPKAMDN		
AUTHORS	VTVQGSATLURCTIDNRVTKAWLNSTILYAGNDKWCDFRVLLSNTQYQYIEI		
TITLE	QNDVYDEGPTCVSQVDNHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTICAT		
JOURNAL	GRPPTVTRHISPKQFVSEDEYLTIGITREQSGEYCSASNDVAAPVVRKVT		
MEDLINE	VNYPPYSEAKGTGVPVQKCTLOCEASAVPSAFQFQDKDLVEGKGVKVENRPF		
PUBMED	LSKLTFFNVSEHDYGNVTCVASNKLIGHTNASIMLFGPGAVSEVNGTSRRACGIIWLLP		
REFERENCE	LLVLLHLKFP"		
AUTHORS			
TITLE	Query Match		
JOURNAL	Best Local Similarity 66.7%; Score 1119.4; DB 3; Length 1808;		
MEDLINE	Matches 1417; Conservative 0; Mismatches 251; Indels 37; Gaps 11;		
PUBMED	Qy 1 GTTGTGCTCTTCAGCAAAACAGTGAGTTAAATCTCTTTCAGCAAGCTTGAGAGCAACAC		
REFERENCE	60		

Db 59 GTTGTGCTCTTCAGCAAAACAGTGGATTAATCTCTCGACTAGCTTGTAGAGCAAC 118
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Qy 109 AAGAAAAAGAGAAAAAATCATGAACACCATCCAGCCAAATATGCAATCTAT 168
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Qy 349 CACCATCTCTATGTGGGAATGACAAAGTGTGCTCGATCTCTCGGTGCTCTTCTGAG 408
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Qy 409 CAACACCCAAACGAGTACAGATCGAGATCCAGAACCTGTGATGTGTATGAGGGGCC 468
Db 479 TAACACCCAGACCCAGTACAGATTCAGATCCAGAAATGTGGATGTGTACGATGAGGGCCC 538
Qy 469 TTACACCTCTCGGTGACAGACCAACCCAAAGACCTTAGGGTCCACCTCATGT 528
Db 539 TTATACCTCTCGGTGACAGACCAACCCAAAGACCTTAGGGTCCACCTCATGT 598
Qy 529 GCAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTTAATGAAGGAA 588
Db 599 ACAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTTAATGAAGGAA 658
Qy 589 TATTAGCTTACCTGATAGCAATCTGTGTAGACAGAGCTTACGGTTACTTGTGAGACAT 648
Db 659 CATCAGCTCTCTTGCATAGCCACAGGTAGACCGGAGCTTACAGTAACTCGAGACATAT 718
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Db 899 TGTCCCGTGGGCGAAGGGGACTCTGAGTGTGAAGCTTCCGAGTCCCTTACGAGA 958
Qy 889 ATTCCAGTGGTACAGGATGACAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGA 948
Db 959 ATTTCAATGGTTCAAGGATGACAAAGACTGTGCGAAGGAAAGAGGGAGTCAAGTGA 1018
Qy 949 AAACAGACTTCTCTCAAAACTCATCTTCTCAATGTCTCTGACATGACTATGGAA 1008
Db 1019 AAACAGACTTCTCTTCAAAACTCACCTTTTCAACGCTCTCTGAACATGACTATGGAA 1078
Qy 1009 CTACACTTGGTGGCTCTCAACAGCTGGCCACACCAATGCGCATCATCTGCTATTGG 1068
Db 1079 CTACACATGTGTGGCTTCAACAGCTGGGTCAACCAACGCGCATCATCTGCTATTGG 1138
Qy 1069 TCCAGGCGCGTACGAGGTGAGCAACGGCACTGTGAGGAGGGCAGCTCGTCTGGCT 1128

Db 1139 TCCCGTGTCTGTCTCAGTGGGTCAACAATGGGACATCAAGGAGGGCAGGCTGCATTTGGCT 1198
Qy 1129 GCTGCTCTTCTGTGTCTTGCACCTGTCTTCAAAATTTTGTGTGTGAGTGCCACTTCCCCAC 1188
Db 1199 CTTCCCTCTTCTGTGTCTTACACCTGTCTTCAAAATTTTGTGTGTGAGTGCCCTTCCCTGC 1258
Qy 1189 CCGGAAAGGCTGCGGCCACCCACCAACCAACAACAAGCAATGGGCAACACCCAGCAGA 1248
Db 1359 TGGGAGA-GCTGTGCGCACCGCATC--TCNATACACAGCAGCTG-----CAAAATGA 1308
Qy 1249 ACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCTCATGTGGACAGAAATTTG 1308
Db 1309 AGCAACAAGTCAGAAATCAAAATGAAATTCGAGAAATCACAGCC-AATGAGACAGAAATTCG 1367
Qy 1309 AGGAGGGGAACAAGATATCTTTG-----GGGGGAAAAGTTTAAAAAG--AAAT 1360
Db 1368 AGGAGGAGGACAAAGCATATCTGTGGTAAAGGGGAAAAAAGGTTTAAGAAAAAGAAAT 1427
Qy 1361 TGAATAATTCCTTGCAGATATTAGGTACAATGAGATTTTCTTT-TCCCAACCGGAAGA 1419
Db 1428 TGGAAATTCCTTGCAGATATTTCGGTACCGCTGAGTTTCTTCTTTTCCCAAGTGGGA 1487
Qy 1420 ACACAGCACACCCGGCTTGACCCA-CTGCAAGCTGATCGTGCAACCTCTTTGGTGCCA 1478
Db 1488 AGAAGGCACACCTAGCTTGGACCCACCAAGCTGCACCTGTGTGACCTCTCTGTGGCA 1547
Qy 1479 GTGTGGCCAGGGCTCAGCTCTCTGCCAC-AGAGTGGCCCCACAGTGGACATCTTGA 1537
Db 1548 GGGTGGGCAAGGGCTCAGCCACTCTGCCCACTAAAGTGGCCCCACCATGAACAATCTTGA 1607
Qy 1538 GCTGCCCATCCCAATTTCAATCAGTCCATAGACAGCAACAGAAATG---AGACCTTCCGGC 1594
Db 1608 GTTGGCCATCCCAATTTTCATCGTCCATAGACACAGCAGCAGCAAGAACAAAGGCC 1667
Qy 1595 CCAAGCTGGCGCTGCGGGCACTTTGTGTAGACTGTGCCACACCGCGTGTGTGTGAAC 1654
Db 1668 TTAGATGTGCCACGAAGGGCCCTTTGTGGGCTGTGTGACAGTCCGCTGTGTGATGAAGT 1727
Qy 1655 GTGAATAAAAAGAGCAAAAAA 1679
Db 1728 GTGAATCTGGAGGAAGAAAAA 1752

RESULT 3

CR602526
LOCUS full-length cDNA clone CS0DN005YD20 of Adult brain of Homo sapiens (human).
DEFINITION

ACCESSION CR602526.1 GI:50483333

VERSION CR602526

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2512)

Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

CONTACT : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

2 (bases 1 to 2512)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life technologies, a

division of Invitrogen.

Qy	1313	AGGGGACAAAGAATACTTTTGGGGGGAAAAAGAGTTTTTAAAAAAGAAAATTCGAATTGCCT	13172
Db	1001	AGGGGACAAAGAATACTTTTGGGGGGAAAAAGTTTTTAAAAAAGAAAATTCGAATTGCCT	10600
Qy	1373	TGCAGATATTAGGTACAATGGAGTTCTCTTTCCCAACCGGAGAACACACGACACACC	14322
Db	1061	TGCAGATATTAGGTACAATGGAGTTCTCTTTCCCAACCGGAGAACACACGACACACC	11200
Qy	1433	GGCTTGACCCACTGCGAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGCAAGGGC	14922
Db	1121	GGCTTGACCCACTGCGAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGCAAGGGC	11800
Qy	1493	TCAGCTCTCTGCCCCACAGAGTGCCCCCACGCTGGAACATTTCTGAGAGTGGCCATCCCAA	15522
Db	1181	TCAGCTCTCTGCCCCACAGAGTGCCCCCACGCTGGAACATTTCTGAGAGTGGCCATCCCAA	12400
Qy	1553	TTCAATCAGTCCATAGAGACGACAGACGACGACCTTCGGGCCACACGCTGGCGCTCGGG	16122
Db	1241	TTCAATCAGTCCATAGAGACGACGACGACCTTCGGGCCACACGCTGGCGCTCGGG	13000
Qy	1613	GCACTTTGGTAGACTGTGCCACACCGCGCTGTGTGTGTAACCTGAAATTAAGAAGACAA	16722
Db	1301	GCACTTTGGTAGACTGTGCCACACCGCGCTGTGTGTGTAACCTGAAATTAAGAAGACAA	13600
Qy	1673	AAAAAAAA 1679	
Db	1361	AAAAAA 1367	
RESULT 4	AY406347	874 bp DNA linear GSS 12-DEC-2003	
LOCUS	Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY406347		
VERSION	AY406347.1 GI:39762321		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBLISHED	14671302		
REFERENCE	2 (bases 1 to 874)		
AUTHORS	Todd,M.A., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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Matches	Conservative 0; Mismatches 0; Indels 6; Gaps 1;		

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Qy	361	TGCTGGGAATGACAAGTGGTGCCTGGATCTCCGGTGGTCTCTTCTGAGCAACACCCAAAC	420		
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Qy	421	GCAGTACAGCATCGAGATCCAGAACGTTGATGTATGACAGGGCCCTTACACCTGCTC	480		
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DEFINITION	genomic survey sequence.				
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VERSION	AY406348.1	GI:39762322			
KEYWORDS	GSS.				
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ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				

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ACCESSION BM807426
VERSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1033)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLCM1981 row: c column: 08
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laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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REFERENCE
1 (bases 1 to 1083)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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FEATURES

source

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 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 874)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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VERSION BI66583.1 GI:15580816
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
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<http://image.llnl.gov>
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 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 3.8e-163;
Matches 685; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 361 TGCTGGGAATGACAAGTGGTGCCTGATCTCTCGGTGCTCTTCTGAGCAACACCCAAAC 420
Db 410 TGCTGGGAATGACAAGTGGTGCCTGATCTCTCGGTGCTCTTCTGAGCAACACCCAAAC 469
Qy 421 GCAGTACAGCATCGAGATCCAGAAAGCTGGATGTGTATGACGAGGGCCCTTACCTGTCTC 480
Db 470 GCAGTACAGCATCGAGATCCAGAAAGCTGGATGTGTATGACGAGGGCCCTTACCTGTCTC 529
Qy 481 GGTGACGACACACACACCCCAAGACCTCTAGGGTCCACCTCATTTGCGAGTATCTCC 540
Db 530 GGTGACGACACACACACCCCAAGACCTCTAGGGTCCACCTCATTTGCGAGTATCTCC 589
Qy 541 CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCA 599
Db 590 CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCA 649
Qy 600 CCGTATAGCAACTGGTAGACAGAGCGCTACGGTTACTTTGAGAGACACATCTCTCCCAAG 659

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Db 650 CCTGATAGCAACTGGTATAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAG 709
 Qy 660 CGGTGGCTTTGTGAGTGAAGACGAA 685
 Db 710 CGGTGGCTTTGTGAGTGAAGACGAA 735

RESULT 10
 CR736885
 LOCUS
 DEFINITION CR736885 Homo sapiens library (Ebert L) Homo sapiens cDNA clone linear EST 27-AUG-2004
 IMAGP971B1852 ; IMAGE:789137 5', mRNA sequence.
 CR736885
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 673)
 Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E., Peters,M., Radelof,U. and Schneider,D.
 I.M.A.G.E. cDNA Clone Collection
 Unpublished (2004)
 Contact: Inge Axlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Email: www.rzpd.de
 RZPD; IMAGp971B1852.
 RZPDLJB; I.M.A.G.E. cDNA Clone Collection;
 Contact: Inge Axlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTACACAGGAACAGCTATGAC.
 Location/Qualifiers
 1. 673
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGp971B1852 ; IMAGE:789137"
 /clone_lib="Homo sapiens library (Ebert L)"

FEATURES
 source
 1. 673

ORIGIN
 Query Match 39.9%; Score 669.8; DB 7; Length 673;
 Best Local Similarity 99.7%; Pred. No. 4.4e-162;
 Matches 671; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 945 TGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGCTCTGAAACATGATG 1004
 Db 1 TGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGCTCTGAAACATGATG 60

Qy 1005 GGAACATACCTTGGTGGCTTCCAAAGCTGGGGCCACCAATGCGCAGCATCATGCTAT 1064
 Db 61 GGAACATACCTTGGTGGCTTCCAAAGCTGGGGCCACCAATGCGCAGCATCATGCTAT 120

Qy 1065 TTGTGTCAGGGCGCGTTCAGCGAGGTGACCAAGCTGGGAGGAGGCGGCGTCTGCT 1124
 Db 121 TTGTGTCAGGGCGCGTTCAGCGAGGTGACCAAGCTGGGAGGAGGCGGCGTCT 180

Qy 1125 GGCTGCTCCCTCTTCTGCTTCTGACCTGCTTCTCAAAATTTTGAATGAGTGCCACTTCC 1184
 Db 181 GGCTGCTCCCTCTTCTGCTTCTGACCTGCTTCTCAAAATTTTGAATGAGTGCCACTTCC 240

Qy 1185 CCACCCGGGAAGGCTGCGGCGCACCAACCAACCAACCAACCAACCAACCAACCAAC 1244
 Db 241 CCACCCGGGAAGGCTGCGGCGCACCAACCAACCAACCAACCAACCAACCAACCAAC 300

Qy 1245 AGCAACCAATCAGATATATACAAATGAAATTTAGAGAAACACACAGCTCATGGGACAGAA 1304
 Db 301 AGCAACCAATCAGATATATATACAAATGAAATTTAGAGAAACACACAGCTCATGGGACAGAA 360
 Qy 1305 TTTGAGGGAGGGGAAACAAAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAGAAATTGAA 1364
 Db 361 TTTGAGGGAGGGGAAACAAAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAGAAATTGAA 420

Qy 1365 AATTGCCCTTCAGATATTTAGGTACAAATGAGTTTTCTTTTCCAAACGGGAAGACACA 1424
 Db 421 AATTGCCCTTCAGATATTTAGGTACAAATGAGTTTTCTTTTCCAAACGGGAAGACACA 480

Qy 1425 GCACACCCGGCTTGGACCCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGG 1484
 Db 481 GCACACCCGGCTTGGACCCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGG 540

Qy 1485 GCAAGGGCTCAGCCTCTCTGCCCAACAGAGTGCCCGCCAGTGGAACAATTTCTGGAGCTGGCC 1544
 Db 541 GCAAGGGCTCAGCCTCTCTGCCCAACAGAGTGCCCGCCAGTGGAACAATTTCTGGAGCTGGCC 600

Qy 1545 ATCCCAATTCATCAGTCCATAGAGAGCAAGCAAGTCCCGGCCCAAGCGTGG 1604
 Db 601 ATCCCAATTCATCAGTCCATAGAGAGCAAGCAAGTCCCGGCCCAAGCGTGG 660

Qy 1605 CGCTGCGGGCACT 1617
 Db 661 CGCTGCGGGCACT 673

RESULT 11
 BU155617
 LOCUS
 DEFINITION AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone linear EST 03-SEP-2002
 S', mRNA sequence.
 ACCESSION BU155617
 VERSION BU155617
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 856)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTP/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Cloning by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13527 row: m column: 16
 High quality sequence stop: 593.
 Location/Qualifiers
 1. 856
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAG:616839"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN
 Query Match 39.6%; Score 664.8; DB 5; Length 856;
 Best Local Similarity 97.6%; Pred. No. 9.2e-161;

	Matches	728;	Conservative	0;	Mismatches	12;	Indels	6;	Gaps	5;
Qy	214	AGGAGTCCCGTGCGCAGCGGAGATGCCACCTCCCCAAAGCTATGGACAACGTGACGGT	273							
Dd	94	AGGAGTCCCGTGCGCAGCGGAGATGCCACCTCCCCAAAGCTATGGACAACGTGACGGT	153							
Qy	274	CCGCGAGGGGGNAGCGCCACCCTCAGGTGCACCTATTGACNAACCGGCTCACCCGGGTGGC	333							
Dd	154	CCGCGAGGGGGGAGAGCGCCACCCTCAGGTGCACCTATTGACNAACCGGCTCACCCGGGTGGC	213							
Qy	334	CTGGCTAAAACCGCAGCAACCATCTCTATGCTGGGAATGACAAGTGGTGCCTTGGATCTCTCG	393							
Dd	214	CTGGCTAAAACCGCAGCAACCATCTCTATGCTGGGAATGACAAGTGGTGCCTTGGATCTCTCG	273							
Qy	394	CGTGGTCCTTTCTGAGCAACACCCAAAACGCAAGTACAGCATCGAGATCCAGAACCGTGGATGT	453							
Dd	274	CGTGGTCCTTTCTGAGCAACACCCAAAACGCAAGTACAGCATCGAGATCCAGAACCGTGGATGT	333							
Qy	454	GTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGACNAACACCCAAAGACCTCTTAG	513							
Dd	334	GTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGACNAACACCCAAAGACCTCTTAG	393							
Qy	514	GGTCCACTCATTTGTGCAAGTATCTCCAAAAATTGTAGAGATTTCTTCAGATATCTCCAT	573							
Dd	394	GGTCCACTCATTTGTGCAAGTATCTCCAAAAATTGTAGAGATTTCTTCAGATATCTCCAT	453							
Qy	574	TAAATGAAGGAAACAATATTAGCTTCACCTGTCATAGCAAACCTGGTAGACCAAGACCTACGGT	633							
Dd	454	TAAATGAAGGAAACAATATTAGCTTCACCTGTCATAGCAAACCTGGTAGACCAAGACCTACGGT	513							
Qy	634	TACTTGAGACACATCTCTCCCAAGCGGTTGGCTTTGTGANGTGAAGACGAATACTTGGTA	693							
Dd	514	TACTTGAGACACATCTCTCCCAAGCGGTTGGCTTTGTGANGTGAAGACGAATACTTGGTA	573							
Qy	694	AATTTCAGGGCATCACCCGGGAGCAGTTCAGGGGACTACGAGTGCAGTGCCTTCCAATGACGT	753							
Dd	574	AATTTCAGGGCATCACCCGGGAGCAGTTCAGGGGACTACGAGTGCAGTGCCTTCCAATGACGT	633							
Qy	754	GGCCGCGCCCGTGGTACGAGAGGTAAAGTGACCGTGAACTATCCACCATACATTTCCAGA	813							
Dd	634	GGCCGCGCCCGTGGTACGAGAGGTAAAGTGACCGTGAACTATCCACCATACATTTCCAGA	693							
Qy	814	AGCCCAAGGTTACAGGTGT-CCCCTGGGACAAAGGGGACACTGTCAG-TGTGAGACCTCA	871							
Dd	694	AGCCCAAGGTTACAGGTGTCTCCCCGTGGACAAAGGGGACACTGTCAGTTGTGAAACCTCA	753							
Qy	872	GCAGTCCCTCAGCAG-AATTTCAGTGGTACAAGGATG-ACAAAGACTGATT--GAAGG	927							
Dd	754	GCAGTCCCTCAGCAGAAATTCAGTGGTACAGGGATGAACCAAGACTGATTTGAAGGG	813							
Qy	928	AAAGAAAGGGGTGAAGTGGAAACA	953							
Dd	814	AAAAAAAAAGGGGTGAAAGGGGAAAA	839							

RESULT 12	AL533026	1027 bp	mrna	linear	EST 24-MAR-2004
LOCUS	AL533026				
DEFINITION	CS50DN005YD20 5-PRIME, mRNA sequence.				
ACCESSION	AL533026				
VERSION	AL533026.3	GI:45707932			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 13, 2001 this sequence version replaced gi:31070858.				
	Contact: Genoscope				

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
E-mail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6387.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?ac=CSODN005PB100P1&c=6387.f>.

FEATURES

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1. /organism="Homo sapiens"
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   /tissue_type="ADULT BRAIN"
   /dev_stage="adult"
   /clone_lib="Homo sapiens 2"
   /note="Organ: brain; Vector:
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enriched, double-strand cloned
into the Not I and
vector. Library was not

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ORIGIN

Query Match	38.4%;	Score 645;	DB 1;	Length 1027;
Best Local Similarity	86.8%;	Pred. No. 1.3e-155;		
Matches	806;	Conservative 1;	Mismatches 1;	Indels 121;
	Gaps 4;			
Qy	531	AAATATCTCCAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAGGGAACAATA	590	
Db	102	AAATATCTCCAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAGGGAACAATA	161	
Qy	591	TTAGCCTCACCTGCATAGCAACTGGTAGACACGAGGCTACGGTTACTTGGAGACACATCT	650	
Db	162	TTAGCCTCACCTGCATAGCAACTGGTAGACACGAGGCTACGGTTACTTGGAGACACATCT	221	
Qy	651	CTCCAAAGGGTTGGCTTTGTAGTAGGAAGAAATACATTGGAATATCAGGGCATCACCC	710	
Db	222	CTCCAAAGGGTTGGCTTTGTAGTAGGAAGAAATACATTGGAATATCAGGGCATCACCC	281	
Qy	711	GGGAGCAGTCAGGGGACTACGAGTCAGTGCAGTCCCAATGACGTGGCCGCCCGTGGTAC	770	
Db	282	GGGAGCAGTCAGGGGACTACGAGTCAGTGCAGTCCCAATGACGTGGCCGCCCGTGGTAC	341	
Qy	771	GGAGAGTAAAGGTCACCGTGAACTATCCACCACATATTTCAGAAGCCAAGGGGTACAGGTG	830	
Db	342	GGAGAGTAAAGGTCACCGTGAACTATCCACCACATATTTCAGAAGCCAAGGGGTACAGGTG	401	
Qy	831	TCCCGCTGGGACAAAGGGGACATCTCAGTGTGGAAGCCTCAGCAGTCCCTCAGCAGAAAT	890	
Db	402	TCCCGCTGGGACAAAGGGGACATCTCAGTGTGGAAGCCTCAGCAGTCCCTCAGCAGAAAT	461	
Qy	891	TCAGTGTGTAACAGGATGACAAA-----	914	
Db	462	TCAGTGTGTAACAGGATGACAAAAGCTGAAATCTCATTCACAGTTTGGTTATGATGGG	521	
Qy	915	-----	914	
Db	522	AAAGCTTCCTCCCATGGTGGACGAATGGTGTCAAAA CGGCCAGTGGGATCAATCAGCCT	581	
Qy	915	-----GACTGATGAAGGAAGAAAGGGGTGAAGTGGGAAC	952	
Db	582	GACTTGTCTGCAGAAATCTCCCGACTGATTGAAGGAAGAAAGGGGTGAAGTGGGAAC	641	
Qy	953	AGACCTTTCTCTCAAAACTCATCTTTCAATGTCTCTGAACATGACTGACTATGGGAAGTAC	1012	
Db	642	AGACCTTTCTCTCAAAACTCATCTTTCAATGTCTCTGAACATGACTATGGGAAGTAC	701	
Qy	1013	ACTTGGTGGCTTCCAAAGCTGGGGCCACACCAATGCCAGCATCATGTATTGTGGTCCA	1072	

Db 702 ACTTGGCTGGCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTGGTCCA 761
Qy 1073 GGCGCGCTCAGCGAGGTAGCAACGGCACTGTCGAGGAGGCGAGGTGCTGGCTGCTG 1132
Db 762 GGCGCGCTCAGCGAGGTAGCAACGGCACTGTCGAGGAGGCGAGGTGCTGGCTGCTG 821
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Db 822 CCTCTTCTGCTTGTGACCTGCTCTCAAAATTTTGTATGTGAGT-SCATTTCCCGACCGG 880
Qy 1193 GAAAGGCTGCCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1252
Db 881 GAAAGGCTGCCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 939
Qy 1253 ATCAGATATATACAAATGAATTAAGAAACACAGCCCTCATGGACAGAAATTTGAGG 1312
Db 940 ATCAGATATATACAAATGAATTAAGAAACACAGCCCTCATGGACAGAAATTTGAGG 999
Qy 1313 AGGGGAACAAAGAAATACTTTGGGGGAAA 1341
Db 1000 AGGGG-ACAAAGAAATACTTTGGGGGAAA 1027

RESULT 13
BI551784
LOCUS 603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
DEFINITION mRNA sequence.
ACCESSION BI551784
VERSION BI551784.1 GI:15439096
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: LAM11699 row: m column: 20
High quality sequence stop: 732.
Location/Qualifiers
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/clone="IMAGE:5277115"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified
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(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH MGC Library."

FEATURES
source

RESULT 14
CN362539
LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN362539
ACCESSION CN362539
VERSION CN362539.1 GI:47362473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 748)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, W.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

ORIGIN

Query Match 38.3%; Score 643; DB 4; Length 732;

Best Local Similarity 99.4%; Pred. No. 3.9e-155;
Matches 676; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
Qy 1 GTTGTGCTCTTTCAGCAAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTTGAGCAACAC 60
Db 54 GTTGTGCTCTTTCAGCAAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTTGAGCAACAC 113
Qy 61 AATCTATCAGGAAGAAGAAGAAAACCGAACCTTGACAAAAAAGAA-AAAAGAA 119
Db 114 AATCTATCAGGAAGAAGAAGAAAACCGAACCTTGACAAAAAAGAA-AAAAGAA 173
Qy 120 GAAGAAAAAATCATGAATAACCATCCAGCCAAAATGCAAAATTTCTATCTTCTTGGGCAA 179
Db 174 GAAGAAAAAATCATGAATAACCATCCAGCCAAAATGCAAAATTTCTATCTTCTTGGGCAA 233
Qy 180 TCTTTCAGGGGCTGGCTCTGTCTCTTCTTCCAGAGTGCCCGTCGCGAGCGGAGATG 239
Db 234 TCTTTCAGGGGCTGGCTCTGTCTCTTCTTCCAGAGTGCCCGTCGCGAGCGGAGATG 293
Qy 240 CCACCTTCCCAAGCTATGACAAACGTCGCGTCCGCGAGGGGAGAGCGCCACCTCA 299
Db 294 CCACCTTCCCAAGCTATGACAAACGTCGCGTCCGCGAGGGGAGAGCGCCACCTCA 353
Qy 300 GGTGCACCTATTGACAAACCGGGTCAACCGGGTGGCTTGGCTTAAACCGCAGCACCAATCTCT 359
Db 354 GGTGCACCTATTGACAAACCGGGTCAACCGGGTGGCTTGGCTTAAACCGCAGCACCAATCTCT 413
Qy 360 ATGCTGGGAATGACAAAGTGGTGGCTTGGATCTCTCGGTGGTCTCTTCTGAGCAACACCCAAA 419
Db 414 ATGCTGGGAATGACAAAGTGGTGGCTTGGATCTCTCGGTGGTCTCTTCTGAGCAACACCCAAA 473
Qy 420 CGCAGTACAGCATCGAGATCCAGAAACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCT 479
Db 474 CGCAGTACAGCATCGAGATCCAGAAACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCT 533
Qy 480 CGGTGCAGACAGACAAACCCAAAGACCTCTAGGGTCCACTATTTGTGCAAGTATCTC 539
Db 534 CGGTGCAGACAGACAAACCCAAAGACCTCTAGGGTCCACTATTTGTGCAAGTATCTC 593
Qy 540 CCAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAGGGAACATATTAGCCCTCA 599
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Db 654 CTTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAA 713
Qy 659 CGCGTTGGCTTTGTGAGTGA 678
Db 714 CGCG-TGGCTTTGTGAGTGA 732

RESULT 14
CN362539
LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN362539
ACCESSION CN362539
VERSION CN362539.1 GI:47362473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 748)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, W.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

230 Constitution Drive, Menlo Park, CA 94035, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 748 Std Error: 0.00.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model supports real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. Integration: The model integrates seamlessly with existing systems and workflows, facilitating easy adoption.	Model Performance Metrics
7. Customization: The model offers customization options, allowing users to tailor the predictions to their specific needs.	Model Performance Metrics
8. Security: The model adheres to strict security protocols, ensuring that data is protected and handled responsibly.	Model Performance Metrics
9. Support: Comprehensive support and documentation are provided to assist users in utilizing the model effectively.	Model Performance Metrics
10. Continuous Improvement: The model undergoes continuous improvement, incorporating feedback and new data to enhance its performance over time.	Model Performance Metrics

ORIGIN

Query Match	38.1%;	Score 640;	DB 7;	Length 748;
Best Local Similarity	100.0%;	Identical 100.0%;	Mismatches 0;	Gaps 0;
Matches 640;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	214	AGAGNTGCCCGTGGCGAGCGGAGTGCACCTTCCCAAAAGCTATGACAACGTGACGGT	273	
DB	109	AGAGTGTCCCGTGGCGAGCGGAGTGCACCTTCCCAAAAGCTATGACAACGTGACGGT	168	
QY	274	CCGCGAGGGGAGCGCCACCCCTCAGGTGCACATATTGACAACCGGGTCACCCGGGGTGC	333	
DB	169	CCGCGAGGGGAGCGCCACCCCTCAGGTGCACATATTGACAACCGGGTCACCCGGGGTGC	228	
QY	334	CTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG	393	
DB	229	CTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG	288	
QY	394	CGTGGTCTTCTGAGCAACAACCCAAACGCGAGTACAGCATCGAGATCGAGAACGTGGAATG	453	
DB	289	CGTGGTCTTCTGAGCAACAACCCAAACGCGAGTACAGCATCGAGATCGAGAACGTGGAATG	348	
QY	454	GTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGACAACCCCAAGACCTCTAG	513	
DB	349	GTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGACAACCCCAAGACCTCTAG	408	
QY	514	GGTCCACCTCATTTGTGTGCAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCAT	573	
DB	409	GGTCCACCTCATTTGTGTGCAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCAT	468	
QY	574	TAATGAAGGAAACAATATTAGCTCTCACTGCATAGCAACTGGTAGACAGAGCTACGGT	633	
DB	469	TAATGAAGGAAACAATATTAGCTCTCACTGCATAGCAACTGGTAGACAGAGCTACGGT	528	
QY	634	TACTTGGAGACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGA	693	
DB	529	TACTTGGAGACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGA	598	
QY	694	AATTTCAGGGCATCAACCGGGAGCAGTCAAGGGGACTACAGGTGCAGTGCCTTCCAATGACGT	753	
DB	589	AATTTCAGGGCATCAACCGGGAGCAGTCAAGGGGACTACAGGTGCAGTGCCTTCCAATGACGT	648	
QY	754	GGCCGCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAACTATCCACCATATCATTTTCAGA	813	
DB	649	GGCCGCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAACTATCCACCATATCATTTTCAGA	708	
QY	814	AGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	853	
DB	709	AGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	748	

ACCESSION	BE798585
VERSION	BE798585.1
KEYWORDS	GI:10219783
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1039)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTB/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCW779 row: d column: 04 High quality sequence stop: 849

ORIGIN

Query Match	37.8%;	Score 635.2;	DB 2;	Length 1039;
Best Local Similarity	97.6%;	Pred. No. 4.5e-153;		
Matches 656;	Conservative 0;	Mismatches 13;	Indels 3;	Gaps 1
Qy	298	CAGGTGCACATATTGACAAACCGGGTCACCCGGGTGSCCTGGCTTAACCCGACGACCATCTCT	357	
Db	65	CAGGTGCACATATTGACAAACCGGGTCGCCGGGTGSCCTGGCTTAACCCGACGACCATCTCT	124	
Qy	358	CTATGCTGGGAATGACAAAGTGTGTCCCTGGATTCCTCGGTGTGCTTCTTGAGCAACACCCA	417	
Db	125	CTATGCTGGGAATGACAAAGTGTGTCCCTGGATTCCTCGGTGTGCTTCTTGAGCAACACCCA	184	
Qy	418	AAGCGAGTACAGCATTCAGATCCAGAACGTCGGATGTGATCAGCAGGGCCCTTACACCTG	477	
Db	185	AAGCGAGTACAGCATTCAGATCCAGAACGTCGGATGTGATCAGCAGGGCCCTTACACCTG	244	
Qy	478	CTCGGTGCAGACAGACCAACCAACAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATC	537	
Db	245	CTCGGTGCAGACAGACCAACCAACAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATC	304	
Qy	538	TCCGAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT	597	
Db	305	TCCGAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT	364	
Qy	598	CACCTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAA	657	
Db	365	CACCTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAA	424	
Qy	658	AGCGTTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATACACCCGGGAGCA	717	
Db	425	AGCGTTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATACACCCGGGAGCA	484	

Qy	718	GTCAGGGGACTACGAGTCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGGAGAGT	777
Db	485		
Qy	778	AAAGGTCACCGTGAACTATCCACCACATACATTTGAGAAGCCCAAGGGTACAGGTGTCCCCGT	837
Db	545		
Qy	838	GGGACAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTG	897
Db	605		
Qy	898	GTACAAGGATGACAAAAGACTGATTGAAGGAA---AGAAAGGGGTGAAAGTGGAAAAACAG	954
Db	665		
Qy	955	ACCTTTCTCTC	966
Db	725		
		ACCTTTTCTCTC	736

Search completed: June 16, 2005, 06:56:32
Job time : 6280.03 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2005, 02:42:13 ; Search time 4692.58 Seconds
(without alignments)
10687.319 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 atgaaccatccagccaaa.....acctgtctctcaaatgtga 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_or.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1679	6	CQ768055 Sequence
2	1035	100.0	1679	6	AR528639 Sequence
3	1035	100.0	1679	6	AX358872 Sequence
4	1035	100.0	1679	6	AX362365 Sequence
5	1035	100.0	1679	6	AX403748 Sequence
6	1035	100.0	1679	6	AX454470 Sequence
7	1035	100.0	1679	6	AX464242 Sequence
8	1035	100.0	1679	6	AX490948 Sequence
9	1035	100.0	1679	9	AX358331 Homo sapi
10	1035	100.0	1693	6	AR439649 Sequence
11	1032	99.7	1032	6	AR439648 Sequence
12	953.4	92.1	1839	6	AX665342 Sequence
13	953.4	92.1	1839	9	AF126426 Homo sapi
14	939	90.7	939	6	AX439650 Sequence
15	910.4	88.0	1068	6	AX665344 Sequence
16	874.4	84.5	1104	6	AX665346 Sequence
17	868	83.9	868	6	CQ729109 Sequence
18	856	82.7	1325	9	BC050716 Homo sapi
19	851.8	82.3	1140	6	AX665348 Sequence

93	254.2	24.6	5605	9	BC036771	BC036771 Homo sapi	92.6	8.9	214942	10	AC125214	AC125214 Mus muscu	
94	246	23.8	1169	6	AX644999	AX644999 Sequence	89.8	8.7	114269	2	AP002341	AP002341 Homo sapi	
95	238.4	23.0	20731	9	AP0004721	AP0004721 Homo sapi	168	89.8	8.7	152797	2	AC012134	AC012134 Homo sapi
96	238.4	23.0	43087	9	AP0005155	AP0005155 Homo sapi	169	89.8	8.7	159520	9	AC113009	AC113009 Homo sapi
97	235.6	22.8	203572	9	AC016769	AC016769 Homo sapi	170	89.8	8.7	172128	2	AP000762	AP000762 Homo sapi
98	223.2	21.6	2070	5	BC080221	BC080221 Danio rer	171	89.8	8.7	190104	2	AP002831	AP002831 Homo sapi
99	223.2	21.6	2455	5	AF241637	AF241637 Danio rer	172	89.8	8.7	199079	9	AP000844	AP000844 Homo sapi
100	221.8	21.4	4323	10	AK122576	AK122576 Mus muscu	173	89	8.6	987	6	CQ734933	CQ734933 Sequence
101	220.4	21.3	197553	2	AC146103	AC146103 Pan trogl	174	89	8.6	170006	9	AP005122	AP005122 Homo sapi
102	207.6	20.1	786	5	GGA132998	AJ132998 Gallus Ga	175	88	8.5	882	6	CQ732721	CQ732721 Sequence
103	207.2	20.0	168745	2	AC119552	AC119552 Rattus no	176	87.2	8.4	163120	5	BX296535	BX296535 Zebrafish
104	207.2	20.0	248329	2	AC109989	AC109989 Rattus no	177	87.2	8.4	180842	2	CR536619	CR536619 Danio rer
105	205.6	19.9	110000	2	AC102028_1	Continuation (2 of	178	86.6	8.4	169582	2	AC102190	AC102190 Mus muscu
106	193.6	18.7	352	6	AX886912	AX886912 Sequence	179	86.2	8.3	74368	9	AL391239	AL391239 Human DNA
107	193.6	18.7	352	6	BD026532	BD026532 Sequence	180	86.2	8.3	131457	9	AL356600	AL356600 Human DNA
108	180.4	17.4	5666	6	AX740565	AX740565 Sequence	181	86.2	8.3	153852	2	AC009694	AC009694 Homo sapi
109	176.6	17.1	540	6	AX665354	AX665354 Sequence	182	86.2	8.3	315761	2	AL158079	AL158079 Homo sapi
110	176.6	17.1	116069	2	AP000784	AP000784 Homo sapi	183	85.8	8.3	162247	2	AC102328	AC102328 Mus muscu
111	176.6	17.1	123320	9	AP000863	AP000863 Homo sapi	184	85.4	8.3	295	6	CQ732164	CQ732164 Sequence
112	176.6	17.1	176676	2	AC012234	AC012234 Homo sapi	185	84.4	8.2	36000	9	AP003166	AP003166 Homo sapi
113	176.6	17.1	177102	2	AP002808	AP002808 Homo sapi	186	84.4	8.2	189323	2	AC150620	AC150620 Callithri
114	175	16.9	642	6	CQ732119	CQ732119 Sequence	187	84.4	8.2	191545	2	AC151029	AC151029 Callithri
115	173.2	16.7	242555	2	AC094728	AC094728 Rattus no	188	84.2	8.1	246900	2	AC128465	AC128465 Rattus no
116	173.2	16.7	251570	2	AC094463	AC094463 Rattus no	189	84	8.1	189037	2	AC150026	AC150026 Papio anu
117	171.2	16.5	184012	10	AC116523	AC116523 Mus muscu	190	83.4	8.1	162717	10	AC127259	AC127259 Mus muscu
118	166.8	16.1	504	6	CQ715694	CQ715694 Sequence	191	83.4	8.1	258847	2	AC112746	AC112746 Rattus no
119	164.8	15.9	531	6	CQ719449	CQ719449 Sequence	192	83.4	8.1	285603	2	AC104926	AC104926 Mus muscu
120	163.2	15.8	585	6	AX079674	AX079674 Sequence	193	81.8	7.9	110000	2	AC110642_3	Continuation (4 of
121	160	15.5	408	6	AX684132	AX684132 Sequence	194	79.6	7.7	168191	2	AC151813	AC151813 Dasyypus n
122	156	15.1	371	6	CQ731074	CQ731074 Sequence	195	79.6	7.7	215743	2	AC148958	AC148958 Otlemur
123	156	15.1	184716	2	AC018368	AC018368 Homo sapi	196	78.6	7.6	420	6	AX665356	AX665356 Sequence
124	156	15.1	191071	9	AP004248	AP004248 Homo sapi	197	78.6	7.6	113063	2	AC010946	AC010946 Homo sapi
125	149.6	14.5	793	5	BX932289	BX932289 Gallus ga	198	78.6	7.6	191204	9	AP000843	AP000843 Homo sapi
126	140.6	13.6	152686	2	AC018913	AC018913 Homo sapi	199	78.6	7.6	202505	2	AP000912	AP000912 Homo sapi
127	135.2	13.1	268	4	AF271984	AF271984 Bos tauru	200	78.2	7.6	150308	10	AC098294	AC098294 Rattus no
128	135.2	13.1	110000	2	AC102028_0	AC102028 Mus muscu	201	78.2	7.6	225433	2	AC106484	AC106484 Rattus no
129	135.2	13.1	186110	2	AC102204	AC102204 Mus muscu	202	78.2	7.6	237199	10	AC094830	AC094830 Rattus no
130	132	12.8	110000	2	AC110642_2	Continuation (3 of	203	78	7.5	133989	2	AC149777	AC149777 Bos tauru
131	128	12.4	184716	2	AC018368	AC018368 Homo sapi	204	78	7.5	205738	4	AC150499	AC150499 Bos tauru
132	121	11.7	152686	2	AC018913	AC018913 Homo sapi	205	77.8	7.5	177	6	AR030585	AR030585 Sequence
133	113.6	11.0	195993	2	AC134953	AC134953 Pan trogl	206	77.8	7.5	177	6	AR030586	AR030586 Sequence
134	113.6	11.0	212752	9	AC063977	AC063977 Homo sapi	207	76.8	7.4	479	6	AX665358	AX665358 Sequence
135	112.8	10.9	157263	2	BX957285	BX957285 Danio rer	208	76.6	7.4	259743	2	AC113965	AC113965 Mus muscu
136	110.6	10.7	292	6	CQ716587	CQ716587 Sequence	209	71.4	6.9	480	6	AX665357	AX665357 Sequence
137	110.4	10.7	213331	2	AC125960	AC125960 Rattus no	210	69.2	6.7	62350	9	AC067725	AC067725 Homo sapi
138	109.6	10.6	175963	2	AC148913	AC148913 Sus scrof	211	69	6.7	146352	2	CR548641	CR548641 Danio rer
139	109.4	10.6	134184	2	AC150028	AC150028 Canis fam	212	69	6.7	186279	5	BX950870	BX950870 Zebrafish
140	108.8	10.5	168611	2	AC102204	AC102204 Mus muscu	213	69	6.7	191779	2	CR376789	CR376789 Danio rer
141	108	10.4	168861	2	AC130786	AC130786 Papio anu	214	67	6.5	176744	2	AC027631	AC027631 Homo sapi
142	108	10.4	172146	2	AC130272	AC130272 Papio anu	215	65.6	6.3	198	6	AR030587	AR030587 Sequence
143	107.8	10.4	169206	10	AC123550	AC123550 Mus muscu	216	65	6.3	195956	2	AC127626	AC127626 Rattus no
144	107.8	10.4	277603	2	AC079543	AC079543 Mus muscu	217	65	6.3	249701	2	AC106525	AC106525 Rattus no
145	106.2	10.3	229330	2	AC137057	AC137057 Rattus no	218	63.4	6.1	198	6	AR030588	AR030588 Sequence
146	106.2	10.3	238070	2	AC134313	AC134313 Rattus no	219	61.6	6.0	270	6	AX665353	AX665353 Sequence
147	106.2	10.3	242260	2	AC094567	AC094567 Rattus no	220	60.8	5.9	117951	9	AL359821	AL359821 Human DNA
148	106.2	10.3	255120	2	AC127219	AC127219 Rattus no	221	60.8	5.9	199301	2	AC119938	AC119938 Mus muscu
149	106	10.2	142000	9	AC078813	AC078813 Homo sapi	222	58.6	5.7	2000	6	AX655393	AX655393 Sequence
150	105.6	10.2	913	6	AR542162	AR542162 Sequence	223	58.6	5.7	166417	10	AC127685	AC127685 Mus muscu
151	104.4	10.1	237376	2	AC124949	AC124949 Rattus no	224	57.6	5.6	420	6	AX665355	AX665355 Sequence
152	104.4	10.1	277228	2	AC106911	AC106911 Rattus no	225	57.6	5.6	142882	9	AP003029	AP003029 Homo sapi
153	102.2	9.9	131490	10	AC122207	AC122207 Mus muscu	226	56	5.4	193180	2	AC112588	AC112588 Rattus no
154	102.2	9.9	177251	10	AC124565	AC124565 Mus muscu	227	55.4	5.4	34930	2	AC099999	AC099999 Mus muscu
155	102	9.9	187203	2	AP000832	AP000832 Homo sapi	228	53.8	5.2	134609	2	AC021416	AC021416 Homo sapi
156	102	9.9	202505	2	AP000912	AP000912 Homo sapi	229	53.8	5.2	150407	2	AC093228	AC093228 Homo sapi
157	100	9.7	219	6	AR030583	AR030583 Sequence	230	53.8	5.2	163538	9	AC012598	AC012598 Homo sapi
158	99	9.6	219713	2	AC112456	AC112456 Rattus no	231	52.2	5.0	2010	6	CQ586755	CQ586755 Sequence
159	99	9.6	234283	2	AC114113	AC114113 Rattus no	232	52.2	5.0	3927	3	DMU78177	U78177 Drosophila
160	99	9.6	250355	2	AC127766	AC127766 Rattus no	233	52.2	5.0	4052	3	AY060363	AY060363 Drosophila
161	99	9.6	263661	2	AC106603	AC106603 Rattus no	234	52.2	5.0	189627	10	AC122934	AC122934 Mus muscu
162	99	9.6	319104	2	AC106602	AC106602 Rattus no	235	52	5.0	4807	9	HSM808173	BS648027 Homo sapi
163	98.4	9.5	411	6	CQ731080	CQ731080 Sequence	236	52	5.0	180842	2	CR536619	CR536619 Danio rer
164	96.8	9.4	187746	2	AC087123	AC087123 Mus muscu	237	50	4.8	3806	5	AJ720876	AJ720876 Gallus ga
165	95.2	9.2	219	6	AR030584	AR030584 Sequence	238	49.8	4.8	2000	6	AX655393	AX655393 Sequence

239	48.4	4.7	4073	6	AX269342	AX369342 Sequence	312	41.2	4.0	3266	6	CQ728451	CQ728451 Sequence
240	48.4	4.7	8546	6	AX828406	AX828406 Sequence	313	41.2	4.0	3309	6	AX714869	AX714869 Sequence
241	48.4	4.7	8546	9	HS306906	AJ306906 Homo sapi	314	41.2	4.0	3309	9	AK057509	AK057509 Homo sapi
242	48.4	4.7	18207	6	AX828384	AX828384 Sequence	315	41.2	4.0	4050	9	BC047244	BC047244 Homo sapi
243	48.4	4.7	18207	9	AF156100	AF156100 Homo sapi	316	41.2	4.0	4290	9	BC014205	BC014205 Homo sapi
244	47.6	4.6	63585	2	AC026983	AC026983 Homo sapi	317	41.2	4.0	5807	6	AR447664	AR447664 Sequence
c 245	47.6	4.6	84492	2	AC021676	AC021676 Homo sapi	318	41.2	4.0	8513	6	AX207284	AX207284 Sequence
246	47	4.5	157263	2	AX957285	AX957285 Danio rer	c 319	41.2	4.0	168144	2	CR792456	CR792456 Danio rer
247	46.8	4.5	2229	6	CQ729908	CQ729908 Sequence	c 320	41.2	4.0	192097	9	AC008743	AC008743 Homo sapi
248	46.6	4.5	172407	2	AC148515	AC148515 Sub scrofa	321	41	4.0	1140	10	BC034209	BC034209 Mus muscu
249	46.4	4.5	6267	10	AF315558	AF315558 Mus muscu	322	41	4.0	2547	10	BC037721	BC037721 Mus muscu
250	46.4	4.5	6829	10	AY005483	AY005483 Mus muscu	323	41	4.0	3470	10	BC045197	BC045197 Mus muscu
c 251	46.2	4.5	68409	2	AC119994	AC119994 Mus muscu	324	41	4.0	3486	10	AY237727	AY237727 Mus muscu
c 252	46	4.4	4641	10	RNU68726	U68726 Rattus norv	325	41	4.0	6021	10	AY237726	AY237726 Mus muscu
c 253	45.4	4.4	7218	6	I66494	I66494 Sequence 14	326	41	4.0	249562	10	AL627327	AL627327 Mouse DNA
254	45	4.3	4784	5	GU07644	U07644 Gallus gall	c 327	40.6	3.9	262336	2	AC006786	AC006786 Caenorhab
255	45	4.3	41219	9	AL135797	AL135797 Human DNA	c 328	40.6	3.9	163399	2	AC079860	AC079860 Homo sapi
256	44	4.3	3498	10	RNU81035	U81035 Rattus norv	c 329	40.6	3.9	180569	9	AL354949	AL354949 Human DNA
257	44	4.3	3651	10	RNU81036	U81036 Rattus norv	c 330	40.6	3.9	186759	9	AL645608	AL645608 Human DNA
258	44	4.3	3752	10	AY061639	AY061639 Rattus no	c 331	40.6	3.9	187746	2	AC087123	AC087123 Mus muscu
259	44	4.3	4465	10	MMU543322	AJ543322 Mus muscu	c 332	40.6	3.9	200491	2	AB107102	AB107102 Homo sapi
260	44	4.3	4496	6	CQ715482	CQ715482 Sequence	c 333	40.6	3.9	327883	2	BX571684	BX571684 Homo sapi
261	44	4.3	5071	10	AK129207	AK129207 Mus muscu	c 334	40.4	3.9	53661	2	AC134672	AC134672 Homo sapi
262	44	4.3	5822	10	RATANKBLND	L11002 Rat ankryrin	c 335	40.4	3.9	82019	2	AC139567	AC139567 Homo sapi
263	44	4.3	171637	2	AC116691	AC116691 Mus muscu	336	40.4	3.9	216161	9	AC087749	AC087749 Homo sapi
264	44	4.3	228647	2	AC134289	AC134289 Rattus no	337	40.2	3.9	2019	10	BC025840	BC025840 Mus muscu
c 265	44	4.3	229948	2	AC126070	AC126070 Rattus no	338	40.2	3.9	2811	10	AF487347	AF487347 Mus muscu
c 266	44	4.3	262363	2	AC105703	AC105703 Rattus no	339	40.2	3.9	4631	9	HSU72391	U72391 Human neoge
267	43.8	4.2	4041	5	GNEUPASC	X65224 G.gallus mR	340	40.2	3.9	5021	6	CQ729613	CQ729613 Sequence
268	43.8	4.2	143045	9	AC008750	AC008750 Homo sapi	341	40.2	3.9	5292	10	AB093285	AB093285 Mus muscu
269	43.2	4.2	195958	2	BX957263	BX957263 Danio rer	342	40.2	3.9	5297	6	AX587800	AX587800 Sequence
270	43	4.2	157282	2	AC136089	AC136089 Rattus no	343	40.2	3.9	5297	6	AX771417	AX771417 Sequence
271	42.6	4.1	1565	10	AF314149	AF314149 Mus muscu	344	40.2	3.9	5297	9	HSU61262	U61262 Human neoge
272	42.4	4.1	3588	6	CQ870412	CQ870412 Sequence	345	40.2	3.9	5506	6	AR447897	AR447897 Sequence
273	42.4	4.1	4306	9	AK124736	AK124736 Homo sapi	346	40.2	3.9	11850	4	AY136513	AY136513 Canis fam
274	42.4	4.1	4479	9	HSAG1	X68274 Homo sapten	347	40.2	3.9	16799	2	AC020355	AC020355 Drosophil
275	42.4	4.1	4548	6	AR453309	AR453309 Sequence	348	40.2	3.9	68727	3	AC004516	AC004516 Drosophil
276	42.4	4.1	4548	6	AX305052	AX305052 Sequence	c 349	40.2	3.9	71023	2	AC004426	AC004426 Drosophil
277	42.4	4.1	4548	9	HSTAG1A	X67734 H.sapiens m	c 350	40.2	3.9	193262	3	AC007579	AC007579 Drosophil
278	42.4	4.1	6137	6	CQ870414	CQ870414 Sequence	c 351	40.2	3.9	260367	3	AE003808	AE003808 Drosophil
c 279	41.8	4.0	131042	10	AC110166	AC110166 Mus muscu	352	40	3.9	171062	9	AL445587	AL445587 Human DNA
c 280	41.8	4.0	181463	10	AC124452	AC124452 Mus muscu	353	39.8	3.8	1623	6	AX298209	AX298209 Sequence
281	41.8	4.0	268912	2	AC094291	AC094291 Rattus no	354	39.8	3.8	3788	5	CHRXUGG	M63437 Chicken KUG
282	41.6	4.0	1912	3	SARREGALPT	X93601 S.americana	355	39.8	3.8	5040	10	RATTAG1	M31725 Rat axonal
283	41.6	4.0	5374	9	AF289030	AF289030 Homo sapi	356	39.8	3.8	18848	4	OCV14852	Y14852 Oryctolagus
284	41.6	4.0	5387	6	CQ731799	CQ731799 Sequence	357	39.8	3.8	110000	2	BX255276_05	Continuation (6 of
285	41.6	4.0	6110	9	AF023449	AF023449 Homo sapi	358	39.8	3.8	162208	9	AC073321	AC073321 Homo sapi
286	41.6	4.0	6413	9	AF023450	AF023450 Homo sapi	359	39.8	3.8	225416	10	AC131744	AC131744 Mus muscu
c 287	41.6	4.0	6649	9	AF217525	AF217525 Homo sapi	c 360	39.8	3.8	227067	2	AC140391	AC140391 Mus muscu
c 288	41.6	4.0	79444	2	AC150153	AC150153 Gallus ga	361	39.6	3.8	124281	10	AL645976	AL645976 Mouse DNA
289	41.6	4.0	125020	9	AF429315	AF429315 Homo sapi	362	39.4	3.8	741	6	AX756349	AX756349 Sequence
c 290	41.6	4.0	143178	2	AC150117	AC150117 Gallus ga	363	39.4	3.8	2650	6	CQ882042	CQ882042 Sequence
c 291	41.6	4.0	168663	2	AC150140	AC150140 Gallus ga	364	39.4	3.8	5992	10	BC058610	BC058610 Mus muscu
c 292	41.6	4.0	199442	2	AC150038	AC150038 Gallus ga	365	39.4	3.8	234447	2	AC111017	AC111017 Mus muscu
293	41.6	4.0	208621	2	AC150078	AC150078 Gallus ga	366	39.2	3.8	579	11	BV103163	BV103163 MARC 2423
294	41.4	4.0	2753	10	BC060263	BC060263 Mus muscu	367	39.2	3.8	611	11	BV103131	BV103131 MARC 2423
295	41.4	4.0	110000	1	XP000010_02	Continuation (8 of	c 368	39.2	3.8	63585	2	AC026983	AC026983 Homo sapi
c 296	41.4	4.0	110000	1	XP000010_02	Continuation (3 of	c 369	39	3.8	518	6	CQ781104	CQ781104 Sequence
c 297	41.4	4.0	203224	2	AC149607	AC149607 Mus muscu	c 370	39	3.8	518	6	CQ782392	CQ782392 Sequence
c 298	41.4	4.0	215601	2	AC073306	AC073306 Mus muscu	c 371	39	3.8	518	6	BD125813	BD125813 Primer fo
c 299	41.4	4.0	223121	2	AC073726	AC073726 Mus muscu	c 372	39	3.8	518	6	BD127101	BD127101 Primer fo
300	41.2	4.0	2083	6	AX590224	AX590224 Sequence	373	39	3.8	1883	6	CQ598923	CQ598923 Sequence
301	41.2	4.0	2142	6	AX275019	AX275019 Sequence	374	39	3.8	2040	3	AY118318	AY118318 Drosophil
302	41.2	4.0	2397	6	AX392395	AX392395 Sequence	375	39	3.8	2742	6	CQ782949	CQ782949 Sequence
303	41.2	4.0	2450	6	AX590219	AX590219 Sequence	376	39	3.8	2742	6	BD127395	BD127395 Primer fo
304	41.2	4.0	2493	6	AX275017	AX275017 Sequence	377	39	3.8	2742	9	AK074976	AK074976 Homo sapi
305	41.2	4.0	2633	9	HSU63041	U63041 Human neuira	378	39	3.8	3974	3	AY051554	AY051554 Drosophil
306	41.2	4.0	2633	9	HSU63041	U63041 Human neuira	c 379	39	3.8	4012	6	CQ598922	CQ598922 Sequence
307	41.2	4.0	2756	6	AX590252	AX590252 Sequence	c 380	39	3.8	4057	6	CQ598919	CQ598919 Sequence
308	41.2	4.0	2799	9	HSNCAME	X16841 Human mRNA	c 381	39	3.8	148432	3	AC004642	AC004642 Drosophil
309	41.2	4.0	2960	6	AX58287	AX58287 Sequence	c 382	39	3.8	158480	3	AC099018	AC099018 Drosophil
310	41.2	4.0	2960	9	S71824	S71824 N-CAM=145 k	383	39	3.8	157851	2	AC020509	AC020509 Drosophil
311	41.2	4.0	3027	6	AX3922983	AX3922983 Sequence	c 384	39	3.8	160252	2	AC119373	AC119373 Rattus no

C 385	3.85	3.8	163322	9	AC138389	AC138389 Homo sapi	C 458	38	3.7	202023	2	AC141270	AC141270 Homo sapi
C 386	3.86	3.8	186241	9	AC103560	AC103560 Homo sapi	C 459	38	3.7	223432	9	AC126755	AC126755 Homo sapi
C 387	3.87	3.8	265053	2	AC098057	AC098057 Rattus no	C 460	37.8	3.7	1548	12	BT007989	BT007989 Synthetic
C 388	3.88	3.8	303823	3	AE003462	AE003462 Drosophil	C 461	37.8	3.7	1605	6	CQ599856	CQ599856 Sequence
C 389	3.89	3.7	4285	6	CQ607487	CQ607487 Sequence	C 462	37.8	3.7	2167	9	HUMG6PDA	M21248 Human gluco
C 390	3.8	3.7	5913	6	CQ869760	CQ869760 Sequence	C 463	37.8	3.7	2230	9	BC000337	BC000337 Homo sapi
C 391	3.8	3.7	6656	10	AF334385	AF334385 Rattus no	C 464	37.8	3.7	2625	9	HSG6PDR	XQ3674 Human mRNA
C 392	3.8	3.7	13654	1	AE005754	AE005754 Caulobact	C 465	37.8	3.7	2630	6	CQ730121	CQ730121 Sequence
C 393	3.8	3.7	48870	2	AC017807	AC017807 Drosophil	C 466	37.8	3.7	9680	6	CQ599855	CQ599855 Sequence
C 394	3.8	3.7	70712	2	AC135970	AC135970 Homo sapi	C 467	37.8	3.7	20940	2	AC014917	AC014917 Drosophill
C 395	3.8	3.7	155666	3	AC007854	AC007854 Drosophil	C 468	37.8	3.7	36859	3	U80022	U80022 Caenorhabdi
C 396	3.8	3.7	168471	3	AC006170	AC006170 Drosophil	C 469	37.8	3.7	66669	1	AME16952	Y16952 Amycolatops
C 397	3.8	3.7	170056	2	AC087643	AC087643 Homo sapi	C 470	37.8	3.7	110000	1	AF006618	Continuation (60 o
C 398	3.8	3.7	188948	2	AC132884	AC132884 Homo sapi	C 471	37.8	3.7	126899	3	AY130758	AY130758 Caenorhab
C 399	3.8	3.7	231562	3	AE003767	AE003767 Drosophil	C 472	37.8	3.7	159672	3	AC010040	AC010040 Drosophil
C 400	3.8	3.7	607	3	AF254364	AF254364 Drosophil	C 473	37.8	3.7	168989	2	AC147589	AC147589 Atelerix
C 401	3.8	3.7	2303	5	GGNEU9	Y14344 Gallus gall	C 474	37.8	3.7	187555	3	AC010037	AC010037 Drosophill
C 402	3.8	3.7	2313	9	AK097802	AK097802 Homo sapi	C 475	37.8	3.7	281917	3	AE003556	AE003556 Drosophill
C 403	3.8	3.7	2462	6	AX746553	AX746553 Sequence	C 476	37.6	3.6	384	6	E01962	E01962 DNA encodin
C 404	3.8	3.7	2462	9	AK090639	AK090639 Homo sapi	C 477	37.6	3.6	384	6	BD081409	BD081409 Fused pro
C 405	3.8	3.7	3525	6	CQ715490	CQ715490 Sequence	C 478	37.6	3.6	444	6	E01961	E01961 DNA encodin
C 406	3.8	3.7	4398	5	D85084	Cynops pyrr	C 479	37.6	3.6	444	9	BT007189	BT007189 Homo sapi
C 407	3.8	3.7	4955	9	AB018299	AB018299 Homo sapi	C 480	37.6	3.6	444	9	CR456908	CR456908 Homo sapi
C 408	3.8	3.7	115292	9	AL391822	AL391822 Human DNA	C 481	37.6	3.6	444	12	BT007870	BT007870 Synthetic
C 409	3.8	3.7	161034	2	AL359927	AL359927 Homo sapi	C 482	37.6	3.6	483	9	HSTTRM	X59498 H. sapiens t
C 410	3.8	3.7	175522	2	AC018373	AC018373 Homo sapi	C 483	37.6	3.6	501	9	HUMTHYA	M11714 Human trans
C 411	3.8	3.7	182666	5	AL929172	AL929172 Zebrafish	C 484	37.6	3.6	506	9	AF162690	AF162690 Homo sapi
C 412	3.8	3.7	349028	1	BX640413	Bordetell	C 485	37.6	3.6	572	6	AR531501	AR531501 Sequence
C 413	3.8	3.7	366	6	AR393998	AR393998 Sequence	C 486	37.6	3.6	615	9	HUMPALA	X02091 Human preal
C 414	3.8	3.7	591	6	AR393996	AR393996 Sequence	C 487	37.6	3.6	615	9	HUMPALFAP	D00096 Homo sapien
C 415	3.8	3.7	984	6	BD173702	Novel cel	C 488	37.6	3.6	631	6	E00722	E00722 cDNA inuedi
C 416	3.8	3.7	1062	6	CQ738382	CQ738382 Sequence	C 489	37.6	3.6	644	9	BC005310	BC005310 Homo sapi
C 417	3.8	3.7	1523	6	BD173703	Novel cel	C 490	37.6	3.6	650	9	BC020791	BC020791 Homo sapi
C 418	3.8	3.7	1523	9	AK172835	Homo sapi	C 491	37.6	3.6	669	6	E01963	E01963 DNA encodin
C 419	3.8	3.7	2375	6	AX747704	Sequence	C 492	37.6	3.6	817	8	AF517871	AF517871 Griffiths
C 420	3.8	3.7	2375	9	AK092746	Homo sapi	C 493	37.6	3.6	1370	6	AX298211	AX298211 Sequence
C 421	3.8	3.7	2735	6	AX833579	Sequence	C 494	37.6	3.6	5414	10	MMNEOGEN	Y09535 M. musculus
C 422	3.8	3.7	2735	9	AK095432	Homo sapi	C 495	37.6	3.6	5443	10	BC054540	BC054540 Mus muscu
C 423	3.8	3.7	3460	3	BT011190	Drosophil	C 500	37.6	3.6	15085	1	AE002038	AE002038 Deinococc
C 424	3.8	3.7	4808	6	CQ590178	Sequence	C 501	37.6	3.6	163972	8	AC096855	AC096855 Oryza sat
C 425	3.8	3.7	4890	6	AR361390	Sequence	C 502	37.6	3.6	217817	5	BX511298	BX511298 Zebrafish
C 426	3.8	3.7	4943	6	AR361392	Sequence	C 503	37.6	3.6	634	11	BV105635	BV105635 MARC 1613
C 427	3.8	3.7	5170	6	AR361391	Sequence	C 504	37.4	3.6	837	12	AY658737	AY658737 Synthetic
C 428	3.8	3.7	5236	3	AX079187	Drosophil	C 505	37.4	3.6	1829	6	CQ841463	CQ841463 Sequence
C 429	3.8	3.7	5253	3	AX079185	Drosophil	C 506	37.4	3.6	1829	9	AK123191	AK123191 Homo sapi
C 430	3.8	3.7	7031	3	AX079184	Drosophil	C 507	37.4	3.6	2262	10	MMNCAMRI	X15049 Mouse commo
C 431	3.8	3.7	7221	6	CQ590177	Sequence	C 508	37.4	3.6	2472	6	CQ592467	CQ592467 Sequence
C 432	3.8	3.7	78877	9	AC008408	Homo sapi	C 509	37.4	3.6	2544	10	BC011310	BC011310 Mus muscu
C 433	3.8	3.7	90736	3	AC004532	Drosophil	C 510	37.4	3.6	2583	10	MMNCAMR	Y00051 Mouse mRNA
C 434	3.8	3.7	119668	9	AC011422	Homo sapi	C 511	37.4	3.6	3150	9	BC040198	BC040198 Homo sapi
C 435	3.8	3.7	129020	8	AP004871	Oryza sat	C 512	37.4	3.6	3705	6	AX059557	AX059557 Sequence
C 436	3.8	3.7	129201	2	AC017928	Drosophil	C 513	37.4	3.6	4066	3	AF109875	AF109875 Leishmani
C 437	3.8	3.7	155807	9	AC087685	Homo sapi	C 514	37.4	3.6	161644	9	AL161645	AL161645 Human DNA
C 438	3.8	3.7	157948	3	AC007696	Drosophil	C 515	37.4	3.6	180213	2	AC120424	AC120424 Mus muscu
C 439	3.8	3.7	172885	2	AC011340	Homo sapi	C 516	37.4	3.6	180213	2	AC120424	AC120424 Mus muscu
C 440	3.8	3.7	174294	2	AC013659	Homo sapi	C 517	37.4	3.6	190867	9	AC145922	AC145922 Pan trogl
C 441	3.8	3.7	186783	9	AC090355	Homo sapi	C 518	37.4	3.6	280585	2	AC128381	AC128381 Rattus no
C 442	3.8	3.7	210598	2	AC117924	Rattus no	C 519	37.4	3.6	280585	2	AC128381	AC128381 Rattus no
C 443	3.8	3.7	228872	2	AC115412	Rattus no	C 520	37.2	3.6	474	6	AR426536	AR426536 Sequence
C 444	3.8	3.7	251142	3	AE003620	Drosophil	C 521	37.2	3.6	474	6	AX987230	AX987230 Sequence
C 445	3.8	3.7	299800	1	AP005040	Streptomy	C 522	37.2	3.6	474	6	BD122089	BD122089 EST and e
C 446	3.8	3.7	159547	2	AC073674	Mus muscu	C 523	37.2	3.6	110000	1	AF006618	Continuation (30 o
C 447	3.8	3.7	180210	2	AC109156	Mus muscu	C 524	37.2	3.6	110000	2	AC015551	AC015551 Homo sapi
C 448	3.8	3.7	184357	2	AC073728	Mus muscu	C 525	37.2	3.6	178515	9	AC106574	AC106574 Rattus no
C 449	3.8	3.7	950	3	AY052157	Drosophil	C 526	37	3.6	292748	2	AC106574	AC106574 Rattus no
C 450	3.8	3.7	950	3	AY052158	Drosophil	C 527	37	3.6	392	9	AF279756	AF279756 Homo sapi
C 451	3.8	3.7	1242	6	CQ607488	Sequence	C 528	37	3.6	483	5	AY539382	AY539382 Polymixia
C 452	3.8	3.7	3106	3	AY060653	Drosophil	C 529	37	3.6	566	9	AF254748	AF254748 Homo sapi
C 453	3.8	3.7	3987	10	BC070436	Mus muscu	C 530	37	3.6	900	6	CQ717158	CQ717158 Sequence
C 454	3.8	3.7	13716	6	CQ729237	Sequence	C 531	37	3.6	3020	9	BC033697	BC033697 Homo sapi
C 455	3.8	3.7	14233	8	AP003340	Oryza sat	C 532	37	3.6	3619	1	SCVALSFP	Y13070 S.coelicolo
C 456	3.8	3.7	173474	2	AC142081	Homo sapi							
C 457	3.8	3.7	183537	2	AC141266	Homo sapi							

531	37	3.6	3721	6	CQ724481	Sequence	604	36.4	3.5	1685	6	AR410665	Sequence
532	37	3.6	4092	6	AR062746	Sequence	605	36.4	3.5	1685	6	AR439029	Sequence
533	37	3.6	4092	6	AX658306	Sequence	606	36.4	3.5	1685	6	AR439029	Sequence
534	37	3.6	4092	9	HUMROR2A	M97639 Human trans	607	36.4	3.5	1685	6	AR527035	Sequence
535	37	3.6	7195	9	HSWGL17G	X13546 Human HMG-1	608	36.4	3.5	1685	6	AR528625	Sequence
536	37	3.6	11578	1	AE004855	AE004855 Pseudomon	609	36.4	3.5	1685	6	AR566068	Sequence
537	37	3.6	14461	6	AX256438	AX256438 Sequence	610	36.4	3.5	1685	6	AX454458	Sequence
538	37	3.6	35347	3	CE7009B9	Z47070 Caenorhabdi	611	36.4	3.5	1685	6	AX464214	Sequence
539	37	3.6	89319	2	AL329255	AL329255 Homo sapi	612	36.4	3.5	1685	6	AX490936	Sequence
540	37	3.6	91325	2	AC139936	AC139936 Mus muscu	613	36.4	3.5	1685	6	AX697492	Sequence
541	37	3.6	107415	9	AL513365	AL513365 Human DNA	614	36.4	3.5	1685	6	BD075436	Secretory
542	37	3.6	125020	9	AF429315	AF429315 Homo sapi	615	36.4	3.5	1685	6	AY358332	Homo sapi
543	37	3.6	162311	2	AC096877	AC096877 Pan trogl	616	36.4	3.5	1718	6	BD247477	Molecules
544	37	3.6	170669	9	AL592284	AL592284 Human DNA	617	36.4	3.5	1718	6	BD247477	Molecules
545	37	3.6	179545	2	AC146737	AC146737 Otollemur	618	36.4	3.5	1820	6	BD278800	Sequence
546	37	3.6	179620	2	AC146725	AC146725 Otollemur	619	36.4	3.5	1820	6	BD278800	Sequence
547	37	3.6	181427	2	AC027209	AC027209 Homo sapi	620	36.4	3.5	2463	6	BD156426	Primer fo
548	37	3.6	192799	9	AL583841	AL583841 Human DNA	621	36.4	3.5	2463	6	AX876990	Sequence
549	37	3.6	199227	2	AC110876	AC110876 Mus muscu	622	36.4	3.5	2463	6	AK001560	Sequence
550	37	3.6	212031	10	AC113326	AC113326 Mus muscu	623	36.4	3.5	2496	6	BD191411	Secreted
551	37	3.6	236508	2	AC094222	AC094222 Rattus no	624	36.4	3.5	2540	9	AF062733	Homo sapi
552	37	3.6	242227	10	AC124120	AC124120 Mus muscu	625	36.4	3.5	2835	10	AB010384	Mus muscu
553	37	3.6	259028	2	AC103238	AC103238 Rattus no	626	36.4	3.5	3214	10	RATF3A	D38492 Rat mRNA fo
554	37	3.6	262363	2	AC131868	AC131868 Rattus no	627	36.4	3.5	3557	9	AF363367	Homo sapi
555	37	3.6	301525	1	AP005046	AP005046 Streptomy	628	36.4	3.5	7590	6	CQ731281	Sequence
556	36.8	3.6	5201	3	AY069789	AY069789 Drosophil	629	36.4	3.5	10384	1	AE004945	Pseudomon
557	36.8	3.6	5220	6	AR361389	AR361389 Sequence	630	36.4	3.5	34636	2	AC141232	Homo sapi
558	36.8	3.6	5264	3	DME250859	AJ250859 Drosophil	631	36.4	3.5	34653	2	AC140698	Homo sapi
559	36.8	3.6	96157	9	AL138789	AL138789 Human DNA	632	36.4	3.5	34991	2	AC140701	Homo sapi
560	36.8	3.6	98613	2	AC139630	AC139630 Takifugu	633	36.4	3.5	35258	2	AC141240	Homo sapi
561	36.8	3.6	118447	2	AC093508	AC093508 Homo sapi	634	36.4	3.5	36297	2	AC140699	Homo sapi
562	36.8	3.6	132117	9	AC092463	AC092463 Homo sapi	635	36.4	3.5	36613	2	AC141233	Homo sapi
563	36.8	3.6	170000	2	AC004524	AC004524 Homo sapi	636	36.4	3.5	37909	2	AC141239	Homo sapi
564	36.8	3.6	174548	9	AP002342	AP002342 Homo sapi	637	36.4	3.5	89599	2	AC138966	Homo sapi
565	36.8	3.6	208587	2	AC079498	AC079498 Mus muscu	638	36.4	3.5	110000	1	AE016822_04	Continuation (5 of
566	36.8	3.6	209472	2	AC090759	AC090759 Homo sapi	639	36.4	3.5	124437	2	AC141598	Homo sapi
567	36.8	3.6	210000	2	AC004555	AC004555 Homo sapi	640	36.4	3.5	127485	9	HUAC002039	Homo sapi
568	36.8	3.6	256050	1	AL627274	AL627274 Salmonell	641	36.4	3.5	131353	2	AC137642	Homo sapi
569	36.8	3.6	258728	2	AC096957	AC096957 Rattus no	642	36.4	3.5	132781	2	AC141265	Homo sapi
570	36.8	3.6	300928	1	AE016836	AE016836 Salmonell	643	36.4	3.5	133726	2	AC141614	Homo sapi
571	36.8	3.6	301482	1	AE016916	AE016916 Chromobac	644	36.4	3.5	144161	2	AC141602	Homo sapi
572	36.6	3.5	695	3	AP254369	AP254369 Drosophil	645	36.4	3.5	148930	2	AC138949	Homo sapi
573	36.6	3.5	1752	4	AB039957	AB039957 Bos tauru	646	36.4	3.5	159466	2	AC140888	Homo sapi
574	36.6	3.5	2764	8	AF045014	AF045014 Podospora	647	36.4	3.5	174163	2	AC138970	Homo sapi
575	36.6	3.5	176267	9	AC127328	AC127328 Mus muscu	648	36.4	3.5	177920	2	AC137806	Homo sapi
576	36.6	3.5	186950	10	AC127328	AC127328 Mus muscu	649	36.4	3.5	181694	2	AC141466	Homo sapi
577	36.6	3.5	189424	9	AC148664	AC148664 Macaca mu	650	36.4	3.5	189311	10	AC114677	Mus muscu
578	36.6	3.5	197621	9	AC092809	AC092809 Homo sapi	651	36.4	3.5	182965	2	AC138946	Homo sapi
579	36.6	3.5	251845	2	AC097949	AC097949 Rattus no	652	36.4	3.5	186901	2	CR847800	Danio rer
580	36.6	3.5	293695	10	AC137749	AC137749 Mus muscu	653	36.4	3.5	200202	10	AC112154	Mus muscu
581	36.4	3.5	397	6	BD071700	BD071700 Secreted	654	36.4	3.5	204500	2	AC141267	Homo sapi
582	36.4	3.5	820	6	BD148386	BD148386 Primer fo	655	36.4	3.5	204638	2	AC141253	Homo sapi
583	36.4	3.5	820	6	AX688324	AX688324 Sequence	656	36.4	3.5	206404	2	AC136534	Homo sapi
584	36.4	3.5	950	3	AY052156	AY052156 Drosophil	657	36.4	3.5	210053	10	AL807383	Mouse DNA
585	36.4	3.5	950	3	AY052159	AY052159 Drosophil	658	36.4	3.5	216759	9	AC138969	Homo sapi
586	36.4	3.5	950	3	AY052160	AY052160 Drosophil	659	36.4	3.5	240787	2	AC126757	Homo sapi
587	36.4	3.5	950	3	AY052161	AY052161 Drosophil	660	36.4	3.5	242449	10	AC102618	Mus muscu
588	36.4	3.5	950	3	AY052162	AY052162 Drosophil	661	36.4	3.5	245165	2	CR383660	Danio rer
589	36.4	3.5	950	3	AY052163	AY052163 Drosophil	662	36.4	3.5	276787	2	AC113850	Rattus no
590	36.4	3.5	951	12	AL655987	AL655987 Synthetic	663	36.4	3.5	283100	1	SC093110	Streptomy
591	36.4	3.5	1242	9	AY046418	AY046418 Homo sapi	664	36.4	3.5	300684	1	AE017227	Mycobacte
592	36.4	3.5	1299	6	CQ728323	CQ728323 Sequence	665	36.4	3.5	308147	1	AE016915	Chromobac
593	36.4	3.5	1542	6	BD193028	BD193028 207 human	666	36.2	3.5	728	8	AY265313	Amorphoph
594	36.4	3.5	1542	6	CQ822024	CQ822024 Sequence	667	36.2	3.5	1066	5	CR407256	Gallus ga
595	36.4	3.5	1614	6	BD177640	BD177640 MBGPI pol	668	36.2	3.5	2501	1	AF127222	Pseudomon
596	36.4	3.5	1614	6	E37854	E37854 MBGPI polyp	669	36.2	3.5	33294	6	CQ870411	Sequence
597	36.4	3.5	1614	6	AX003003	AX003003 Sequence	670	36.2	3.5	84997	9	AL583832	Human DNA
598	36.4	3.5	1680	9	BC033819	BC033819 Homo sapi	671	36.2	3.5	87244	9	AC104670	Homo sapi
599	36.4	3.5	1685	6	BD172296	BD172296 Secreted	672	36.2	3.5	90458	8	AC140671	Medicago
600	36.4	3.5	1685	6	BD172615	BD172615 Secreted	673	36.2	3.5	90450	8	AC140548	Medicago
601	36.4	3.5	1685	6	BD172934	BD172934 Secreted	674	36.2	3.5	110000	1	AP006840_16	Continuation (17 o
602	36.4	3.5	1685	6	BD173253	BD173253 Secreted	675	36.2	3.5	110000	2	AL330427	Homo sapi
603	36.4	3.5	1685	6	BD175287	BD175287 Secretory	676	36.2	3.5	113587	9	AL590702	Human DNA

677	36.2	3.5	151329	9	BS000541	Pan trogl	c	750	35.8	3.5	300600	1	AP005935	AP005935 Bradyrhiz		
678	36.2	3.5	151766	4	AC150635	Bos tauru		751	35.8	3.5	300600	1	AP005952	AP005952 Bradyrhiz		
679	36.2	3.5	152252	2	AC147683	Pan trogl		752	35.6	3.4	718	6	BD220830	BD220830 Human gen		
c	680	36.2	3.5	161034	2	AL359927	Homo sapi	c	753	35.6	3.4	1157	8	SBU23787	U23787 Sorghum bic	
c	681	36.2	3.5	165128	2	AC147139	Pan trogl		754	35.6	3.4	1932	6	AX078612	AX078612 Sequence	
c	682	36.2	3.5	169292	2	AC136036	Rattus no		755	35.6	3.4	3967	5	GDAXONIN	X63101 G.domesticu	
c	683	36.2	3.5	181148	9	AC147668	Pan trogl		756	35.6	3.4	4734	6	CQ592466	CQ592466 Sequence	
c	684	36.2	3.5	188603	9	AC147164	Pan trogl		757	35.6	3.4	15597	3	AF074901	AF074901 Caenorhab	
685	36.2	3.5	190050	1	AL646080	Ralstonia		758	35.6	3.4	41345	3	CEP15G9	Z47068 Caenorhabdi		
686	36.2	3.5	196946	2	AC067934	Homo sapi		759	35.6	3.4	60978	2	AC017675	AC017675 Drosophil		
687	36.2	3.5	202249	9	AC147115	Pan trogl		760	35.6	3.4	80182	5	AL772356	AL772356 Zebrafish		
c	688	36.2	3.5	212954	9	AC144376	Pan trogl		761	35.6	3.4	91688	8	AC006446	AC006446 Arabidops	
c	689	36.2	3.5	220216	9	AC021019	Homo sapi		762	35.6	3.4	110000	1	AP006618	Continuation (51 o	
c	690	36.2	3.5	238976	2	AC106187	Rattus no		763	35.6	3.4	115768	2	AP000712	AP000712 Homo sapi	
691	36.2	3.5	241758	2	AC150518	Bos tauru		764	35.6	3.4	157043	2	AC013692	AC013692 Homo sapi		
692	36.2	3.5	243864	2	AC096925	Rattus no		765	35.6	3.4	165147	2	AC021342	AC021342 Homo sapi		
c	693	36.2	3.5	254314	2	AC122953	Rattus no		766	35.6	3.4	184266	2	EX571737	EX571737 Danilo rer	
c	694	36.2	3.5	258707	2	AC095455	Rattus no		767	35.6	3.4	185967	2	BX640499	BX640499 Danilo rer	
c	695	36.2	3.5	347625	1	BX248356	Corynebac		768	35.6	3.4	187131	2	AP001535	AP001535 Homo sapi	
c	696	36.2	3.5	349142	1	BX572599	Rhodopsu		769	35.6	3.4	204548	5	AC145960	AC145960 Gallus ga	
697	36	3.5	828	8	AF517881	Griffithsu		770	35.6	3.4	209071	3	AC005285	AC005285 Drosophil		
698	36	3.5	2895	5	AY029403	Danio rer		771	35.6	3.4	214621	3	AC093100	AC093100 Drosophil		
699	36	3.5	7585	1	SCV14206	Streptomyce		772	35.6	3.4	230267	5	BX324146	BX324146 Zebrafish		
c	700	36	3.5	148984	9	AC097335	Chimpanze		773	35.6	3.4	280096	3	AE003613	AE003613 Drosophil	
c	701	36	3.5	174326	2	AC135387	Rattus no		774	35.6	3.4	305520	1	AE016780	AE016780 Pseudomon	
702	36	3.5	182573	2	AC120353	Mus muscu		775	35.4	3.4	465	1	AY120214	AY120214 Neisseria		
703	36	3.5	190575	2	AC135024	Rattus no		776	35.4	3.4	465	1	AY120240	AY120240 Neisseria		
c	704	36	3.5	192213	2	CR847542	Danio rer		777	35.4	3.4	465	1	AY120263	AY120263 Neisseria	
c	705	36	3.5	194328	2	AC139902	Rattus no		778	35.4	3.4	465	1	AY120272	AY120272 Neisseria	
706	36	3.5	199175	2	AC113055	Mus muscu		779	35.4	3.4	843	6	CQ605682	CQ605682 Sequence		
c	707	36	3.5	200673	10	AC131676	Mus muscu		780	35.4	3.4	2315	8	AK105496	AK105496 Oryza sat	
c	708	36	3.5	235086	2	AC097672	Rattus no		781	35.4	3.4	3324	6	AR384490	AR384490 Sequence	
c	709	36	3.5	310550	1	SC0939113	Streptomy		782	35.4	3.4	6741	6	E32987	AE010162 Pyrococu	
710	35.8	3.5	444	9	HSNRCAM			783	35.4	3.4	9685	3	AF369890	AF369890 Branchios		
711	35.8	3.5	975	6	BD179599	Homo sapi		c	784	35.4	3.4	16524	3	AF369890	AF369890 Branchios	
c	712	35.8	3.5	1731	6	AX433258	Sequence		785	35.4	3.4	37941	1	AQPCA361	AJ223398 Amycolato	
713	35.8	3.5	1774	9	AF016029	Homo sapi		786	35.4	3.4	58645	9	AC002068	AC002068 Homo sapi		
714	35.8	3.5	2734	6	AX954539	Sequence		787	35.4	3.4	63780	9	AC131957	AC131957 Homo sapi		
715	35.8	3.5	3170	10	RNNCAM14			788	35.4	3.4	110000	2	AE017180	Continuation (13 o		
c	716	35.8	3.5	3531	9	AF030112	Homo sapi		789	35.4	3.4	110000	2	AP006486	AP006486 Cyanidios	
717	35.8	3.5	3574	4	BTADGVC			c	790	35.4	3.4	110000	8	CR382131	Continuation (24 o	
718	35.8	3.5	3900	9	HSC7NRCAM			791	35.4	3.4	136982	8	AC123974	AC123974 Oryza sat		
719	35.8	3.5	4197	6	A87637	Sequence		792	35.4	3.4	141988	2	AC109703	AC109703 Rattus no		
720	35.8	3.5	4334	9	HSU55258	Human bBRAV		793	35.4	3.4	155628	1	AE016876	AE016876 Pseudomon		
721	35.8	3.5	6218	9	AB002341	Homo sapi		c	794	35.4	3.4	158391	10	AC115051	AC115051 Mus muscu	
722	35.8	3.5	6219	6	CQ716062	Sequence		c	795	35.4	3.4	177206	9	AC005105	AC005105 Homo sapi	
723	35.8	3.5	6240	9	HSM806153	Homo sapi		c	796	35.4	3.4	184896	10	AC141641	AC141641 Mus muscu	
724	35.8	3.5	6254	6	BD190781	Secreted		c	797	35.4	3.4	232240	2	AC150191	AC150191 Gallus ga	
725	35.8	3.5	6254	6	AX099489	Sequence		c	798	35.4	3.4	258596	2	AC150042	AC150042 Gallus ga	
726	35.8	3.5	6384	6	AR448063	Sequence		c	799	35.4	3.4	289308	1	AE017242	AE017242 Mycobacte	
c	727	35.8	3.5	6384	6	AR531706	Sequence		c	800	35.4	3.4	300425	1	AP005044	AP005044 Streptomy
c	728	35.8	3.5	11085	1	AE004450	Pseudomon		c	801	35.2	3.4	1247	10	AY262758	AY262758 Mus muscu
c	729	35.8	3.5	15259	9	HSL6009A	Human DNA s		c	802	35.2	3.4	2556	10	AY269789	AY269789 Mus muscu
730	35.8	3.5	36890	2	AC113351	Homo sapi		c	803	35.2	3.4	2868	5	GSTRKC	X59669 G.gallus tr	
c	731	35.8	3.5	59339	9	AF287967	Homo sapi		c	804	35.2	3.4	3157	5	S74248	S74248 trkC-tyrosi
c	732	35.8	3.5	74673	9	AC005683	Homo sapi		c	805	35.2	3.4	3606	10	AB107882	AB107882 Mus muscu
733	35.8	3.5	110000	1	AE017333	31 Continuation (32 o		c	806	35.2	3.4	4500	1	HMA277440	AJ2777440 Halaearcul	
734	35.8	3.5	110000	2	CP000002	31 Continuation (32 o		c	807	35.2	3.4	10242	6	CQ600663	CQ600663 Sequence	
c	735	35.8	3.5	110000	2	AC109410	2 Continuation (3 of		c	808	35.2	3.4	11087	1	HMA429077	AJ429077 Halaearcul
736	35.8	3.5	145151	9	AL645949	Human DNA		c	809	35.2	3.4	20978	6	CQ600662	CQ600662 Sequence	
737	35.8	3.5	148042	2	AC115038	Mus muscu		c	810	35.2	3.4	23759	1	AE008802	AE008802 Salmonell	
c	738	35.8	3.5	150151	9	AL356115	Human DNA		c	811	35.2	3.4	27060	3	AB055927	AB055927 Procambri
c	739	35.8	3.5	159246	9	AL590235	Human DNA		c	812	35.2	3.4	39115	2	AC051972	AC051972 Drosophil
c	740	35.8	3.5	168215	9	AC009789	Homo sapi		c	813	35.2	3.4	70398	3	DME271740	AJ2717140 Drosophil
c	741	35.8	3.5	168656	9	AC009108	Homo sapi		c	814	35.2	3.4	83495	3	AC087076	AC087076 Caenorhab
742	35.8	3.5	177203	9	AC074321	Homo sapi		c	815	35.2	3.4	107595	10	EX571734	BX571734 Mouse DNA	
743	35.8	3.5	178403	10	AL845283	Mouse DNA		c	816	35.2	3.4	110000	2	AP006840	Continuation (13 o	
c	744	35.8	3.5	187386	9	AC103702	Homo sapi		c	817	35.2	3.4	110000	2	AC103663	Continuation (2 of
c	745	35.8	3.5	191032	2	AC074370	Homo sapi		c	818	35.2	3.4	120180	5	BX323592	BX323592 Zebrafish
c	746	35.8	3.5	208824	2	AC110687	Rattus no		c	819	35.2	3.4	136884	2	AC013397	AC013397 Homo sapi
747	35.8	3.5	227054	9	AF172277	Homo sapi		c	820	35.2	3.4	144056	3	AC091222	AC091222 Drosophil	
748	35.8	3.5	268294	2	AC020885	Mus muscu		c	821	35.2	3.4	167281	2	AP001147	AP001147 Homo sapi	
c	749	35.8	3.5	299750	1	AP005964	Bradyrhiz		c	822	35.2	3.4	173572	2	AC135112	AC135112 Mus muscu

C 823	35.2	3.4	179661	2	AC134788	Mus muscu	C 896	34.8	3.4	153950	8	AC104429	Oryza sat
C 824	35.2	3.4	184794	2	AP000849	Homo sapi	897	34.8	3.4	154719	2	CR457445	Danio rer
C 825	35.2	3.4	190289	14	MCU60315	U60315 Molluscum c	898	34.8	3.4	168318	2	AC024042	Homo sapi
C 826	35.2	3.4	215434	2	AC1019214	AC0119214	899	34.8	3.4	170801	3	AC095014	Drosophill
C 827	35.2	3.4	233861	2	AC148064	Bob tauru	900	34.8	3.4	173690	2	AC011307	Homo sapi
C 828	35.2	3.4	300550	1	AP005021	Streptomy	901	34.8	3.4	178137	9	AC011302	Homo sapi
C 829	35.2	3.4	315108	3	AE003473	Drosophill	902	34.8	3.4	179937	9	CNS051CV	AL355840 Human chr
C 830	35	3.4	879	6	E09376	BD179636 Highly th	C 903	34.8	3.4	183272	2	AC150298	Callithri
C 831	35	3.4	1251	6	BC009462	BC009462 Homo sapi	C 904	34.8	3.4	183351	9	AC015801	Homo sapi
C 832	35	3.4	1383	9	BC009462	BC009462 Homo sapi	C 905	34.8	3.4	183351	9	AC015801	Homo sapi
C 833	35	3.4	1749	6	AR388820	Sequence	C 906	34.8	3.4	187733	9	AC151388	Callithri
C 834	35	3.4	2116	9	AC094031	AC094031 Homo sapi	C 907	34.8	3.4	188877	9	AC091902	Homo sapi
C 835	35	3.4	2771	9	HSC1P216	XS9906 H.sapiens C	C 908	34.8	3.4	192763	3	AC007474	Drosophill
C 836	35	3.4	2989	1	AF262989	AF262989 Klebsiell	909	34.8	3.4	194634	2	AC020286	Drosophill
C 837	35	3.4	2989	1	AF262990	AF262990 Klebsiell	910	34.8	3.4	196673	5	EX248396	Zebrafish
C 838	35	3.4	3000	1	AF193871	Thermus t	911	34.8	3.4	201972	2	CR391979	Danio rer
C 839	35	3.4	3324	1	KPNASTAB	M31938 K.aerogenes	C 912	34.8	3.4	205920	9	AC096570	Homo sapi
C 840	35	3.4	3832	1	KPN131525	AJ131525 Klebsiell	C 913	34.8	3.4	211029	2	AC126840	Rattus no
C 841	35	3.4	4044	9	BC002377	BC002377 Homo sapi	914	34.8	3.4	215458	2	AC127783	Rattus no
C 842	35	3.4	4044	9	BC014626	BC014626 Homo sapi	C 915	34.8	3.4	220527	5	AL929322	Zebrafish
C 843	35	3.4	7447	1	AF012100	AF012100 Pseudomon	916	34.8	3.4	222740	2	AC111134	Mus muscu
C 844	35	3.4	11558	1	AE004652	AE004652 Pseudomon	917	34.8	3.4	230755	2	AC024618	Mus muscu
C 845	35	3.4	1630	3	U97592	U97592 Caenorhabdi	C 918	34.8	3.4	252153	2	AC128765	Rattus no
C 846	35	3.4	59030	9	AC067959	AC067959 Homo sapi	C 919	34.8	3.4	266099	2	AC094795	Rattus no
C 847	35	3.4	63882	7	AY349011	AY349011 Burkholder	C 920	34.8	3.4	291000	1	SC0939105	Streptomy
C 848	35	3.4	72165	10	AL844574	AL844574 Mouse DNA	C 921	34.8	3.4	292919	3	AE003823	Drosophill
C 849	35	3.4	79405	10	AL928721	AL928721 Mouse DNA	922	34.8	3.4	298020	3	AE003674	Drosophill
C 850	35	3.4	90906	9	AC079767	AC079767 Homo sapi	C 923	34.8	3.4	300800	1	AP005036	Streptomy
C 851	35	3.4	110000	1	EX571966_24	Continuation (25 o	C 924	34.8	3.4	310005	2	AC098428	Rattus no
C 852	35	3.4	110000	1	CP000011_03	Continuation (4 of	925	34.8	3.4	321250	1	SC0939111	Streptomy
C 853	35	3.4	110542	10	AC087042	AC087042 Rattus no	926	34.8	3.4	348971	1	EX572594	Rhodospir
C 854	35	3.4	129696	9	AC008662	AC008662 Homo sapi	927	34.6	3.3	664	3	AY743229	Hemirich
C 855	35	3.4	150797	2	AC026817	AC026817 Homo sapi	928	34.6	3.3	731	8	AY265314	Amorphoph
C 856	35	3.4	157463	8	AC136377	AC136377 Oryza sat	929	34.6	3.3	736	8	AY191004	Amorphoph
C 857	35	3.4	159875	9	AC148692	AC148692 Macaca mu	930	34.6	3.3	2644	8	AKU32104	Neurospora
C 858	35	3.4	164176	2	AC080447	AC080447 Homo sapi	931	34.6	3.3	3396	8	AKU32104	Oryza sat
C 859	35	3.4	164396	2	AC024961	AC024961 Homo sapi	932	34.6	3.3	3613	9	HSMB02220	Homo sapi
C 860	35	3.4	165866	2	AC073202	AC073202 Homo sapi	933	34.6	3.3	3951	9	AY245430	Homo sapi
C 861	35	3.4	170665	5	EX072563	EX072563 Zebrafish	934	34.6	3.3	9805	9	AF244132	Homo sapi
C 862	35	3.4	174149	2	AC009688	AC009688 Homo sapi	C 935	34.6	3.3	12665	1	AE012784	Chlorobiu
C 863	35	3.4	174959	5	AL845312	AL845312 Zebrafish	936	34.6	3.3	29280	3	AB079865	Streptomy
C 864	35	3.4	175291	9	AC103925	AC103925 Homo sapi	C 937	34.6	3.3	34644	1	AF080235	Streptomy
C 865	35	3.4	176129	9	AP003061	AP003061 Homo sapi	C 938	34.6	3.3	39130	3	CBRG42821	Caenorhab
C 866	35	3.4	177623	2	CR394571	CR394571 Danio rer	C 939	34.6	3.3	103308	9	AC092491	Homo sapi
C 867	35	3.4	196137	10	AC097257	AC097257 Rattus no	C 940	34.6	3.3	104939	2	AC138556	Takifugu
C 868	35	3.4	199446	10	AC125069	AC125069 Mus muscu	C 941	34.6	3.3	110000	1	AE016822_24	Continuation (25 o
C 869	35	3.4	229065	2	EX284665	EX284665 Danio rer	C 942	34.6	3.3	110000	1	AY316747_0	Rhizobium
C 870	35	3.4	231332	10	AC096070	AC096070 Rattus no	C 943	34.6	3.3	120988	9	AL137182	Human DNA
C 871	35	3.4	270418	1	AE017303	AE017303 Thermus t	C 944	34.6	3.3	127075	9	AC097374	Homo sapi
C 872	35	3.4	296300	1	AP005035	AP005035 Streptomy	C 945	34.6	3.3	133574	9	AC138558	Takifugu
C 873	35	3.4	315041	2	AC106711	AC106711 Homo sapi	946	34.6	3.3	133574	9	HS20N2	Human DNA
C 874	34.8	3.4	1110	6	CQ575874	CQ575874 Sequence	947	34.6	3.3	146505	2	CR352287	Danio rer
C 875	34.8	3.4	1563	3	AY051911	AY051911 Drosophill	948	34.6	3.3	155120	2	AL929459	Danio rer
C 876	34.8	3.4	2020	8	AK121289	AK121289 Oryza sat	949	34.6	3.3	160000	3	AB090307	Bombyx mo
C 877	34.8	3.4	2135	3	DROAMA	M23561 D.melanogas	950	34.6	3.3	164144	2	AC092432	Homo sapi
C 878	34.8	3.4	3426	6	CQ575873	CQ575873 Sequence	951	34.6	3.3	172116	2	AC009472	Homo sapi
C 879	34.8	3.4	3496	1	RLB427840	AJ427840 Rhizobium	C 952	34.6	3.3	174425	2	AC146284	Lemur cat
C 880	34.8	3.4	3718	1	AF005842	AF005842 Rhodobact	953	34.6	3.3	179893	2	AL139043	Homo sapi
C 881	34.8	3.4	4640	3	DMDTRK	X63453 D.melanogas	C 954	34.6	3.3	179993	9	AC018360	Homo sapi
C 882	34.8	3.4	4645	6	CQ591393	CQ591393 Sequence	C 955	34.6	3.3	182741	2	AC120426	Mus muscu
C 883	34.8	3.4	4645	6	CQ847776	CQ847776 Sequence	C 956	34.6	3.3	192554	2	AC024170	Homo sapi
C 884	34.8	3.4	4775	3	BT015249	BT015249 Drosophill	957	34.6	3.3	196311	9	CNS01DVP	Human chr
C 885	34.8	3.4	6228	2	AC020270	AC020270 Drosophill	C 958	34.6	3.3	196642	2	AC012587	Homo sapi
C 886	34.8	3.4	11203	1	AE011939	AE011939 Xanthomon	959	34.6	3.3	197311	2	AC074207	Mus muscu
C 887	34.8	3.4	20248	6	CQ591392	CQ591392 Sequence	960	34.6	3.3	199030	2	AC111324	Rattus no
C 888	34.8	3.4	37500	2	AC068068	AC068068 Leishmani	961	34.6	3.3	207067	5	EX232601	Zebrafish
C 889	34.8	3.4	83726	9	AC113391	AC113391 Homo sapi	962	34.6	3.3	221717	2	AC074357	Mus muscu
C 890	34.8	3.4	84246	3	AC002512	AC002512 Drosophill	C 963	34.6	3.3	225984	2	AC138325	Mus muscu
C 891	34.8	3.4	98816	10	AL928861	AL928861 Mouse DNA	C 964	34.6	3.3	238327	2	AC151718	Mus muscu
C 892	34.8	3.4	110000	1	AE016822_11	Continuation (12 o	965	34.6	3.3	295150	1	SC0939126	Streptomy
C 893	34.8	3.4	110000	3	AE001572_2	Continuation (3 of	C 966	34.6	3.3	295150	1	SC0939126	Streptomy
C 894	34.8	3.4	133079	8	AC146581	AC146581 Oryza sat	C 967	34.6	3.3	299425	1	AP005037	Streptomy
C 895	34.8	3.4	147205	8	AC146702	AC146702 Genomic s	C 968	34.6	3.3	320658	2	AC145527	Atelerix

c 969	34.6	3.3	349116	1	AP003003	1042	34.4	3.3	206784	2	AC100182	AC100182 Mus muscu
c 970	34.4	3.3	481	3	AF103755	1043	34.4	3.3	215555	2	CR354444	Danio rer
	34.4	3.3	618	9	AB083330	c1044	34.4	3.3	217273	2	AC113182	AC113182 Mus muscu
	34.4	3.3	1179	6	BD167330	c1045	34.4	3.3	220050	1	AL646074	RA1646074 Ralsconia
	34.4	3.3	1179	6	BD093548	c1046	34.4	3.3	224076	2	AC084019	AC084019 Mus muscu
	34.4	3.3	1181	6	ES11166	c1047	34.4	3.3	228972	2	AC114611	AC114611 Mus muscu
	34.4	3.3	1181	6	ES11184	c1048	34.4	3.3	231639	2	AC095118	AC095118 Rattus no
	34.4	3.3	1181	6	AR399385	c1049	34.4	3.3	232874	2	AC124663	AC124663 Mus muscu
	34.4	3.3	1181	6	AR399385	c1050	34.4	3.3	235438	2	AC129004	AC129004 Rattus no
	34.4	3.3	1182	6	BD2335295	c1051	34.4	3.3	236397	2	AC101880	AC101880 Mus muscu
	34.4	3.3	1182	6	BD2335295	c1052	34.4	3.3	236536	10	AC139941	AC139941 Mus muscu
	34.4	3.3	1182	6	IS3761	c1053	34.4	3.3	236892	2	AC123191	AC123191 Rattus no
	34.4	3.3	1182	6	BD057228	c1054	34.4	3.3	252370	2	AC098545	AC098545 Rattus no
	34.4	3.3	1359	8	AV154299	c1055	34.4	3.3	256673	2	AC087146	AC087146 Mus muscu
	34.4	3.3	1360	6	AR381644	c1056	34.4	3.3	256673	2	AC087146	AC087146 Mus muscu
	34.4	3.3	1431	6	IS7379	c1057	34.4	3.3	256150	1	SC0939125	SC0939125 Streptomy
	34.4	3.3	1431	6	IS7379	c1058	34.4	3.3	300395	1	AE016785	AE016785 Pseudomon
	34.4	3.3	1926	6	BD2335301	c1059	34.4	3.3	301925	1	AP005046	AP005046 Streptomy
	34.4	3.3	1926	6	BD2335308	c1060	34.4	3.3	321435	2	AC094119	AC094119 Rattus no
	34.4	3.3	2327	6	AR363785	c1061	34.4	3.3	321435	2	AC094119	AC094119 Rattus no
	34.4	3.3	2327	6	AR365583	c1062	34.2	3.3	640	6	E12641	E12641 cDNA encodi
	34.4	3.3	2328	1	AFAKTLAACA	c1063	34.2	3.3	1266	8	AK103964	AK103964 Oryza sat
	34.4	3.3	2328	6	E29399	c1064	34.2	3.3	1271	8	AK058594	AK058594 Oryza sat
	34.4	3.3	2328	6	E38217	c1065	34.2	3.3	1298	8	AK071859	AK071859 Oryza sat
	34.4	3.3	2328	6	AR242841	c1066	34.2	3.3	1353	6	AX653421	AX653421 Sequence
	34.4	3.3	2328	6	AX105330	c1067	34.2	3.3	14574	1	AE001928	AE001928 Deinococc
	34.4	3.3	2328	6	AX105577	c1068	34.2	3.3	31422	6	E38021	E38021 Avermectin
	34.4	3.3	2328	6	BD015028	c1069	34.2	3.3	31422	6	BD097650	BD097650 A method
	34.4	3.3	2714	5	GN0113	c1070	34.2	3.3	64957	1	AB032367	AB032367 Streptomy
	34.4	3.3	2879	5	BC075300	c1071	34.2	3.3	96745	2	AC074219	AC074219 Mus muscu
	34.4	3.3	3456	6	AR381643	c1072	34.2	3.3	110000	8	BX323455	BX323455 Mus muscu
	34.4	3.3	3834	1	AF348135	c1073	34.2	3.3	110000	8	CR382130	CR382130_07
	34.4	3.3	4901	9	HS0803665	c1074	34.2	3.3	119148	5	BX005411	BX005411 Zebrafish
	34.4	3.3	4983	6	IS7083	c1075	34.2	3.3	145009	2	CR548634	CR548634 Danio rer
	34.4	3.3	4984	6	ES1164	c1076	34.2	3.3	145011	2	AP005608	AP005608 Oryza sat
	34.4	3.3	4984	6	ES1182	c1077	34.2	3.3	146008	8	AP005608	AP005608 Oryza sat
	34.4	3.3	4984	6	AR399383	c1078	34.2	3.3	167133	2	AC026186	AC026186 Homo sapi
	34.4	3.3	4984	6	AX137499	c1079	34.2	3.3	174131	2	AC129126	AC129126 Rattus no
	34.4	3.3	7928	6	AX039412	c1080	34.2	3.3	174310	2	BX572630	BX572630 Danio rer
	34.4	3.3	12738	9	HS0475429	c1081	34.2	3.3	177191	2	AC147521	AC147521 Otolomur
	34.4	3.3	20435	9	HS0475429	c1082	34.2	3.3	177466	1	AE001826	AE001826 Deinococc
	34.4	3.3	34569	1	AJ627420	c1083	34.2	3.3	183431	2	AC138788	AC138788 Sus scrofa
	34.4	3.3	68015	2	AC120038	c1084	34.2	3.3	186161	2	AC151887	AC151887 Salimiri s
	34.4	3.3	70070	2	AC022761	c1085	34.2	3.3	187807	5	BX569780	BX569780 Zebrafish
	34.4	3.3	80091	9	AC094088	c1086	34.2	3.3	189538	2	AC148045	AC148045 Otolomur
	34.4	3.3	104114	9	CR788250	c1087	34.2	3.3	190969	2	AC098337	AC098337 Rattus no
	34.4	3.3	106648	2	AC004588	c1088	34.2	3.3	194029	10	AL773523	AL773523 Mouse chr
	34.4	3.3	109682	9	BX120007	c1089	34.2	3.3	199429	10	AL606977	AL606977 Mouse chr
	34.4	3.3	110000	1	AE017180_20	c1090	34.2	3.3	205573	10	AL591032	AL591032 Mouse chr
	34.4	3.3	110000	1	AE017282_13	c1091	34.2	3.3	215873	2	AC124222	AC124222 Rattus no
	34.4	3.3	110000	2	AC106549_1	c1092	34.2	3.3	223248	2	AC055778	AC055778 Mus muscu
	34.4	3.3	110000	2	AC123076_5	c1093	34.2	3.3	227538	10	AC002397	AC002397 Mouse chr
	34.4	3.3	112309	9	AC003025	c1094	34.2	3.3	227743	2	CR847529	CR847529 Danio rer
	34.4	3.3	112830	2	AC151678	c1095	34.2	3.3	241529	2	AC103153	AC103153 Rattus no
	34.4	3.3	115165	9	AC106789	c1096	34.2	3.3	250893	2	AC094453	AC094453 Rattus no
	34.4	3.3	137729	10	AC079223	c1097	34.2	3.3	252070	2	AC098426	AC098426 Rattus no
	34.4	3.3	141682	2	CR391931	c1098	34.2	3.3	253812	2	AC094991	AC094991 Rattus no
	34.4	3.3	152152	5	BX005478	c1099	34.2	3.3	266114	2	AC103150	AC103150 Rattus no
	34.4	3.3	159693	10	AL646042	c1100	34.2	3.3	300129	1	AE017309	AE017309 Desulfovi
	34.4	3.3	163024	2	AP006260	c1101	34.2	3.3	301950	1	AP006570	AP006570 Globobact
	34.4	3.3	165255	2	AC102762	c1102	34.2	3.3	302077	1	SC0939132	SC0939132 Streptomy
	34.4	3.3	166867	9	AP003733	c1103	34.2	3.3	302675	1	AP005024	AP005024 Streptomy
	34.4	3.3	167098	2	AC023952	c1104	34.2	3.3	349008	1	BX640444	BX640444 Bordetell
	34.4	3.3	168745	5	BX005239	c1105	34	3.3	648	6	C0602403	C0602403 Sequence
	34.4	3.3	170028	2	AP002435	c1106	34	3.3	1141	6	AX083744	AX083744 Sequence
	34.4	3.3	170415	2	AC123299	c1107	34	3.3	1226	8	SU020596	SU020596 Soltanum lyc
	34.4	3.3	170871	2	AC084135	c1108	34	3.3	1259	8	BT014354	BT014354 Lycopersi
	34.4	3.3	182507	9	AC013441	c1109	34	3.3	1352	10	S77822	S77822 alpha-1-ant
	34.4	3.3	184681	2	AC084409	c1110	34	3.3	1746	6	AR306274	AR306274 Sequence
	34.4	3.3	197067	2	BS711806	c1111	34	3.3	1746	6	AX040926	AX040926 Sequence
	34.4	3.3	199789	2	AC074168	c1112	34	3.3	1746	6	AX040932	AX040932 Sequence
	34.4	3.3	201331	2	AC073687	c1113	34	3.3	1884	6	AR306272	AR306272 Sequence
	34.4	3.3	204272	2	CR762441	c1114	34	3.3	1884	6	AR306273	AR306273 Sequence

1115	34	3.3	1884	6	AR306275	Sequence	1188	33.8	3.3	465	1	AF086754	Neisseria
1116	34	3.3	1884	6	AR306276	Sequence	1189	33.8	3.3	465	1	AF165319	Neisseria
1117	34	3.3	1884	6	AX040922	Sequence	1190	33.8	3.3	465	1	AF165320	Neisseria
1118	34	3.3	1884	6	AX040923	Sequence	1191	33.8	3.3	465	1	AF165321	Neisseria
1119	34	3.3	1884	6	AX040928	Sequence	1192	33.8	3.3	465	1	AF165321	Neisseria
1120	34	3.3	1884	6	AX040930	Sequence	1193	33.8	3.3	465	1	AV120194	Neisseria
1121	34	3.3	2027	1	AVU30799	U30799 Azotobacter	1194	33.8	3.3	465	1	AV120195	Neisseria
1122	34	3.3	2561	1	AF205854	AF205854 Streptomy	1195	33.8	3.3	465	1	AV120196	Neisseria
1123	34	3.3	2870	6	AX405859	Sequence	1196	33.8	3.3	465	1	AV120197	Neisseria
1124	34	3.3	2900	9	AF169301	AF169301 Homo sapi	1197	33.8	3.3	465	1	AV120198	Neisseria
1125	34	3.3	2927	6	BD242874	BD242874 Secreted	1198	33.8	3.3	465	1	AV120199	Neisseria
1126	34	3.3	3470	6	CG062402	CG062402 Sequence	1199	33.8	3.3	465	1	AV120201	Neisseria
1127	34	3.3	4341	6	AX306429	AX306429 Sequence	1200	33.8	3.3	465	1	AV120202	Neisseria
1128	34	3.3	4343	6	AX306428	AX306428 Sequence	1201	33.8	3.3	465	1	AV120207	Neisseria
1129	34	3.3	4376	6	AX523794	AX523794 Sequence	1202	33.8	3.3	465	1	AV120212	Neisseria
1130	34	3.3	4384	6	AX523795	AX523795 Sequence	1203	33.8	3.3	465	1	AV120215	Neisseria
1131	34	3.3	4717	4	AF162445	AF162445 Canis fam	1204	33.8	3.3	465	1	AV120217	Neisseria
1132	34	3.3	30449	2	AC012859	AC012859 Drosophil	1205	33.8	3.3	465	1	AV120218	Neisseria
1133	34	3.3	40236	2	AC136401	AC136401 Rattus no	1206	33.8	3.3	465	1	AV120222	Neisseria
1134	34	3.3	95383	8	AC105259	AC105259 Oryza sat	1207	33.8	3.3	465	1	AV120223	Neisseria
1135	34	3.3	106186	8	AF448416	AF448416 Zea mays	1208	33.8	3.3	465	1	AV120224	Neisseria
1136	34	3.3	106977	9	HS9E21	AL008639 Human DNA	1209	33.8	3.3	465	1	AV120225	Neisseria
1137	34	3.3	110000	1	BS571966-20	AP006840 Symbiobac	1210	33.8	3.3	465	1	AV120232	Neisseria
1138	34	3.3	110000	1	BS571966-20	Continuation (21 o	1211	33.8	3.3	465	1	AV120233	Neisseria
1139	34	3.3	110983	2	AC110549	AC110549 Mus muscu	1212	33.8	3.3	465	1	AV120234	Neisseria
1140	34	3.3	110983	2	AC110549	AC110549 Mus muscu	1213	33.8	3.3	465	1	AV120239	Neisseria
1141	34	3.3	113372	9	AL161613	AL161613 Human DNA	1214	33.8	3.3	465	1	AV120242	Neisseria
1142	34	3.3	143320	9	AB042234	AB042234 Homo sapi	1215	33.8	3.3	465	1	AV120243	Neisseria
1143	34	3.3	158737	9	AL365276	AL365276 Human DNA	1216	33.8	3.3	465	1	AV120246	Neisseria
1144	34	3.3	167247	2	AC023579	AC023579 Homo sapi	1217	33.8	3.3	465	1	AV120247	Neisseria
1145	34	3.3	168136	2	AC138388	AC138388 Mus muscu	1218	33.8	3.3	465	1	AV120248	Neisseria
1146	34	3.3	170085	2	AC118718	AC118718 Mus muscu	1219	33.8	3.3	465	1	AV120253	Neisseria
1147	34	3.3	172172	9	AP006201	AP006201 Homo sapi	1220	33.8	3.3	465	1	AV120254	Neisseria
1148	34	3.3	176631	2	AC136204	AC136204 Sus scrof	1221	33.8	3.3	465	1	AV120255	Neisseria
1149	34	3.3	176711	10	AC137969	AC137969 Mus muscu	1222	33.8	3.3	465	1	AV120256	Neisseria
1150	34	3.3	177242	2	AC147237	AC147237 Mus muscu	1223	33.8	3.3	465	1	AV120262	Neisseria
1151	34	3.3	177431	2	EX571794	EX571794 Danio rer	1224	33.8	3.3	465	1	AV120264	Neisseria
1152	34	3.3	179563	9	AC006433	AC006433 Homo sapi	1225	33.8	3.3	465	1	AV120265	Neisseria
1153	34	3.3	183317	2	AL356861	AL356861 Homo sapi	1226	33.8	3.3	465	1	AV120266	Neisseria
1154	34	3.3	186822	10	AL837505	AL837505 Mouse DNA	1227	33.8	3.3	465	1	AV120267	Neisseria
1155	34	3.3	190110	2	AC101751	AC101751 Mus muscu	1228	33.8	3.3	465	1	AV120270	Neisseria
1156	34	3.3	190694	2	AC104543	AC104543 Mus muscu	1229	33.8	3.3	465	1	AV120273	Neisseria
1157	34	3.3	192350	3	AC008182	AC008182 Drosophil	1230	33.8	3.3	465	1	AV120274	Neisseria
1158	34	3.3	197901	3	AC009523	AC009523 Drosophil	1231	33.8	3.3	552	4	AAJ33149	Sorex ara
1159	34	3.3	199236	2	AC109237	AC109237 Mus muscu	1232	33.8	3.3	711	9	AF529206	Homo sapi
1160	34	3.3	200502	2	AC084830	AC084830 Mus muscu	1233	33.8	3.3	906	6	BD180234	BD180234 Highly th
1161	34	3.3	208196	2	AC098088	AC098088 Rattus no	1234	33.8	3.3	909	1	TT551423	Thermus t
1162	34	3.3	215895	2	AC121688	AC121688 Rattus no	1235	33.8	3.3	909	1	TT576036	Thermus t
1163	34	3.3	217393	9	AP001122	AP001122 Homo sapi	1236	33.8	3.3	1029	6	AX959811	Sequence
1164	34	3.3	222741	2	AC128894	AC128894 Rattus no	1237	33.8	3.3	1230	4	AB046174	Sus scrof
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1167	34	3.3	228824	2	AC137163	AC137163 Rattus no	1240	33.8	3.3	1439	5	SSSK181K	Y14647 Scyllorhinu
1168	34	3.3	234635	3	AE003623	AE003623 Drosophil	1241	33.8	3.3	1663	1	PSEPE1	D12711 P.aeruginos
1169	34	3.3	235043	2	AC103302	AC103302 Rattus no	1242	33.8	3.3	2016	5	CR390117	Callus ga
1170	34	3.3	251417	2	AC106252	AC106252 Rattus no	1243	33.8	3.3	2093	3	PEXARTP60A	L1557 Pseudomicro
1171	34	3.3	257983	2	AC106913	AC106913 Rattus no	1244	33.8	3.3	2133	4	OCU78768	U78768 Oryctolagus
1172	34	3.3	259794	2	AC121388	AC121388 Rattus no	1245	33.8	3.3	2196	10	AB064671	AB064671 Rattus no
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1174	34	3.3	289156	2	AC096058	AC096058 Rattus no	1247	33.8	3.3	3147	6	AR146118	AR146118 Sequence
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1184	33.8	3.3	465	1	AF086739	AF086739 Neisseria	1257	33.8	3.3	5510	6	AX409111	AX409111 Sequence
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c1409	33.6	3.2	172029	3	AC092494	AC092494 Drosophila	1482	33.4	3.2	4044	9	HUMCP210HC	M28548 Human mutan
c1410	33.6	3.2	173270	3	AC024886	AC024886 Homo sapi	1483	33.4	3.2	4071	9	AF531869	AF531869 Homo sapi
c1411	33.6	3.2	173988	3	AC011251	AC011251 Drosophila	1484	33.4	3.2	4191	6	C0789354	C0789354 Sequence
c1412	33.6	3.2	175582	2	AC016977	AC016977 Homo sapi	1485	33.4	3.2	4191	9	AF531868	AF531868 Homo sapi
c1413	33.6	3.2	176081	2	AC121053	Rattus no	1486	33.4	3.2	4191	9	HSU40271	U40271 Homo sapien
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c1415	33.6	3.2	189557	3	AC007356	Drosophila	1488	33.4	3.2	4236	9	HSU33635	U33635 Human colon
c1416	33.6	3.2	194516	2	AC102355	Mus muscu	1489	33.4	3.2	4238	9	BCO71557	BCO71557 Homo sapi
c1417	33.6	3.2	202676	2	CR788311	Danio rer	1490	33.4	3.2	5141	9	HUMHCP42	M12792 Homo sapien
c1418	33.6	3.2	208050	1	AL646083	CR847953	1491	33.4	3.2	5147	9	HUMHCP41	M12793 Homo sapien
c1419	33.6	3.2	210930	5	EX119315	zebrafish	c1492	33.4	3.2	5163	8	SCU32508	U32508 Saccharomyc
c1420	33.6	3.2	211583	9	AC069025	Homo sapi	1493	33.4	3.2	7478	9	AF077974	AF077974 Homo sapi
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c1422	33.6	3.2	212799	2	AC119477	Rattus no	1495	33.4	3.2	31595	6	AX780060	AX780060 Sequence
c1423	33.6	3.2	222489	2	CR847953	Danio rer	c1496	33.4	3.2	35325	3	U23514	U23514 Caenorhabdi
c1424	33.6	3.2	222938	2	AC095075	Rattus no	1497	33.4	3.2	3539	9	EX936373	EX936373 Human DNA
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c1426	33.6	3.2	235249	2	AC123564	Rattus no	1499	33.4	3.2	40127	9	HSF0811	Z97184 Human DNA s
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c1430	33.6	3.2	276492	2	AC111574	Rattus no							
c1431	33.6	3.2	280487	2	AC095311	Rattus no							
c1432	33.6	3.2	294169	3	AE003821	Drosophila							
c1433	33.6	3.2	300181	1	AE017318	Desulfovi							
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RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches 1035;

Conservative

Score 1035;

DB 6;

Length 1679;

Pred. No. 6.2e-284;

Mismatches 0;

Indels 0;

Gaps 0;

Qy

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60

Db

134

ATGAAAACCATCCAGCCAAATAATGCACAAATCTATCTCTTGGGCAATCTTACGGGGCTG

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61

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QY	781	AGATGTATTGAAGAAAGAAAGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAATCTC	840
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QY	841	ATCTTCTCAATGTCTCTGAAACATGACTATGGAACTACATTTGGTCCAGGCGCGTCCAAACAAG	900
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QY	901	CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCCAGCGAGGTGAGC	960
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RESULT 2
AR528639
LOCUS AR528639 1679 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 375 from patent US 6725730.
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Bollinger, C.L., Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 375 27-APR-2004;
FEATURES
 Location/Qualifiers
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ORIGIN

Query Match	100.0%;	Score 1035;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 6.2e-284;		
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QY	61	GCTGCTCTGTGTCTCTTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA	120	
Db	194			
QY	121	GCTATGACAAACGTCAGCGTCCCGCAGGGGAGAGCGCACCTTCAGGTGCACATTTTAC	180	
Db	254			
QY	181	AACCGGGTCAACCCGGGTGGCTTAAACCGCAGCACCAATCTCTTATGTGGGAATGAC	240	
Db	314			
QY	241	AAAGTGGTCCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGACGTACAGCATC	300	
Db	374			
QY	301	GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	360	
Db	434			
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Db	494			
QY	421	ATTTCTTCAGATATCTCCATTAAGAGGAAACAATATTAGCCTCACCTGCATAGCAACT	480	
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Db	734			
QY	661	TATCCACCATACATTTTCAGAAAGCCAAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA	720	
Db	794			
QY	721	CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGTAACAGGATGACAAA	780	
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QY	781	AGATGTATTGAAGAAAGAAAGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAATCTC	840	
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Db	974			
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Db	1094			
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Db	1154	CTTCTCAAAATTTTGA 1168		


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Db 1154 CTTCTCAAAATTTTGA 1168
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AX358872
LOCUS AX358872 1679 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 125 from Patent WO0193983.
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 100.0%; Score 1035; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.2e-284;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGCAGCGAGATGCCACCTTCCCAAAA 120
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGCAGCGAGATGCCACCTTCCCAAAA 253
QY 121 GCTATGGAACAAGTGCAGCGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATTTGAC 180
Db 254 GCTATGGAACAAGTGCAGCGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATTTGAC 313
QY 181 AACCGGGTCACCGGGTGCCTGAGTAAACCGCAGCACCACCTCTATGCTGGGAATGAC 240
Db 314 AACCGGGTCACCGGGTGCCTGAGTAAACCGCAGCACCACCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db 374 AAGTGGTGCCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
Db 434 GAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCATGTGCGAAGTATCTCCCAAAATTTGAG 420
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATGTGCGAAGTATCTCCCAAAATTTGAG 553
QY 421 ATTCTCTCAGATATCTCCATTAAAGGGAAACAATATTAGCTCACCCTGCATAGCAACT 480
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Db 674 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCGGAGCAGTCAAGGGACTACGAG 733
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QY 1021 CTTCTCAAAATTTTGA 1035
Db 1154 CTTCTCAAAATTTTGA 1168
RESULT 4
AX362365
LOCUS AX362365 1679 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 1035; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.2e-284;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 60
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LOCUS
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Sequence 55 from Patent WO208284.
ACCESSION
AX454470.1 GI:21713859
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REFERENCE
AUTHORS
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL
Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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Best Local Similarity 100.0%; Pred. No. 6.2e-284;
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DEFINITION
Sequence 375 from Patent WO0140466.
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VERSION
AX464242.1 GI:21899137
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
REFERENCE
AUTHORS
Baker, K.P., Beresini, M., Deforge, L., Deanoyers, L., Filvaroff, E.,
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Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L., and Zhang, Z.,
Secreted and transmembrane polypeptides and nucleic acids encoding same

JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;

Genentech Inc. (US)

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source

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Query Match 100.0%; Score 1035; DB 6; Length 1679;

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DEFINITION Sequence 55 from Patent WO0200690.
ACCESSION AX490948
VERSION AX490948.1 GI:22323811
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
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TITILE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 55 03-JAN-2002;
Genentech, Inc. (US)
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REFERENCE			
AUTHORS			
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,			
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,			
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Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,			
Goddard, A., Wood, W.I. and Godowski, P.			
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale			
Effort to Identify Novel Human Secreted and Transmembrane Proteins:			
A Bioinformatics Assessment			

JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)
PUBMED	12975309
REFERENCE	2 (bases 1 to 1679)
AUTHORS	Clark, H.F.
TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
	Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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LOCUS AR439649 1693 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 2 from patent US 6664383.

ACCESSION AR439649

VERSION AR439649.1 GI:42665573

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1693)

AUTHORS Fukushima,D., Shibayama,S. and Tada,H.

TITLE Polypeptides, cDNA encoding the same and utilization thereof

JOURNAL Patent: US 6664383-A 2 16-DEC-2003;

FEATURES

source

1..1693

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1035; DB 6; Length 1693;

Best Local Similarity 100.0%; Pred. No. 6.2e-284;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAAATGACAAATTCATCTCTTGGGCAATCTTCACGGGGCTG 60

Db 130 ATGAAACCATCCAGCCAAAATGACAAATTCATCTCTTGGGCAATCTTCACGGGGCTG 189

Qy 61 GCTGCTCTGTGTCTCTTCAAGAGTGCCTGGTGGGAGATGCCACCTTCCCAAAA 120

Db 190 GCTGCTCTGTGTCTCTTCAAGAGTGCCTGGTGGGAGATGCCACCTTCCCAAAA 249

Qy 121 GCTATGGAACAAGTACAGTGCCTGGGAGAGCGCCCTCAGGTGCACTATTGAC 180

Db 250 GCTATGGAACAAGTACAGTGCCTGGGAGAGCGCCCTCAGGTGCACTATTGAC 309

Qy 181 AACCGGGTCAACCGGGTGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240

Db 310 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTCTATGCTGGGAATGAC 369

Qy 241 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGGACACCCAAACCGCAGGTACAGCATC 300

Db 370 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACCGATGACAGCATC 429

Qy 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACAG 360

Db 430 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACAG 489

Qy 361 AACCAACCAAGACCTCTAGGGTCCACCTATTTGGCAAGTATCTCCCAAAATTTGTAGAG 420

Db 490 AACCAACCAAGACCTCTAGGGTCCACCTATTTGGCAAGTATCTCCCAAAATTTGTAGAG 549

Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Db 550 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 609

Qy 481 GGTAGACAGAGCCTTACGGTTTACTTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTG 540

Db 610 GGTAGACAGAGCCTTACGGTTTACTTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTG 669

Qy 541 AGTCAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGAGAGCATCAGGGGACTACGAG 600

Db 670 AGTCAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGAGAGCATCAGGGGACTACGAG 729

Qy 601 TGCAGTGCCTCCATGAGTGGCGCGCGCTGGTACGAGAGTAAAGGTGCTACCGTGAAC 660

Db 730 TGCAGTGCCTCCATGAGTGGCGCGCGCTGGTACGAGAGTAAAGGTGCTACCGTGAAC 789

Qy 661 TATCCACCATACATTTTCAGAAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 849

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Db 850 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTCAAGGATGACAAA 909

Qy 781 AGACTGATGTAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCTC 840

Db 910 AGACTGATGTAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCTC 969

Qy 841 ATCTTTCTTCAATGTCTCTGAACATGACTATGGAACACTACCTTGGTGGCCCTCACAACAG 900

Db 970 ATCTTTCTTCAATGTCTCTGAACATGACTATGGAACACTACCTTGGTGGCCCTCACAACAG 1029

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Db 1030 CTGGGGCACACAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1089

Qy 961 AACGCGACGTGAGGAGGCGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 1020

Db 1090 AACGCGACGTGAGGAGGCGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 1149

Qy 1021 CTCTCTCAAAATTTTGA 1035

Db 1150 CTCTCTCAAAATTTTGA 1164

RESULT 11

AR439648

LOCUS AR439648 1032 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 1 from patent US 6664383.

ACCESSION AR439648

VERSION AR439648.1 GI:42665572

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1032)

AUTHORS Fukushima,D., Shibayama,S. and Tada,H.

TITLE Polypeptides, cDNA encoding the same and utilization thereof

JOURNAL Patent: US 6664383-A 1 16-DEC-2003;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.1e-283;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCAATCCAGCCAAATATGACAAATCTATCTCTGGGCAATCTTACCGGGCTG 60
DB 1 ATGAACCAATCCAGCCAAATATGACAAATCTATCTCTGGGCAATCTTACCGGGCTG 60

QY 61 GCTGCTCTGTCTCTTCCAAAGAGTCCCGTGCAGCGAGAGTCCACCTTCCCCAAA 120
DB 61 GCTGCTCTGTCTCTTCCAAAGAGTCCCGTGCAGCGAGAGTCCACCTTCCCCAAA 120

QY 121 GCTATGGACAGTGCAGCGTCCGCGAGGGGAGAGCGCACCTCAGGTGCACTATTGAC 180
DB 121 GCTATGGACAGTGCAGCGTCCGCGAGGGGAGAGCGCACCTCAGGTGCACTATTGAC 180

QY 181 AACCGGTCACCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 181 AACCGGTCACCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240

QY 241 AAGTGGTCCCTGGATCCCTCGGTGTCTCTTCTGAGCAACACCCAAACGACGATC 300
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QY 301 GAGATCCAGAACGTGGATGTATGACAGGGCCCTTACCTGCTCGGTGCAGACAGAC 360
DB 301 GAGATCCAGAACGTGGATGTATGACAGGGCCCTTACCTGCTCGGTGCAGACAGAC 360

QY 361 AACCACCAAGAGCTCTAGGTCACCTCATTTGCAAGTATCTCCCAAAATTTGAG 420
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QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTTAGCTCACCCTGCATAGCAACT 480
DB 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTTAGCTCACCCTGCATAGCAACT 480

QY 481 GGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGT 540
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QY 541 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACGAG 600
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QY 601 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACCGTGAAC 660
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QY 661 TATCCACCATATCTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
DB 661 TATCCACCATATCTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720

QY 721 CTGCAAGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTACAGAGTGAACAAA 780
DB 721 CTGCAAGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTACAGAGTGAACAAA 780

QY 781 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATCTC 840
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QY 961 AACGCGACGTCGAGGAGGCGAGGCTGCGTCTGGCTGCTCTTCTGCTTTCGACCTG 1020
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QY 1021 CTTCTCAAAATTT 1032
DB 1021 CTTCTCAAAATTT 1032

RESULT 12
AX665342
LOCUS AX665342 1839 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 100 from Patent WO03002765.
ACCESSION AX665342
VERSION AX665342.1 GI:29290464
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
SELLAR, G.C. and GABRA, H.
Cancer
Patent: WO 03002765-A 100 09-JAN-2003;
Cancer Research Technology Limited (GB)
Location/Qualifiers
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FEATURES
source

ORIGIN

Query Match 92.1%; Score 953.4; DB 6; Length 1839;
Best Local Similarity 99.9%; Pred. No. 1.3e-260;
Matches 954; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 AGGAGTGCCCGTGGCGCAGCGAGATGCCACCTTCCCAAAGCTATGGACAACGTCACGGT 140
DB 345 AGGAGTGCCCGTGGCGCAGCGAGATGCCACCTTCCCAAAGCTATGGACAACGTCACGGT 404

QY 141 CCGCAGGGGAGAGCGCCACCTCAGGTGACATTTGACAACCGGGTCAACCGGGTGGC 200
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QY 201 CTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGGATCTCTCG 260
DB 465 CTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGGATCTCTCG 524

QY 261 CGTGGTCCCTTCTGAGCAACACCCAAACGCACTACGAGATCCAGAACGTCGATGT 320
DB 525 CGTGGTCCCTTCTGAGCAACACCCAAACGCACTACGAGATCCAGAACGTCGATGT 584

QY 321 GTATGACAGAGGGCCCTTACACCTGCTGGTGCAGACAGAACCAACCCAAAGACCTCTAG 380
DB 585 GTATGACAGAGGGCCCTTACACCTGCTGGTGCAGACAGAACCAACCCAAAGACCTCTAG 644

QY 381 GGTCCACTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCCAGATATCTCCAT 440
DB 645 GGTCCACTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCCAGATATCTCCAT 704

QY 441 TAATGAAGGGAACAATATTAGCCCTCACCTGCATAGCAACTGCTAGACAGAGCTTACCGT 500
DB 705 TAATGAAGGGAACAATATTAGCCCTCACCTGCATAGCAACTGCTAGACAGAGCTTACCGT 764

QY 501 TACTTGGAGACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATATTCTGGA 560
DB 765 TACTTGGAGACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATATTCTGGA 824

QY 561 AATTTCAGGGCATACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAAAGCCT 620
DB 825 AATTTCAGGGCATACCCGGGGAACAGTCAGGGGGAACCTACGAGTGCAGTGCCTCCAAAGCCT 884

Qy 621 GGCCGCGCCGCTGGTACGAGGAGTAAAGGTACCGTGAACATATCACCATACATTTTCAGA 680
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Db 1005 AGTCCCTCAGCAGATTCAGAGTGTGTAAGATGACAAAGACTGATTGAAGGAAGAA 1064
Qy 801 AGGGTGAAGTGGAAAACAGACCTTCTCTCAAACTCATCTCTCAATGCTCTGA 860
Db 1065 AGGGTGAAGTGGAAAACAGACCTTCTCTCAAACTCATCTCTCAATGCTCTGA 1124
Qy 861 ACATGACTATGGGAATCACTATGCGTGGCTCCAAACAGCTGGGCCACCAATGCCAG 920
Db 1125 ACATGACTATGGGAATCACTATGCGTGGCTCCAAACAGCTGGGCCACCAATGCCAG 1184
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Db 1185 CATCATGCTATTTGGTCCAGGCGCGTCCAGCGAGGTGAGCAACCGCAGCTCGAGAGGCG 1244
Qy 981 AGGCTGCGTCTGGCTGCTGCTCTCTGCTCTTGACCTGCTCTCAAAATTTTGA 1035
Db 1245 AGGCTGCGTCTGGCTGCTGCTCTCTGCTCTTGACCTGCTCTCAAAATTTTGA 1299

RESULT 13
LOCUS AF126426 1839 bp mRNA linear PRI 10-JUN-2002
DEFINITION Homo sapiens neurotrophin (HNT) mRNA, complete cds.
ACCESSION AF126426
VERSION AF126426.1 GI:7158997
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li.G., Jin,J., Tan,X., Hu.S., Yuan,J. and Qiang,B.
TITLE Cloning and identification of human neurotrophin full length cDNA
JOURNAL Unpublished
REFERENCE
AUTHORS Li.G., Jin,J., Tan,X., Hu.S., Yuan,J. and Qiang,B.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China

FEATURES
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/mol_type="mRNA"
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ORIGIN

Query Match 92.1%; Score 953.4; DB 9; Length 1839;

Best Local Similarity 99.9%; Pred. No. 1.3e-260;
Matches 954; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 81 AGGAGTCCCGTGGCGAGGAGATGCCACTTCCCAAGCTATGGAACAACGCGT 140
Db 345 AGGAGTCCCGTGGCGAGGAGATGCCACTTCCCAAGCTATGGAACAACGCGT 404
Qy 141 CCGGACGGGAGAGCCCACTTATGACAAACCGGTTCACCCGGGTGGC 200
Db 405 CCGGACGGGAGAGCCCACTTATGACAAACCGGTTCACCCGGGTGGC 464
Qy 201 CTGCTCTAAACCGCAGCAGCCTCTCTATGCTGGGAATGACAAAGTGGTCCCTCG 260
Db 465 CTGCTCTAAACCGCAGCAGCCTCTCTATGCTGGGAATGACAAAGTGGTCCCTCG 524
Qy 261 CGTGGTCTTCTGAGCAACCCAAACGCGAGTACAGATCGAGATCCAGACGTGGATGT 320
Db 525 CGTGGTCTTCTGAGCAACCCAAACGCGAGTACAGATCGAGATCCAGACGTGGATGT 584
Qy 321 GTATGACGAGGCGCTTACACCTGCTCGTGCAGACAGCAACCAACCAAGACCTCTAG 380
Db 585 GTATGACGAGGCGCTTACACCTGCTCGTGCAGACAGCAACCAACCAAGACCTCTAG 644
Qy 381 GGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT 440
Db 645 GGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT 704
Qy 441 TAATGAAGGGAACAATATTTAGCCTCACCTGCATAGCAACCAACCAAGACCTCTAG 500
Db 705 TAATGAAGGGAACAATATTTAGCCTCACCTGCATAGCAACCAACCAAGACCTCTAG 764
Qy 501 TACTTTGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATCTCTGA 560
Db 765 TACTTTGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATCTCTGA 824
Qy 561 AATTGAGGGAATCACCGGAGAGTACGAGGAGTACGAGTGCAGTGCCTCCAATGACGT 620
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Qy 981 AGGCTGCGTCTGGCTGCTGCTCTCTGCTCTTGACCTGCTCTCAAAATTTTGA 1035
Db 1245 AGGCTGCGTCTGGCTGCTGCTCTCTGCTCTTGACCTGCTCTCAAAATTTTGA 1299

RESULT 14
LOCUS AR439650
DEFINITION Sequence 5 from patent US 6664383.
ACCESSION AR439650

linear

DNA

939 bp

PAT 20-FEB-2004

VERSION AR439650.1 GI:42665574
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 939)
TITLE Fukushima,D., Shibayama,S. and Tada,H.
JOURNAL Polypeptides, cDNA encoding the same and utilization thereof
FEATURES Patent: US 664393-A 5 16-DEC-2003;
Location/Qualifiers
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source /organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 90.7%; Score 939; DB 6; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.5e-256;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 CGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAAGTGAACGGTCCGGCAGGGGAG 153
DB 1 CGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAAGTGAACGGTCCGGCAGGGGAG 60
QY 154 AGCGCCACCTCAGGTGCACTATTGACACCGGTCACCGGTCCTGGCTTAACCGC 213
DB 61 AGCGCCACCTCAGGTGCACTATTGACACCGGTCACCGGTCCTGGCTTAACCGC 120
QY 214 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTCTCGATCTCGGTCGCTTCTG 273
DB 121 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTCTCGATCTCGGTCGCTTCTG 180
QY 274 AGCAACCCCAACCGAGTACAGCATCGAGATCCAGAAAGTGGATGTGTATGACGAGGC 333
DB 181 AGCAACCCCAACCGAGTACAGCATCGAGATCCAGAAAGTGGATGTGTATGACGAGGC 240
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DB 241 CTTTACACTCTCGGTGAGACAGACACACCCCAAGACCTCTAGGTCACCTCATTT 300
QY 394 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 453
DB 301 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 360
QY 454 AATATTAGCCTCACTCGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACAC 513
DB 361 AATATTAGCCTCACTCGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACAC 420
QY 514 ATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGGCATC 573
DB 421 ATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGGCATC 480
QY 574 ACCCGGAGCAGTCAGGGGACTACAGATGTCAGTGCCTCCAATGAGTGGCCGCGCCGTG 633
DB 481 ACCCGGAGCAGTCAGGGGACTACAGATGTCAGTGCCTCCAATGAGTGGCCGCGCCGTG 540
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DB 541 GTACGAGAGTAAAGGTCAACCGTGAATATCAATCAATTCAGAGCCCAAGGGTACA 600
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QY 874 AACTACACTTGGTGGCTCCCAAGCTGGGGCAACCAATGCGCAGCATCATGTATTT 933

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QY 994 CTGCTGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1032
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RESULT 15
AX665344
LOCUS AX665344
DEFINITION Sequence 102 from Patent WO03002765.
ACCESSION AX665344
VERSION AX665344.1 GI:29290465
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Sellar,G.C. and Gabra,H.
AUTHORS Cancer
TITLE Patent: WO 03002765-A 102 09-JAN-2003;
JOURNAL Cancer Research Technology Limited (GB)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 88.0%; Score 910.4; DB 6; Length 1068;
Best Local Similarity 96.6%; Pred. No. 2.2e-248;
Matches 954; Conservative 0; Mismatches 1; Indels 33; Gaps 1;
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Qy	741	AGTCCCTCAGCAGAAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGAAAGAA	800
Db	741		800
Qy	801	AGGGTGAAGTGGAAACAGACCTTTCCTCTCAAACTCATCTTCTCAATGTCTCTGA	860
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Qy	861	ACATGACTATGGGAACACTTTCGTGGCCCTCCAAAGCTGGGCCACACCAATGCCAG	920
Db	861		920
Qy	921	CATCATGCTATT-----GGTCCAGGGCGGT	947
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Qy	948	CAGCGAGTGAGCAACGGCAGTCGAGGAGGCGAGGCTGGCTGGCTGGCTCTTCT	1007
Db	948		1007
Qy	1008	GGTCTTGACCTGCTTCTCAAATTTGA	1035
Db	1008		1035
Qy	1041	GGTCTTGACCTGCTTCTCAAATTTGA	1068
Db	1041		1068

Search completed: June 16, 2005, 10:22:55
 Job time : 4832.58 secs

Run on: June 15, 2005, 23:29:46 ; Search time 605.593 Seconds (without alignments)
 Title: US-10-017-084a-522_COPY_134_1168
 Perfect score: 1035
 Sequence: 1 atgaataaccatccgacaa.....acctgtctctcaatttga 1035
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 4390206 seqs, 2959870657 residues
 Total number of hits satisfying chosen parameters: 8780412
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries
 Database : N_Geneseq_16Dec04:.*
 1: geneseqn1980a:.*
 2: geneseqn1990a:.*
 3: geneseqn2000a:.*
 4: geneseqn2001a:.*
 5: geneseqn2001bs:.*
 6: geneseqn2002a:.*
 7: geneseqn2002bs:.*
 8: geneseqn2003a:.*
 9: geneseqn2003bs:.*
 10: geneseqn2003cs:.*
 11: geneseqn2003ds:.*
 12: geneseqn2004a:.*
 13: geneseqn2004bs:.*
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1
 ID AA34324 standard; cDNA; 1679 BP.
 DE Human PRO337 nucleotide sequence.
 PN WO9946281-A2.
 PD 16-SEP-1999.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 2; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 2
 ID AAC78590 standard; cDNA; 1679 BP.
 DE Human PRO337 nucleotide sequence SEQ ID NO:522.
 PN WO200053756-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 3; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 3
 ID AAC87037 standard; cDNA; 1679 BP.
 DE Nucleotide sequence of human polypeptide PRO337.
 PN WO200077037-A2.
 PD 21-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 4; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 4
 ID AAS21431 standard; cDNA; 1679 BP.
 DE Human cDNA sequence encoding for PRO337 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 4; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 5
 ID ABK33598 standard; cDNA; 1679 BP.
 DE cDNA encoding human PRO protein, Seq ID No 125.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1035; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 6
 ID ABL88099 standard; cDNA; 1679 BP.
 DE Human PRO337 cDNA sequence SEQ ID NO:55.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 7
 ID ABL95588 standard; cDNA; 1679 BP.
 DE Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1035; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 8
 ID ACA63892 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2002192706-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 9
 ID ACA03790 standard; cDNA; 1679 BP.
 DE cDNA encoding human PRO polypeptide #188.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 10
 ID ACA04996 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 11
 ID ACA72056 standard; cDNA; 1679 BP.
 DE Human secreted and transmembrane PRO polypeptide #37 cDNA.
 PN US200217553-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 12
 ID ABX89328 standard; cDNA; 1679 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO337.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;

RESULT 13
ID ABX92696 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 14
ID ACD41982 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #188.
FN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 15
ID ACA60526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 16
ID ACA04516 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 DNA.
FN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 17
ID ACA66437 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 18
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 19
ID ACA04211 standard; cDNA; 1679 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
FN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 20
ID ACA65657 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 21
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US200302328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 22
ID ADA76325 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 23
ID ABY44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 24
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 25
ID ADA61598 standard; cDNA; 1679 BP.
DE Homo sapiens.
FN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 26
ID AD819383 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 27
ID ADB27924 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 28
ID ADA86403 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 29
ID AD815967 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 30
ID ADA47753 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 31
ID ADA67548 standard; cDNA; 1679 BP.

PN US2003050241-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 41
 ID ADA47275 standard; cDNA; 1679 BP.
 DE Human secreted/transmembrane polypeptide PRO337 cDNA.
 PN US2003044844-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 42
 ID ADB18824 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2003073211-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 43
 ID ADA94039 standard; cDNA; 1679 BP.
 DE Human PRO polynucleotide #188.
 PN US2003077722-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 44
 ID ADB19935 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2003082691-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 45
 ID ADB13247 standard; cDNA; 1679 BP.
 DE Human PRO polynucleotide #188.
 PN US2003082710-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 46
 ID ACD98611 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2003044945-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 47
 ID ACD30038 standard; cDNA; 1679 BP.
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 PN US2003050240-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 48
 ID ADA12722 standard; cDNA; 1679 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.
 PN US2003055216-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;
 RESULT 49
 ID ADA74501 standard; cDNA; 1679 BP.
 DE Human PRO polynucleotide #188.
 PN US2003068798-A1
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1035; DB 9; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-309;

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 50
ID ADB24734 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 51
ID ADA82258 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 52
ID ADA75221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 53
ID ADA85299 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 54
ID ADA84747 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 55
ID ADB30003 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 56
ID ADA80531 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 57
ID ADA75773 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 58
ID ADA46998 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 59
ID ADB25294 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 60
ID ADA93470 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 61
ID ADB26820 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 62
ID ADB31107 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 63
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 64
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 65
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 66
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 67
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 68
ID ADA95959 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 69
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 70
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 71
ID ACD82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 72
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 73
ID ADA77532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 74
ID ADB18272 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 75
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 76
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 77
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 78
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 79
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 80
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 81
ID ADA8610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 82
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 83
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003022319-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 84
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 85
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
PN US2003044502-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 86
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.
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PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 87
  ID ADA66996 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003068793-A1.
  PD 10-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 88
  ID ADB22857 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003077711-A1.
  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 89
  ID ADB23630 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide SEQ ID NO 375.
  PN US2003077712-A1.
  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 90
  ID ADA92352 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082712-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 91
  ID ADB15415 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003087352-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 92
  ID ADB83615 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003073814-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 93
  ID ADB80721 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US200308068-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 94
  ID ADB73262 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003096968-A1.
  PD 22-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 95
  ID ADB38667 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082766-A1.

PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 96
  ID ADB78344 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003092889-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 97
  ID ADB38115 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087347-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 98
  ID ADB6587 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082689-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 9; Length 1679;
  RESULT 99
  ID ADB84992 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #63.
  PN US2003073817-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 100
  ID ADB89667 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003082698-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 101
  ID ADB90399 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003082762-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 102
  ID ADB39500 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082764-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 103
  ID ADB78098 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003092886-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 104
  ID ADB74028 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide sequence #133.
  PN US2003045462-A1.
  PD 06-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 105
ID ADB87164 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 106
ID ADB84746 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 107
ID ADB47123 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 108
ID ADB83861 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 109
ID ADB86730 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 110
ID ADB73016 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 111
ID ADB76744 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 112
ID ADB77335 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 113
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 114
ID ADB35596 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 115
ID ADB33940 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 116
ID ADB35044 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 117
ID ADB36148 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 118
ID ADB46543 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 119
ID ADC44170 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 120
ID ADC61930 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 121
ID ADC63894 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 122
ID ADC66994 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;

Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 123
ID ADC69118 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 124
ID ADC63178 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 125
ID ADC68243 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 126
ID ADC41563 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 127
ID ADC67618 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 128
ID ADC62554 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 129
ID ADC36854 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US200308065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 130
ID ADC42187 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 131
ID ADC21844 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 132
ID ADC50416 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 133
ID ADC71963 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 134
ID ADC59942 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 135
ID ADC49875 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 136
ID ADC49074 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 137
ID ADC49591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 138
ID ADC47452 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 139
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID3375.
FN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 140
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID3375.
FN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 141

ID ADC50494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 142
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 143
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 144
ID ADC34594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 145
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 146
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 147
ID ADC55956 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 148
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 149
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 150
ID ADD03200 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 151
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 152
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 153
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 154
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 155
ID ADC78072 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 156
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 157
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 158
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 159
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 160
ID ADL10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 161
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 162
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 163
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 164
ID ADL11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 165
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 166
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 167
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 168
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 169
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 170
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 171
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 172
ID ADD37097 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 173
ID ADD51777 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 174
ID ADD02576 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 175
ID ADD50516 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 176
ID ADD02010 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
RESULT 177
ID ADD54492 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 178
ID ADE50270 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 179
ID ADE51281 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 180
ID ADE49556 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 181
ID ADE92509 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 182
ID ADE91405 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 183
ID ADE04019 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 184
ID ADE32316 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 185
ID ADE22248 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 186
ID ADE79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 187
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 188
ID ADE16724 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 189
ID ADE73339 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 190
ID ADE42008 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 191
ID ADE17825 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 192
ID ADE91957 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 193
ID ADE33420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 194
ID ADE33972 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 195
ID ADE80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 196
ID ADE80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 196
ID ADP93061 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 197
ID ADP72697 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 198
ID ADE19481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 199
ID ADE18929 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 200
ID ADE43125 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 201
ID ADP95914 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 202
ID ADE22800 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 203
ID ADP78918 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 204
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 205
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 206
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 207
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 208
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 209
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 210
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 211
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 212
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 213
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 214

ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 215
ID ADF97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 216
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 217
ID ADG53119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 218
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 219
ID ADG50013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 220
ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 221
ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 222
ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 223
ID ADI61199 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 224
ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 225
ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 226
ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 227
ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 228
ID ADH81386 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 229
ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 230
ID ACA66903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 231
ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 232
ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

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PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 233
  ID AC068655 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003045687-A1.
  PD 06-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 234
  ID AC067181 standard; cDNA; 1679 BP.
  DE cDNA encoding human PRO polypeptide #188.
  PN US2003004311-A1.
  PD 02-JAN-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
  RESULT 235
  ID ADM82555 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087355-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 11; Length 1679;
  RESULT 236
  ID ADN15954 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087353-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 11; Length 1679;
  RESULT 237
  ID ADN16593 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087385-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 11; Length 1679;
  RESULT 238
  ID ADN15402 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087356-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 11; Length 1679;
  RESULT 239
  ID ADN14850 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087357-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 11; Length 1679;
  RESULT 240
  ID ADC48828 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003092888-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 241
  ID ADC81112 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003092115-A1.
  PD 22-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 242
  ID ADE20999 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003100735-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 243
  ID ADE05843 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #63.
  PN US2003100728-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 244
  ID ADD76560 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003100087-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 245
  ID ADD75072 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #63.
  PN US2003100712-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 246
  ID ADD75818 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003100717-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 247
  ID ADD85050 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003100722-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 248
  ID ADD86876 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003100738-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 249
  ID ADE20753 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003100734-A1.
  PD 29-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
  RESULT 250
  ID ADE39050 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003096362-A1.
  PD 22-MAY-2003.
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[illegible]

Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 269
ID ADE24547 standard; cDNA; 1679 BP.
DE Human PRO polypeptide #188.
FN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 270
ID ADD87372 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 271
ID ADE05105 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 272
ID ADD75318 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 273
ID ADD76862 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 274
ID ADD86630 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 275
ID ADE89238 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 276
ID ADE41198 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
FN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 277
ID ADD78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 278
ID ADE18377 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 279
ID ADE88686 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 280
ID ADE89957 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 281
ID ADD77606 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 282
ID ADD77852 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 283
ID ADE85310 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;

Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 284
ID ADD73842 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 285
ID ADD74580 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 286
ID ADD77108 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 287
ID ADD85802 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 288
ID ADE05351 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 289
ID ADD74826 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 290
ID ADF61597 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 291
ID ADF40289 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 292
ID ADF46085 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 293
ID ADE94706 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 294
ID ADE91117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 295
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 296
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 297
ID ADF24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 298
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 299
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 300
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 301
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 303

ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 303
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 304
ID ADF22264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 305
ID ADF90565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 306
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 307
ID ADF33216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 308
ID ADF25582 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 309
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 310
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 311
ID ADF46709 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 312
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 313
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 314
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 315
ID ADG02291 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 316
ID ADG2077 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 317
ID ADG20147 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 318
ID ADF98053 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 319
ID ADG24270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 320
ID ADF98624 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

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PN US2003208055-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 321
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 322
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 323
ID ADG16761 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 324
ID ADG05220 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 325
ID ADG19487 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 326
ID ADG11255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 327
ID ADG13324 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 328
ID ADG08381 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 329
ID ADG15551 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003219885-A1.

PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 330
ID ADG12034 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 331
ID ADF96949 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 332
ID ADG06134 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 333
ID ADG23718 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 334
ID ADG04007 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 335
ID ADG24908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 336
ID ADF94591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 337
ID ADG07205 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 338
ID ADG07757 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 339
ID ADG060687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096966-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 340
ID ADG55252 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 341
ID ADG60916 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 342
ID ADG62020 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 343
ID ADG82221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 344
ID ADG57460 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 345
ID ADG56908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 346
ID ADG55804 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 347
ID ADG58564 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 348
ID ADG70930 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 349
ID ADH39031 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 350
ID ADG58012 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 351
ID ADG53596 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 352
ID ADG71482 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 353
ID ADG50695 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 354
ID ADG81669 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 355
ID ADH30631 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 356
ID ADG63633 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
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RESULT 357
ID ADH11998 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 358
ID ADG50071 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 359
ID ADG51943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 360
ID ADG52420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 361
ID ADG54148 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 362
ID ADG49447 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 363
ID ADG81117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 364
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 365
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 366
ID ADH11998 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein, PRO337.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 367
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 368
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003202331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 369
ID ADG54700 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 370
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 371
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 372
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 373
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 374
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 375
ID ADG62719 standard; cDNA; 1679 BP.
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DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 376
ID AD181164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 377
ID AD133591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 378
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 379
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 380
ID ADG09907 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 381
ID AD115378 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 382
ID ADG09255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 383
ID AD114710 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 384
ID AD129846 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 385
ID AD118305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 386
ID ADM27243 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 387
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 388
ID ADJ77481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 389
ID ADX82833 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 390
ID ADK66601 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 391
ID ADJ65603 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 392
ID ADM27739 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1035; DB 12; Length 1679;
RESULT 393
ID ADM17521 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004048332-A1.

PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 394
ID ADL07355 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 395
ID ADM24463 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 396
ID ADM28325 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004077054-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 397
ID ADI95807 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 398
ID ADI96359 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1035; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 399
ID AA247893 standard; cDNA; 1693 BP.
DE Human protein encoding cDNA SEQ ID NO:3.
PN WO9558668-A1.
PD 18-NOV-1999.
PA (ONOY) ONO PHARM CO LTD.
Query Match 100.0%; Score 1035; DB 3; Length 1693;
Best Local Similarity 100.0%; Pred. No. 1.4e-309;
RESULT 400
ID AA88790 standard; cDNA; 1603 BP.
DE Human SECX cDNA Clone 11753149.0.6.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 1033.4; DB 3; Length 1603;
Best Local Similarity 99.9%; Pred. No. 4.4e-309;
RESULT 401
ID ADD18288 standard; DNA; 1603 BP.
DE Human molecule (MOL) protein MOL10 DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 1033.4; DB 10; Length 1603;
Best Local Similarity 99.9%; Pred. No. 4.4e-309;
RESULT 402
ID AA88791 standard; cDNA; 2012 BP.
DE Human SECX cDNA Clone 11753149.0.37.
PN WO200061754-A2.
PD 19-OCT-2000.

PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 1033.4; DB 3; Length 1612;
Best Local Similarity 99.9%; Pred. No. 5e-309;
RESULT 403
ID ADD18290 standard; DNA; 2012 BP.
DE Human molecule (MOL) protein MOL11 DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 1033.4; DB 10; Length 1612;
Best Local Similarity 99.9%; Pred. No. 5e-309;
RESULT 404
ID AA247892 standard; cDNA; 1032 BP.
DE Human protein encoding cDNA SEQ ID NO:2.
PN WO9558668-A1.
PD 18-NOV-1999.
PA (ONOY) ONO PHARM CO LTD.
Query Match 99.7%; Score 1032; DB 3; Length 1032;
Best Local Similarity 100.0%; Pred. No. 9.3e-309;
RESULT 405
ID AAI59655 standard; cDNA; 1690 BP.
DE Human polynucleotide SEQ ID NO 3644.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.7%; Score 1001; DB 4; Length 1690;
Best Local Similarity 99.7%; Pred. No. 5e-299;
RESULT 406
ID ADI21360 standard; cDNA; 1690 BP.
DE Novel human expressed sequence tag, EST #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 96.7%; Score 1001; DB 10; Length 1690;
Best Local Similarity 99.7%; Pred. No. 5e-299;
RESULT 407
ID ABT17393 standard; DNA; 1061 BP.
DE Human IG gene related nucleic acid SEQ ID NO 19.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 92.3%; Score 955; DB 8; Length 1061;
Best Local Similarity 100.0%; Pred. No. 7e-285;
RESULT 408
ID AAI57869 standard; cDNA; 1678 BP.
DE Human polynucleotide SEQ ID NO 72.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 92.3%; Score 955; DB 4; Length 1678;
Best Local Similarity 100.0%; Pred. No. 9e-285;
RESULT 409
ID ADI21817 standard; cDNA; 2884 BP.
DE Novel human protein cDNA #76.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 92.3%; Score 955; DB 10; Length 2884;
Best Local Similarity 100.0%; Pred. No. 1.2e-284;
RESULT 410
ID ABT17390 standard; DNA; 1839 BP.
DE Human IG gene related nucleic acid SEQ ID NO 16.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 92.1%; Score 953.4; DB 8; Length 1839;
Best Local Similarity 99.9%; Pred. No. 3e-284;
RESULT 411
ID ABX76448 standard; DNA; 1839 BP.
DE Lung cancer-associated polynucleotide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 92.1%; Score 953.4; DB 8; Length 1839;
Best Local Similarity 99.9%; Pred. No. 3e-284;
RESULT 412
ID ADG63208 standard; DNA; 1839 BP.
DE Human neurotrophin DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 92.1%; Score 953.4; DB 10; Length 1839;
Best Local Similarity 99.9%; Pred. No. 3e-284;
RESULT 413
ID ADN39137 standard; cDNA; 1839 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EXEL-) EOS BIOTECHNOLOGY INC.
Query Match 92.1%; Score 953.4; DB 11; Length 1839;
Best Local Similarity 99.9%; Pred. No. 3e-284;
RESULT 414
ID ADQ22984 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 92.1%; Score 953.4; DB 12; Length 3987;
Best Local Similarity 99.9%; Pred. No. 4.6e-284;
RESULT 415
ID ADQ24601 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 92.1%; Score 953.4; DB 12; Length 3987;
Best Local Similarity 99.9%; Pred. No. 4.6e-284;
RESULT 416
ID ABK49272 standard; cDNA; 1873 BP.
DE Human Kruppel associated DNA binding protein 42 cDNA.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 91.1%; Score 943; DB 6; Length 1873;
Best Local Similarity 99.9%; Pred. No. 5e-281;
RESULT 417
ID AA247894 standard; cDNA; 939 BP.
DE Human protein encoding cDNA SEQ ID NO:5.
PN WO9958668-A1.
PD 18-NOV-1999.
PA (ONQY) ONO PHARM CO LTD.
Query Match 90.7%; Score 939; DB 3; Length 939;
Best Local Similarity 100.0%; Pred. No. 6e-280;
RESULT 418
ID ABT17391 standard; DNA; 1094 BP.
DE Human IG gene related nucleic acid SEQ ID No 17.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 88.1%; Score 912; DB 8; Length 1094;
Best Local Similarity 96.7%; Pred. No. 1.5e-271;
RESULT 419
ID ADG63210 standard; DNA; 1068 BP.
DE Human neurotrophin DNA +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 88.0%; Score 910.4; DB 10; Length 1068;
Best Local Similarity 96.6%; Pred. No. 4.7e-271;
RESULT 420
ID ADJ35771 standard; DNA; 2129 BP.
DE Human neurotrophin DNA.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.0%; Score 910.4; DB 10; Length 2129;

Best Local Similarity 96.6%; Pred. No. 6.9e-271;
RESULT 421
ID ADG63212 standard; DNA; 1104 BP.
DE Human neurotrophin DNA +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 84.5%; Score 874.4; DB 10; Length 1104;
Best Local Similarity 93.2%; Pred. No. 7e-260;
RESULT 422
ID ABT17392 standard; DNA; 1130 BP.
DE Human IG gene related nucleic acid SEQ ID No 18.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 84.3%; Score 872.8; DB 8; Length 1130;
Best Local Similarity 93.1%; Pred. No. 2.2e-259;
RESULT 423
ID ADG63214 standard; DNA; 1140 BP.
DE Human neurotrophin DNA +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 82.3%; Score 851.8; DB 10; Length 1140;
Best Local Similarity 99.8%; Pred. No. 7.2e-253;
RESULT 424
ID AAA44536 standard; cDNA; 832 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1111.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 64.8%; Score 670.8; DB 3; Length 832;
Best Local Similarity 99.7%; Pred. No. 7.8e-197;
RESULT 425
ID ADB07017 standard; DNA; 3298 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 54.1%; Score 559.8; DB 10; Length 3298;
Best Local Similarity 72.5%; Pred. No. 4.3e-162;
RESULT 426
ID AAQ51015 standard; cDNA; 3069 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match 52.1%; Score 539; DB 2; Length 3069;
Best Local Similarity 71.2%; Pred. No. 1.2e-155;
RESULT 427
ID ABT17409 standard; DNA; 1478 BP.
DE Human IG gene related nucleic acid SEQ ID No 35.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 51.9%; Score 537.2; DB 8; Length 1478;
Best Local Similarity 73.3%; Pred. No. 2.8e-155;
RESULT 428
ID ABT17406 standard; DNA; 3110 BP.
DE Human IG gene related nucleic acid SEQ ID No 32.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 51.9%; Score 537.2; DB 8; Length 3110;
Best Local Similarity 73.3%; Pred. No. 4.3e-155;
RESULT 429
ID ADG63206 standard; DNA; 3110 BP.
DE Opioid-binding protein/cell adhesion molecule-like DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

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Query Match          51.9%; Score 537.2; DB 10; Length 3110;
Best Local Similarity 73.3%; Pred. No. 4.3e-155;
RESULT 430
ID ABT17408 standard; DNA; 1071 BP.
DE Human IG gene related nucleic acid SEQ ID NO 34.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match          51.7%; Score 535.6; DB 8; Length 1071;
Best Local Similarity 73.2%; Pred. No. 7.4e-155;
RESULT 431
ID ABT17407 standard; DNA; 1080 BP.
DE Human IG gene related nucleic acid SEQ ID NO 33.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match          51.7%; Score 535.6; DB 8; Length 1080;
Best Local Similarity 73.2%; Pred. No. 7.4e-155;
RESULT 432
ID AAQ51017 standard; cDNA; 2179 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match          50.4%; Score 521.2; DB 2; Length 2179;
Best Local Similarity 72.2%; Pred. No. 3.2e-150;
RESULT 433
ID AAQ51016 standard; cDNA; 2337 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match          50.4%; Score 521.2; DB 2; Length 2337;
Best Local Similarity 72.2%; Pred. No. 3.3e-150;
RESULT 434
ID AAQ34325 standard; DNA; 503 BP.
DE Human EST DNA42301.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 435
ID AAC78591 standard; cDNA; 503 BP.
DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 436
ID ACA63893 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein DNA42301.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 437
ID ACA72057 standard; DNA; 503 BP.
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 438
ID ABX92697 standard; cDNA; 503 BP.
DE Human PRO337 EST polynucleotide sequence.
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PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 439
ID ACA66438 standard; cDNA; 503 BP.
DE Human secreted/transmembrane protein EST DNA42301.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 440
ID ADA25063 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 441
ID ACD30039 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 442
ID ADA12724 standard; cDNA; 503 BP.
DE Human secreted/transmembrane polypeptide PRO337 EST.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 443
ID ACD29454 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #134.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 444
ID ADB74030 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 445
ID ADB76746 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 446
ID ADC44172 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match          47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 447
ID ADC61932 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 448
ID ADC63896 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 449
ID ADC66996 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 450
ID ADC69120 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 451
ID ADC63180 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 452
ID ADC68245 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 453
ID ADC41565 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 454
ID ADC67620 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 455
ID ADC62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 456
ID ADC62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 457
ID ADC42189 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 457
ID ADE49558 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 458
ID ADE35612 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 459
ID ADE16726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 460
ID ADD73341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 461
ID ADD72699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 462
ID ADE17350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 463
ID ADE47364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 464
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 465
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;

Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 466
ID ADI61201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 467
ID ACD42858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 468
ID ADE48858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 469
ID ADE89959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FER/) FERARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLAJ/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 470
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 471
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 472
ID ADF46087 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 473
ID ADF24483 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 474
ID ADF40915 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 475
ID ADF23859 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 476
ID ADF33842 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 477
ID ADF27309 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 478
ID ADF27945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 479
ID ADF41539 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 480
ID ADF33218 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;

Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 481
ID ADF25584 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 482
ID ADF26685 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 483
ID ADF34474 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 484
ID ADF46711 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 485
ID ADG50697 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 486
ID ADG50073 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 487
ID ADG51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 488
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 489
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;

RESULT 490
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 491
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 492
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 493
ID ADH25746 standard; cDNA; 503 BP.
DE Human DNA2301 expressed sequence tag (EST) SEQ ID NO:524.
FN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 494
ID ADM17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 495
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 47.5%; Score 492; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
RESULT 496
ID ADM47274 standard; DNA; 617 BP.
DE Oestrogen regulated protein like NOVX 25b gene.
FN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 43.4%; Score 449.4; DB 11; Length 617;
Best Local Similarity 97.6%; Pred. No. 2.9e-128;
RESULT 497
ID ACH15238 standard; cDNA; 437 BP.
DE Human adult brain cDNA #2450.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 39.0%; Score 404; DB 9; Length 437;
Best Local Similarity 97.4%; Pred. No. 2.8e-114;
RESULT 498
ID AAC91321 standard; cDNA; 537 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
FN WO200073509-A2.
PD 07-DEC-2000.

PA (INCY-) INCYTE GENOMICS INC.
Query Match 35.0%; Score 362.2; DB 4; Length 537;
Best Local Similarity 99.2%; Pred. No. 2.9e-101;
RESULT 499
ID AAS78035 standard; cDNA; 484 BP.
DE DNA encoding novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 34.3%; Score 355.4; DB 5; Length 484;
Best Local Similarity 92.3%; Pred. No. 3.5e-99;
RESULT 500
ID ACH46276 standard; cDNA; 409 BP.
DE Human infant brain cDNA #339.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 34.2%; Score 353.8; DB 9; Length 409;
Best Local Similarity 98.1%; Pred. No. 1e-98;
RESULT 501
ID AAL50356 standard; cDNA; 1411 BP.
DE Human limbic system associated membrane protein 36-85 coding sequence.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 33.1%; Score 343; DB 6; Length 1411;
Best Local Similarity 63.6%; Pred. No. 4.4e-95;
RESULT 502
ID AAT42080 standard; cDNA to mRNA; 1238 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 33.0%; Score 342; DB 2; Length 1238;
Best Local Similarity 61.9%; Pred. No. 8.4e-95;
RESULT 503
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.9%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 1.9e-94;
RESULT 504
ID AAT42079 standard; cDNA to mRNA; 977 BP.
DE Human LAMP residues 8-332 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.9%; Score 340.6; DB 2; Length 977;
Best Local Similarity 63.3%; Pred. No. 2e-94;
RESULT 505
ID AAT42081 standard; cDNA to mRNA; 1014 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.9%; Score 340.6; DB 8; Length 1014;
Best Local Similarity 61.9%; Pred. No. 2e-94;
RESULT 506
ID ABT17402 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 28.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.9%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2e-94;
RESULT 507
ID ABT17404 standard; DNA; 1017 BP.

DE Human IG gene related nucleic acid SEQ ID No 30.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.9%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2e-94;
RESULT 508
ID ABX63560 standard; cDNA; 1195 BP.
DE Human cDNA #560 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 32.9%; Score 340.6; DB 8; Length 1195;
Best Local Similarity 63.3%; Pred. No. 2.2e-94;
RESULT 509
ID ADL12674 standard; cDNA; 1195 BP.
DE Human steroid-induced C3A liver cell cDNA #403.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 32.9%; Score 340.6; DB 12; Length 1195;
Best Local Similarity 63.3%; Pred. No. 2.2e-94;
RESULT 510
ID AAT42086 standard; cDNA to mRNA; 861 BP.
DE Human LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.7%; Score 338.6; DB 2; Length 861;
Best Local Similarity 63.7%; Pred. No. 7.8e-94;
RESULT 511
ID AAT42082 standard; cDNA to mRNA; 912 BP.
DE Human mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.7%; Score 338.6; DB 2; Length 912;
Best Local Similarity 63.7%; Pred. No. 8e-94;
RESULT 512
ID AAT42085 standard; cDNA to mRNA; 945 BP.
DE Rat LAMP residues 1-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.6%; Score 337.4; DB 2; Length 945;
Best Local Similarity 63.1%; Pred. No. 1.9e-93;
RESULT 513
ID ABZ76264 standard; cDNA; 1757 BP.
DE Human GENSET cDNA clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 32.6%; Score 337.4; DB 8; Length 1757;
Best Local Similarity 63.8%; Pred. No. 2.7e-93;
RESULT 514
ID AAT42083 standard; cDNA to mRNA; 930 BP.
DE Rat mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.6%; Score 337; DB 2; Length 930;
Best Local Similarity 62.1%; Pred. No. 2.5e-93;
RESULT 515
ID ABT17403 standard; DNA; 1075 BP.
DE Human IG gene related nucleic acid SEQ ID No 29.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 32.4%; Score 335; DB 8; Length 1075;
Best Local Similarity 63.5%; Pred. No. 1.1e-92;
RESULT 516
ID AAT42087 standard; cDNA to mRNA; 861 BP.
DE Rat LAMP residues 29-315 coding sequence.

PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.3%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 2.4e-92;
RESULT 517
ID AAT42116 standard; cDNA to mRNA; 1307 BP.
DE Rat LAMP clone 6c coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 32.1%; Score 331.8; DB 2; Length 1307;
Best Local Similarity 63.3%; Pred. No. 1.3e-91;
RESULT 518
ID AAF93346 standard; cDNA; 452 BP.
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 330; DB 5; Length 452;
Best Local Similarity 100.0%; Pred. No. 2.5e-91;
RESULT 519
ID AAH34425 standard; cDNA; 1153 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 31.4%; Score 325.2; DB 4; Length 1153;
Best Local Similarity 62.7%; Pred. No. 1.3e-89;
RESULT 520
ID AAC19214 standard; cDNA; 333 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23289.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSE-) GENSET.
Query Match 30.6%; Score 316.2; DB 3; Length 333;
Best Local Similarity 97.0%; Pred. No. 4e-87;
RESULT 521
ID ABRI7405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID No 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 30.3%; Score 313.8; DB 8; Length 898;
Best Local Similarity 63.2%; Pred. No. 3.9e-86;
RESULT 522
ID AAT42094 standard; cDNA to mRNA; 756 BP.
DE Human LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 29.3%; Score 303.6; DB 2; Length 756;
Best Local Similarity 63.5%; Pred. No. 5.1e-83;
RESULT 523
ID AAT42095 standard; cDNA to mRNA; 756 BP.
DE Rat LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 28.8%; Score 298.2; DB 2; Length 756;
Best Local Similarity 63.0%; Pred. No. 2.4e-81;
RESULT 524
ID AAS78034 standard; cDNA; 443 BP.
DE DNA encoding novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 28.5%; Score 295.4; DB 5; Length 443;
Best Local Similarity 89.8%; Pred. No. 1.3e-80;
RESULT 525
ID ABRI7401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID No 27.
PN WO200299040-A2.

PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 27.0%; Score 279; DB 8; Length 1809;
Best Local Similarity 57.8%; Pred. No. 3.5e-75;
RESULT 526
ID ADS82049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) LG LIFE SCI LTD.
Query Match 26.5%; Score 274.2; DB 13; Length 4891;
Best Local Similarity 58.6%; Pred. No. 1.9e-73;
RESULT 527
ID ABQ82338 standard; cDNA; 1165 BP.
DE Human NOVI2b encoding cDNA SEQ ID NO:25.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.3%; Score 272.6; DB 6; Length 1165;
Best Local Similarity 58.4%; Pred. No. 2.7e-73;
RESULT 528
ID ADI28059 standard; cDNA; 1327 BP.
DE ECMCAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 26.3%; Score 272.6; DB 6; Length 1327;
Best Local Similarity 58.4%; Pred. No. 2.9e-73;
RESULT 529
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 4; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 530
ID ABK33536 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 6; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 531
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 532
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 533
ID ACA04534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 534
ID ACA68497 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 535
ID ACAC5675 standard; cDNA; 4834 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO6004.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 536
ID ABT44226 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 537
ID ADA47301 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 538
ID ABT44509 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 539
ID ACDB2176 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO 6004 cDNA.
PN US2003049344-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 540
ID ACD30291 standard; cDNA; 4834 BP.
DE Human cDNA encoding Pro6004.
PN US2003049302-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 541
ID ABT43882 standard; cDNA; 4834 BP.
DE Human membrane bound receptor/protein PRO6004 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 542
ID ADB83491 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 543
ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 544
ID ADB73138 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 545
ID ADB78220 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 9; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 546
ID ADB84868 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 547
ID ADB77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 548
ID ADB87040 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 549
ID ADB84622 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 550
ID ADB83737 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 551
ID ADB72892 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 552
ID ADC36730 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 553
ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 553
ID ADC21720 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 554
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200308064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 555
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200308070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 556
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200308071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 557
ID ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200308072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 558
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 559
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 560
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 561
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200308066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 562
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 563
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 564
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 565
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 566
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 567
ID ADG63810 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 568
ID ACA66841 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO polypeptide #1.
FN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 569
ID ACD42405 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 570
ID ACD68593 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 571

ID ADC48704 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 572
ID ADE20875 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 573
ID ADE05719 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 574
ID ADD74948 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 575
ID ADD75694 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 576
ID ADD84926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 577
ID ADD86752 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 578
ID ADE20629 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 579
ID ADE38926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 580
ID ADE05473 standard; cDNA; 4834 BP.

DE Human PRO polynucleotide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 581
ID ADD73458 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 582
ID ADD78298 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 583
ID ADE21121 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 584
ID ADD77236 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 585
ID ADE20383 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 586
ID ADD75448 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 587
ID ADD73964 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 588
ID ADD74210 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 589
ID ADD75940 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

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PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 590
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 600
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 601
ID ADD74456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 602
ID ADD76984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 603
ID ADD85678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 604
ID ADE05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 605
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 606
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 607
ID ADG27068 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 591
ID ADS04981 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 592
ID ADD75194 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 593
ID AD76738 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 594
ID ADD86506 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 595
ID ADE41224 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 596
ID ADD77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 597
ID ADD77482 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 598
ID ADD77728 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100730-A1.
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PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 608
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 609
ID ADG11910 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 610
ID ADP94467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 611
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 612
ID ADH38907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 613
ID ADG3658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 614
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 615
ID ADI33467 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 616
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 617
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 618
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 619
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5.8e-73;
RESULT 620
ID ABQ82337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.3%; Score 272.2; DB 6; Length 1196;
Best Local Similarity 58.3%; Pred. No. 3.6e-73;
RESULT 621
ID ABN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.2%; Score 271; DB 6; Length 1119;
Best Local Similarity 58.3%; Pred. No. 8.1e-73;
RESULT 622
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBBF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 26.2%; Score 271; DB 10; Length 2383;
Best Local Similarity 58.3%; Pred. No. 1.2e-72;
RESULT 623
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 3; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 624
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 625
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.

Query Match 26.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 626
ID ABX92783 standard; cDNA; 2840 BP.
DE cDNA encoding human PRO4993 polypeptide.
FN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 627
ID ACA66524 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO4993.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 628
ID ADA25149 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
FN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 629
ID ADC30125 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
FN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 630
ID ADA12811 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO4993.
FN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 631
ID ADC29540 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #139.
FN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 9; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 632
ID ADB74117 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
FN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 633
ID ADB76833 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
FN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 634
ID ADC44259 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;

RESULT 635
ID ADC62019 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 636
ID ADC63983 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 637
ID ADC67083 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 638
ID ADC69207 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 639
ID ADC63267 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 640
ID ADC68332 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 641
ID ADC41652 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 642
ID ADC67707 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 643
ID ADC62643 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 644

ID ADC42276 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 645
ID ADE49645 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 646
ID ADE35699 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 647
ID ADE16813 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 648
ID ADD73428 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 649
ID ADD72786 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 650
ID ADE17437 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 651
ID ADF47451 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 652
ID ADG53208 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 653
ID ADG60528 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 654
ID ADI61288 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 655
ID ADC42944 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 656
ID ADE48945 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 657
ID ADE90046 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PRON/) PRONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 658
ID ADF61686 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 659

ID ADF40378 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 660
ID ADF46174 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 661
ID ADF24570 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 662
ID ADF41002 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 663
ID ADF23946 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 664
ID ADF33929 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 665
ID ADF27396 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 666
ID ADF28032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 667
ID ADF41626 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 668
ID ADF33305 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 669
ID ADF25671 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 670
ID ADF26772 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 671
ID ADF34561 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 672
ID ADF46798 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 673
ID ADG50784 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 674
ID ADG50160 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 675
ID ADG52032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 676
ID ADG49536 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 677
ID ADG48912 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.


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PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 678
ID ADG51408 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 679
ID ADG59352 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 680
ID ADG62808 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 681
ID ADL07610 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 682
ID ADL07444 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 4.3e-72;
RESULT 683
ID ADP28685 standard; DNA; 834 BP.
DE Human secreted protein encoding sequence SEQ ID #683.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 25.2%; Score 260.4; DB 12; Length 834;
Best Local Similarity 59.5%; Pred. No. 1.3e-69;
RESULT 684
ID ADH71401 standard; DNA; 926 BP.
DE Human gene of the invention NOV11i SEQ ID NO:297.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 926;
Best Local Similarity 59.5%; Pred. No. 1.4e-69;
RESULT 685
ID ADH71405 standard; DNA; 927 BP.
DE Human gene of the invention NOV11k SEQ ID NO:301.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 927;
Best Local Similarity 59.5%; Pred. No. 1.4e-69;
RESULT 686
ID ADH71409 standard; DNA; 946 BP.
DE Human gene of the invention NOV11m SEQ ID NO:305.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 946;
Best Local Similarity 59.5%; Pred. No. 1.4e-69;
RESULT 687
ID ADH71393 standard; DNA; 946 BP.
DE Human gene of the invention NOV11f SEQ ID NO:289.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 946;
Best Local Similarity 59.5%; Pred. No. 1.4e-69;
RESULT 688
ID ADH71395 standard; DNA; 976 BP.
DE Human gene of the invention NOV11f SEQ ID NO:291.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 689
ID ADH71415 standard; DNA; 976 BP.
DE Human gene of the invention NOV11p SEQ ID NO:311.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 690
ID ADH71389 standard; DNA; 976 BP.
DE Human gene of the invention NOV11c SEQ ID NO:285.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 691
ID ADH71397 standard; DNA; 976 BP.
DE Human gene of the invention NOV11g SEQ ID NO:293.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 692
ID ABS71699 standard; DNA; 1017 BP.
DE DNA encoding human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 6; Length 1017;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 693
ID ADL35978 standard; cDNA; 1017 BP.
DE Human NOVX cDNA #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 25.2%; Score 260.4; DB 11; Length 1017;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 694
ID ADH71417 standard; DNA; 1030 BP.
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DE Human gene of the invention NOV11q SEQ ID NO:313.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 1030;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 695
ID ADH71411 standard; DNA; 1033 BP.
DE Human gene of the invention NOV11n SEQ ID NO:307.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 696
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV11b SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 697
ID ADH71413 standard; DNA; 1035 BP.
DE Human gene of the invention NOV11o SEQ ID NO:309.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.2%; Score 260.4; DB 12; Length 1035;
Best Local Similarity 59.5%; Pred. No. 1.5e-69;
RESULT 698
ID ABS76364 standard; DNA; 1427 BP.
DE DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 25.2%; Score 260.4; DB 6; Length 1427;
Best Local Similarity 59.5%; Pred. No. 1.8e-69;
RESULT 699
ID AAD47371 standard; DNA; 2653 BP.
DE Human LP289 DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 25.2%; Score 260.4; DB 8; Length 2653;
Best Local Similarity 59.5%; Pred. No. 2.5e-69;
RESULT 700
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 25.0%; Score 258.8; DB 6; Length 1018;
Best Local Similarity 59.4%; Pred. No. 4.7e-69;
RESULT 701
ID ADL35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M.
PA (SHEN) SHENOV S G.
PA (SPVT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATY) PATTURAJAN M.
PA (GUOX) GUO X.
PA (KEKU) KEKUDA R.
PA (GANG) GANGOLLI E A.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (LILU) LI L.
PA (PADI) PADIGARU M.
Query Match 25.0%; Score 258.8; DB 11; Length 1018;
Best Local Similarity 59.4%; Pred. No. 4.7e-69;

RESULT 702
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV11h SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 25.0%; Score 258.8; DB 12; Length 1018;
Best Local Similarity 59.4%; Pred. No. 4.7e-69;
RESULT 703
ID ABS71700 standard; DNA; 1136 BP.
DE DNA encoding human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 24.9%; Score 257.2; DB 6; Length 1136;
Best Local Similarity 59.3%; Pred. No. 1.6e-68;
RESULT 704
ID ADH71403 standard; DNA; 1171 BP.
DE Human gene of the invention NOV11j SEQ ID NO:299.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 24.9%; Score 257.2; DB 12; Length 1171;
Best Local Similarity 59.3%; Pred. No. 1.6e-68;
RESULT 705
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11a SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 24.9%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 1.7e-68;
RESULT 706
ID ADH71421 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11s SEQ ID NO:317.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 24.9%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 1.7e-68;
RESULT 707
ID ADH71419 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11r SEQ ID NO:315.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 24.7%; Score 255.6; DB 12; Length 1271;
Best Local Similarity 59.1%; Pred. No. 5.2e-68;
RESULT 708
ID ABK35606 standard; DNA; 1011 BP.
DE Gene encoding novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 23.8%; Score 246; DB 6; Length 1011;
Best Local Similarity 58.4%; Pred. No. 4.3e-65;
RESULT 709
ID ABS71701 standard; DNA; 1169 BP.
DE DNA encoding human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 23.8%; Score 246; DB 6; Length 1169;
Best Local Similarity 58.4%; Pred. No. 4.7e-65;
RESULT 710
ID ADH71407 standard; DNA; 1169 BP.
DE Human gene of the invention NOV11l SEQ ID NO:303.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 23.8%; Score 246; DB 12; Length 1169;

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Best Local Similarity 58.4%; Pred. No. 4.7e-65;
RESULT 711
ID ABA06475 standard; cDNA; 2813 BP.
DE Human cDNA SEQ ID NO: 141.
FN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.3%; Score 240.8; DB 4; Length 2813;
Best Local Similarity 58.3%; Pred. No. 3.1e-63;
RESULT 712
ID ABV83812 standard; cDNA; 2813 BP.
DE Human polynucleotide SEQ ID NO 141.
FN US2002090872-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 23.3%; Score 240.8; DB 6; Length 2813;
Best Local Similarity 58.3%; Pred. No. 3.1e-63;
RESULT 713
ID ADH71391 standard; DNA; 760 BP.
DE Human gene of the invention NOV11d SEQ ID NO:287.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 22.9%; Score 236.6; DB 12; Length 760;
Best Local Similarity 59.9%; Pred. No. 3e-62;
RESULT 714
ID AAD47374 standard; DNA; 2601 BP.
DE Human LP319b DNA.
FN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 22.6%; Score 234; DB 8; Length 2601;
Best Local Similarity 58.3%; Pred. No. 3.8e-61;
RESULT 715
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.
FN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 22.4%; Score 232; DB 6; Length 1056;
Best Local Similarity 58.1%; Pred. No. 9.7e-61;
RESULT 716
ID ADJ35982 standard; cDNA; 1168 BP.
DE Human NOVX cDNA #14.
FN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 22.3%; Score 231.2; DB 11; Length 1168;
Best Local Similarity 58.1%; Pred. No. 1.8e-60;
RESULT 717
ID ADJ35980 standard; cDNA; 1133 BP.
DE Human NOVX cDNA #13.
FN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 21.7%; Score 224.8; DB 11; Length 1133;
Best Local Similarity 59.3%; Pred. No. 1.7e-58;
RESULT 718
ID AAS28811 standard; cDNA; 4656 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.
FN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.3%; Score 220.6; DB 4; Length 4656;
Best Local Similarity 57.5%; Pred. No. 7.5e-57;
RESULT 719
ID ADB31536 standard; cDNA; 4656 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 57.
FN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.3%; Score 220.6; DB 10; Length 4656;
Best Local Similarity 57.5%; Pred. No. 7.5e-57;
RESULT 720
ID AAS78003 standard; cDNA; 2883 BP.
DE DNA encoding novel human diagnostic protein #13807.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.0%; Score 217.8; DB 5; Length 2883;
Best Local Similarity 71.1%; Pred. No. 4.3e-56;
RESULT 721
ID ADE08816 standard; DNA; 754 BP.
DE Novel DNA-related contig nucleotide sequence #60.
FN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 21.0%; Score 217.8; DB 10; Length 2883;
Best Local Similarity 71.1%; Pred. No. 4.3e-56;
RESULT 722
ID AAD47372 standard; DNA; 754 BP.
DE Human LP289 splice variant (LP343) DNA.
FN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 20.4%; Score 211.4; DB 8; Length 754;
Best Local Similarity 61.1%; Pred. No. 2e-54;
RESULT 723
ID ADP28686 standard; DNA; 666 BP.
DE Human secreted protein encoding sequence SEQ ID #684.
FN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 20.3%; Score 210; DB 12; Length 666;
Best Local Similarity 60.2%; Pred. No. 5e-54;
RESULT 724
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
FN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 20.2%; Score 208.6; DB 8; Length 2597;
Best Local Similarity 58.1%; Pred. No. 2.9e-53;
RESULT 725
ID AAC02777 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2775.
FN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Query Match 18.7%; Score 193.6; DB 3; Length 352;
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Best Local Similarity 82.5%; Pred. No. 4.2e-49;
RESULT 726
ID ABU99899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 17.4%; Score 180.4; DB 6; Length 5666;
Best Local Similarity 56.1%; Pred. No. 2.4e-44;
RESULT 727
ID ADG63283 standard; DNA; 540 BP.
DE Human OBCAM gene exon 2.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 17.1%; Score 176.6; DB 10; Length 540;
Best Local Similarity 74.9%; Pred. No. 1e-43;
RESULT 728
ID AD083739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 16.9%; Score 175; DB 12; Length 919;
Best Local Similarity 58.0%; Pred. No. 4.2e-43;
RESULT 729
ID AAF93597 standard; cDNA; 585 BP.
DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 15.8%; Score 163.2; DB 5; Length 585;
Best Local Similarity 62.0%; Pred. No. 1.5e-39;
RESULT 730
ID ABS52769 standard; cDNA; 408 BP.
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
PN WO200246475-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 160; DB 6; Length 408;
Best Local Similarity 63.7%; Pred. No. 1.2e-38;
RESULT 731
ID ADQ21981 standard; DNA; 125 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.7%; Score 110.8; DB 12; Length 125;
Best Local Similarity 97.6%; Pred. No. 1.1e-23;
RESULT 732
ID AAS78037 standard; cDNA; 767 BP.
DE DNA encoding novel human diagnostic protein #13841.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 106.8; DB 5; Length 767;
Best Local Similarity 94.1%; Pred. No. 5.3e-22;
RESULT 733
ID ABX71182 standard; cDNA; 913 BP.
DE Novel human cDNA sequence #407.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 10.2%; Score 105.6; DB 8; Length 913;
Best Local Similarity 61.1%; Pred. No. 1.4e-21;
RESULT 734
ID ADQ54463 standard; DNA; 351 BP.
DE Novel canine microarray-related DNA sequence SeqID5765.
PN WO2004063324-A2.
PD 29-JUL-2004.

PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 10.1%; Score 104.6; DB 13; Length 351;
Best Local Similarity 60.8%; Pred. No. 1.7e-21;
RESULT 735
ID AAS78038 standard; cDNA; 693 BP.
DE DNA encoding novel human diagnostic protein #13842.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 102; DB 5; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
RESULT 736
ID AAS78592 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #14396.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 102; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
RESULT 737
ID AAS71904 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #7708.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 102; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
RESULT 738
ID AAS78036 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #13840.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 102; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
RESULT 739
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 9.7%; Score 100; DB 2; Length 219;
Best Local Similarity 67.0%; Pred. No. 3.4e-20;
RESULT 740
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 9.2%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 1e-18;
RESULT 741
ID AAS67246 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 7.4e-18;
RESULT 742
ID AAS71723 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 7.4e-18;
RESULT 743
ID AAS64445 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 8.1e-18;
RESULT 744
ID AAS64798 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #602.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 8.1e-18;
RESULT 745
ID ADM18382 standard; DNA; 2026 BP.
DE Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.
FN WO20040429283-A2.
PD 08-APR-2004.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 8.6%; Score 89; DB 12; Length 2026;
Best Local Similarity 100.0%; Pred. No. 3e-16;
RESULT 746
ID ADG63285 standard; DNA; 420 BP.
DE Human OBCAM gene exon 4.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 7.6%; Score 78.6; DB 10; Length 420;
Best Local Similarity 70.5%; Pred. No. 2.1e-13;
RESULT 747
ID AAT42050 standard; cDNA to mRNA; 177 BP.
DE Human LAMP residues 156-204 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 7.5%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 2.3e-13;
RESULT 748
ID AAT42091 standard; cDNA to mRNA; 177 BP.
DE Rat LAMP residues 156-204 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 7.5%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 2.3e-13;
RESULT 749
ID ADG63287 standard; DNA; 480 BP.
DE Human OBCAM gene exon 6.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 7.4%; Score 76.8; DB 10; Length 480;
Best Local Similarity 70.8%; Pred. No. 8.2e-13;
RESULT 750
ID AAS28866 standard; cDNA; 293 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 112.
FN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 9.4e-12;
RESULT 751
ID ABA06681 standard; cDNA; 293 BP.
DE Human cDNA SEQ ID NO: 347.
FN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 9.4e-12;
RESULT 752
ID ABV84018 standard; cDNA; 293 BP.
DE Human polynucleotide SEQ ID NO 347.
FN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 7.1%; Score 73; DB 6; Length 293;
Best Local Similarity 62.9%; Pred. No. 9.4e-12;
RESULT 753
ID ADR31591 standard; cDNA; 293 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 112.
FN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 73; DB 10; Length 293;
Best Local Similarity 62.9%; Pred. No. 9.4e-12;
RESULT 754
ID ADG63286 standard; DNA; 480 BP.
DE Human OBCAM gene exon 5.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 71.4; DB 10; Length 480;
Best Local Similarity 74.4%; Pred. No. 3.9e-11;
RESULT 755
ID AAT42092 standard; cDNA to mRNA; 198 BP.
DE Human LAMP residues 232-297 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 6.2%; Score 64.6; DB 2; Length 198;
Best Local Similarity 61.3%; Pred. No. 3e-09;
RESULT 756
ID AAT42093 standard; cDNA to mRNA; 198 BP.
DE Rat LAMP residues 232-297 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 6.1%; Score 63.4; DB 2; Length 198;
Best Local Similarity 60.7%; Pred. No. 7.1e-09;
RESULT 757
ID ADG63282 standard; DNA; 270 BP.
DE Human OBCAM gene exon 1.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.0%; Score 61.6; DB 10; Length 270;
Best Local Similarity 88.6%; Pred. No. 3.1e-08;
RESULT 758
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene SEQ ID 5263.
FN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 58.6; DB 8; Length 2000;
Best Local Similarity 9.5%; Pred. No. 7.9e-07;
RESULT 759
ID ADG63284 standard; DNA; 420 BP.
DE Human OBCAM gene exon 3.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 5.6%; Score 57.6; DB 10; Length 420;
Best Local Similarity 65.6%; Pred. No. 6.8e-07;
RESULT 760
ID ACH15235 standard; cDNA; 514 BP.
DE Human adult brain cDNA #2447.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 5.3%; Score 54.4; DB 9; Length 514;
Best Local Similarity 62.3%; Pred. No. 7.5e-06;
RESULT 761

ID ABL11515 standard; cDNA; 2010 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 52.2; DB 4; Length 2010;
Best Local Similarity 45.6%; Pred. No. 7.6e-05;
RESULT 762
ID ABX56303 standard; DNA; 8243 BP.
DE Human NOV25b CG93858-02 DNA SEQ ID 85.
FN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 50; DB 8; Length 8243;
Best Local Similarity 49.7%; Pred. No. 0.0008;
RESULT 763
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
FN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) STINGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 49.8; DB 8; Length 2000;
Best Local Similarity 7.7%; Pred. No. 0.00042;
RESULT 764
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 12; Length 2136;
Best Local Similarity 49.4%; Pred. No. 0.0012;
RESULT 765
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
FN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 8; Length 2153;
Best Local Similarity 49.4%; Pred. No. 0.0012;
RESULT 766
ID ADH72101 standard; DNA; 2153 BP.
DE Human gene of the invention NOV43a SEQ ID NO:997.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 12; Length 2153;
Best Local Similarity 49.4%; Pred. No. 0.0012;
RESULT 767
ID ADO08270 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
FN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERRHUSEN B D.
Query Match 4.7%; Score 48.4; DB 12; Length 2153;
Best Local Similarity 49.4%; Pred. No. 0.0012;
RESULT 768
ID AAS68120 standard; cDNA; 3910 BP.
DE DNA encoding novel human diagnostic protein #3924.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 48.4; DB 5; Length 3910;
Best Local Similarity 49.4%; Pred. No. 0.0017;
RESULT 769
ID AAI72024 standard; cDNA; 4073 BP.
DE Human thrombospondin protein, BTL 012, coding sequence.
FN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Query Match 4.7%; Score 48.4; DB 6; Length 4073;
Best Local Similarity 49.4%; Pred. No. 0.0017;
RESULT 770
ID ADJ93996 standard; cDNA; 5877 BP.
DE Human G-coupled protein receptor-related gene #44.
FN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 4.7%; Score 48.4; DB 12; Length 5877;
Best Local Similarity 49.4%; Pred. No. 0.0021;
RESULT 771
ID ADE16057 standard; DNA; 5935 BP.
DE G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.
FN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 10; Length 5935;
Best Local Similarity 49.4%; Pred. No. 0.0021;
RESULT 772
ID ABX56304 standard; DNA; 6343 BP.
DE Human NOV25c CG56914-03 DNA SEQ ID 87.
FN WO200281625-A2.
PD 17-OCT-2002.

PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 8; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.0022;
RESULT 773
ID ADH72107 standard; DNA; 6343 BP.
DE Human gene of the invention NOV43d SEQ ID NO:1003.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 12; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.0022;
RESULT 774
ID ADK60477 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
FN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 4.7%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.0026;
RESULT 775
ID ADK60778 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
FN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 4.7%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.0026;
RESULT 776
ID ADP73100 standard; DNA; 8546 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N52.
FN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 4.7%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.0026;
RESULT 777
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
FN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 4.7%; Score 48.4; DB 13; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.0026;
RESULT 778
ID AD008272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
FN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.

PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 4.7%; Score 48.4; DB 12; Length 15659;
Best Local Similarity 49.4%; Pred. No. 0.0036;
RESULT 779
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
FN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 8; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.0036;
RESULT 780
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 48.4; DB 12; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.0036;
RESULT 781
ID ABQ86156 standard; DNA; 16908 BP.
DE Novel human gene. SEQ ID 27.
FN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.7%; Score 48.4; DB 6; Length 16908;
Best Local Similarity 49.4%; Pred. No. 0.0037;
RESULT 782
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
FN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 4.7%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.0039;
RESULT 783
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
FN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 4.7%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.0039;
RESULT 784
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
FN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 4.7%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.0039;
RESULT 785
ID ADQ22570 standard; DNA; 18248 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 48.4; DB 12; Length 18248;
Best Local Similarity 49.4%; Pred. No. 0.0039;
RESULT 786
ID ACH14951 standard; cDNA; 467 BP.
DE Human adult brain cDNA #2163.

PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 42.8; DB 9; Length 467;
Best Local Similarity 50.5%; Pred. No. 0.028;
RESULT 787
ID ABD33040 standard; cDNA; 3588 BP.
DE Human cancer-associated cDNA HR22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.1%; Score 42.4; DB 13; Length 3588;
Best Local Similarity 47.4%; Pred. No. 0.11;
RESULT 788
ID AA164283 standard; DNA; 4548 BP.
DE Human transient axonal glycoprotein (tag-1) DNA.
PN WO200188546-A2.
PD 22-NOV-2001.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.1%; Score 42.4; DB 6; Length 4548;
Best Local Similarity 47.4%; Pred. No. 0.13;
RESULT 789
ID ABD33041 standard; cDNA; 6137 BP.
DE Human cancer-associated cDNA HR22-025.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.1%; Score 42.4; DB 13; Length 6137;
Best Local Similarity 47.4%; Pred. No. 0.15;
RESULT 790
ID ADQ23368 standard; DNA; 7625 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 42.4; DB 12; Length 7625;
Best Local Similarity 47.4%; Pred. No. 0.17;
RESULT 791
ID ADQ24513 standard; DNA; 7625 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 42.4; DB 12; Length 7625;
Best Local Similarity 47.4%; Pred. No. 0.17;
RESULT 792
ID ADQ28580 standard; cDNA; 7650 BP.
DE Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 42.4; DB 12; Length 7650;
Best Local Similarity 47.4%; Pred. No. 0.17;
RESULT 793
ID AAV31988 standard; cDNA; 6413 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 4.0%; Score 41.6; DB 2; Length 6413;
Best Local Similarity 45.8%; Pred. No. 0.28;
RESULT 794
ID AAV31981 standard; cDNA; 6604 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 4.0%; Score 41.6; DB 2; Length 6604;
Best Local Similarity 45.8%; Pred. No. 0.28;
RESULT 795
ID ADK71086 standard; DNA; 6649 BP.
DE Human MP21 polypeptide encoding DNA.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.0%; Score 41.6; DB 12; Length 6649;
Best Local Similarity 45.8%; Pred. No. 0.29;
RESULT 796
ID AAL57278 standard; DNA; 1267 BP.
DE DKFZp761A179 'human modifier of p53 pathway' DNA.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 4.0%; Score 41.2; DB 8; Length 1267;
Best Local Similarity 54.7%; Pred. No. 0.15;
RESULT 797
ID ABX34766 standard; cDNA; 1869 BP.
DE Human cDNA for novel secreted protein, SEQ ID 535.
PN WO200177290-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 4.0%; Score 41.2; DB 6; Length 1869;
Best Local Similarity 54.7%; Pred. No. 0.19;
RESULT 798
ID ABX03572 standard; DNA; 2083 BP.
DE Human nervous system leucine rich repeat protein (HLRRNS1) EST.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.0%; Score 41.2; DB 6; Length 2083;
Best Local Similarity 54.7%; Pred. No. 0.2;
RESULT 799
ID AAS62318 standard; cDNA; 2090 BP.
DE cDNA sequence #105 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 4.0%; Score 41.2; DB 6; Length 2090;
Best Local Similarity 54.7%; Pred. No. 0.2;
RESULT 800
ID ABX70472 standard; DNA; 2316 BP.
DE DNA encoding human GPCR related protein NOV31a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 41.2; DB 8; Length 2316;
Best Local Similarity 54.7%; Pred. No. 0.21;
RESULT 801
ID ADL24096 standard; cDNA; 2316 BP.
DE Human NOVX cDNA #71.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.

PA (SMIT//) SMITHSON G.
PA (ZERRH//) ZERRHUSEN B D.
PA (GERL//) GERLACH V.
PA (POCH//) POCHART P F.
PA (FERN//) FERNANDES E R.
PA (SHIM//) SHIMKETS R A.
PA (RAST//) RASTELLI L.
PA (SPAD//) SPADERNA S K.
PA (LARO//) LAROCHELLE W J.
PA (ZHON//) ZHONG M.
PA (KHRA//) KHRAMTSOV N V.
PA (VOSS//) VOSS B Z.
PA (HERR//) HERRMANN J L.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 12; Length 2316;
Pred. No. 0.21;
RESULT 802
ID ABK62093 standard; cDNA; 2397 BP.
DE Human cDNA encoding novel secreted protein LP223 (b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL//) LILLY & CO ELI.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 6; Length 2397;
Pred. No. 0.22;
RESULT 803
ID ABX03571 standard; DNA; 2450 BP.
DE DNA encoding human nervous system leucine rich repeat protein #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM//) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 6; Length 2450;
Pred. No. 0.22;
RESULT 804
ID AAD21287 standard; cDNA; 2493 BP.
DE Human leucine-rich repeat (LRR) family member cDNA.
PN WO200175105-A2.
PD 11-OCT-2001.
PA (MILL//) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 5; Length 2493;
Pred. No. 0.22;
RESULT 805
ID AAD54734 standard; cDNA; 2522 BP.
DE Human CGDD-1 cDNA.
PN WO2002102310-A2.
PD 27-DEC-2002.
PA (INCY//) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 10; Length 2522;
Pred. No. 0.22;
RESULT 806
ID ADD25618 standard; DNA; 2633 BP.
DE Binding domain-immunoglobulin fusion protein-associated DNA #93.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE//) GENE-CRAFT INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 10; Length 2633;
Pred. No. 0.23;
RESULT 807
ID ADI31624 standard; cDNA; 2633 BP.
DE Human cDNA #950.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY//) INCYTE CORP.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 11; Length 2633;
Pred. No. 0.23;
RESULT 808
ID ABX03577 standard; DNA; 2756 BP.
DE DNA encoding human nervous system leucine rich repeat protein #2.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM//) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 6; Length 2756;
Pred. No. 0.23;
RESULT 809
ID ADI24496 standard; cDNA; 2960 BP.

DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL//) EXELIXIS INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 12; Length 2960;
Pred. No. 0.24;
RESULT 810
ID ABK62087 standard; cDNA; 3027 BP.
DE Human cDNA encoding novel secreted protein LP223 (a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL//) LILLY & CO ELI.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 6; Length 3027;
Pred. No. 0.25;
RESULT 811
ID ADO24300 standard; DNA; 3110 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7120.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT//) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 12; Length 3110;
Pred. No. 0.25;
RESULT 812
ID ADA53985 standard; cDNA; 3309 BP.
DE Human coding sequence, SEQ ID 1553.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI//) HELIX RES INST.
PA (REAS//) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 10; Length 3309;
Pred. No. 0.26;
RESULT 813
ID AAL62047 standard; cDNA; 3360 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY//) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 9; Length 3360;
Pred. No. 0.26;
RESULT 814
ID AAH98595 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 452.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE//) HYSEQ INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 4; Length 4710;
Pred. No. 0.31;
RESULT 815
ID AAH98610 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 467.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE//) HYSEQ INC.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 4; Length 4710;
Pred. No. 0.31;
RESULT 816
ID ABX63089 standard; cDNA; 4978 BP.
DE Human cDNA #89 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND//) BANDMAN O.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 8; Length 4978;
Pred. No. 0.32;
RESULT 817
ID ADL12516 standard; cDNA; 5807 BP.
DE Human steroid-induced C3a liver cell cDNA #245.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY//) INCYTE CORP.
Query Match
Best Local Similarity 4.0%; Score 41.2; DB 12; Length 5807;
Pred. No. 0.35;
RESULT 818
ID AAD14203 standard; DNA; 8513 BP.

DE MESVR/EGFP/IBESNCAMPro(ori) vector.
PN WO200155371-A1.
PD 02-AUG-2001.
PA (SCRI) SCRIPPS RES INST.
Query Match 4.0%; Score 41.2; DB 4; Length 8513;
Best Local Similarity 50.0%; Pred. No. 0.44;
RESULT 819
ID ABT17038 standard; DNA; 4620 BP.
DE Human MP21 gene neogenin SEQ ID NO 12.
PN WO2003006990-A1.
PD 23-JAN-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.9%; Score 40.2; DB 10; Length 4620;
Best Local Similarity 49.3%; Pred. No. 0.63;
RESULT 820
ID AAS70835 standard; cDNA; 4650 BP.
DE DNA encoding novel human diagnostic protein #6639.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 40.2; DB 5; Length 4650;
Best Local Similarity 49.3%; Pred. No. 0.64;
RESULT 821
ID ADR09880 standard; DNA; 4650 BP.
DE Novel DNA-related contig nucleotide sequence #602.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 40.2; DB 10; Length 4650;
Best Local Similarity 49.3%; Pred. No. 0.64;
RESULT 822
ID ABV94279 standard; cDNA; 5297 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:270.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 3.9%; Score 40.2; DB 6; Length 5297;
Best Local Similarity 49.3%; Pred. No. 0.68;
RESULT 823
ID ADS99922 standard; cDNA; 5297 BP.
DE Human neogenin homologue 1 (NEO1), cDNA.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.9%; Score 40.2; DB 7; Length 5297;
Best Local Similarity 49.3%; Pred. No. 0.68;
RESULT 824
ID ABX10384 standard; DNA; 5297 BP.
DE DNA encoding protein differentially regulated in prostate cancer #53.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 3.9%; Score 40.2; DB 8; Length 5297;
Best Local Similarity 49.3%; Pred. No. 0.68;
RESULT 825
ID ADQ18519 standard; DNA; 5297 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1338.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 40.2; DB 12; Length 5297;
Best Local Similarity 49.3%; Pred. No. 0.68;
RESULT 826
ID ADL12801 standard; cDNA; 5506 BP.
DE Human steroid-induced C3A liver cell cDNA #530.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.9%; Score 40.2; DB 12; Length 5506;
Best Local Similarity 49.3%; Pred. No. 0.7;

ID AAL62014 standard; cDNA; 5543 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-2 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 40.2; DB 9; Length 5543;
Best Local Similarity 49.3%; Pred. No. 0.7;
RESULT 828
ID ADQ23000 standard; DNA; 5544 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5820.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 40.2; DB 12; Length 5544;
Best Local Similarity 49.3%; Pred. No. 0.7;
RESULT 829
ID ABS76362 standard; DNA; 5553 BP.
DE DNA encoding human immunoglobulin superfamily protein IGSFP-7.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 40.2; DB 6; Length 5553;
Best Local Similarity 49.3%; Pred. No. 0.7;
RESULT 830
ID ADF83428 standard; DNA; 1623 BP.
DE Bread wheat phytase enzyme coding sequence #1.
PN WO200183763-A2.
PD 08-NOV-2001.
PA (RISO-) RISOE FORSKNINGSCENTER.
Query Match 3.8%; Score 39.8; DB 6; Length 1623;
Best Local Similarity 49.8%; Pred. No. 0.47;
RESULT 831
ID ABV75372 standard; DNA; 31024 BP.
DE Human IGFEBP-2 gene sequence.
PN WO200290580-A1.
PD 14-NOV-2002.
PA (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (ARGA/) ARGAEY V P.
Query Match 3.8%; Score 39.8; DB 10; Length 31024;
Best Local Similarity 47.1%; Pred. No. 2.4;
RESULT 832
ID ADC08783 standard; DNA; 741 BP.
DE Wheat DNA sequence Seq ID1088 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.8%; Score 39.4; DB 10; Length 741;
Best Local Similarity 46.8%; Pred. No. 0.41;
RESULT 833
ID ADQ18218 standard; DNA; 2650 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1035.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.8%; Score 39.4; DB 12; Length 2650;
Best Local Similarity 46.0%; Pred. No. 0.83;
RESULT 834
ID ADF25365 standard; cDNA; 2650 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:479.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 39.4; DB 13; Length 2650;
Best Local Similarity 46.0%; Pred. No. 0.83;
RESULT 835
ID ADS19466 standard; DNA; 2650 BP.
DE Glucose-6-phosphate dehydrogenase DNA, a therapeutic gene.
PN WO2004083404-A2.
PD 30-SEP-2004.
PA (ISOG-) ISOGENIS INC.
Query Match 3.8%; Score 39.4; DB 13; Length 2650;
Best Local Similarity 46.0%; Pred. No. 0.83;

RESULT 836
ID AAK92784 standard; cDNA; 518 BP.
DE Human cDNA 3'-end sequence, SEQ ID NO: 1244.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.8%; Score 39; DB 4; Length 518;
Best Local Similarity 53.6%; Pred. No. 0.45;
RESULT 837
ID AAK94072 standard; cDNA; 518 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 2532.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.8%; Score 39; DB 4; Length 518;
Best Local Similarity 53.6%; Pred. No. 0.45;
RESULT 838
ID ADL29211 standard; cDNA; 518 BP.
DE 3' end of a human cDNA molecule SeqID 1244.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 39; DB 12; Length 518;
Best Local Similarity 53.6%; Pred. No. 0.45;
RESULT 839
ID ADL30499 standard; cDNA; 518 BP.
DE 3' end of a representative human cDNA cluster SeqID 2532.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 39; DB 12; Length 518;
Best Local Similarity 53.6%; Pred. No. 0.45;
RESULT 840
ID ABL19627 standard; DNA; 1883 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10354.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 39; DB 4; Length 1883;
Best Local Similarity 49.7%; Pred. No. 0.91;
RESULT 841
ID AAK94366 standard; cDNA; 2742 BP.
DE Human full-length cDNA, SEQ ID NO: 3089.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.8%; Score 39; DB 4; Length 2742;
Best Local Similarity 53.6%; Pred. No. 1.1;
RESULT 842
ID ADL31056 standard; cDNA; 2742 BP.
DE Full length human cDNA clone SeqID 3089.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 39; DB 12; Length 2742;
Best Local Similarity 53.6%; Pred. No. 1.1;
RESULT 843
ID ADL44512 standard; cDNA; 3390 BP.
DE Bacterial polynucleotide #19263.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.8%; Score 39; DB 13; Length 3390;
Best Local Similarity 48.1%; Pred. No. 1.3;
RESULT 844
ID ABL19626 standard; DNA; 4012 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10351.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 39; DB 4; Length 4012;
Best Local Similarity 49.7%; Pred. No. 1.4;
RESULT 845
ID ABL19624 standard; DNA; 4057 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10345.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 39; DB 4; Length 4057;
Best Local Similarity 49.7%; Pred. No. 1.4;
RESULT 846
ID ADL42073 standard; cDNA; 2952 BP.
DE Bacterial polynucleotide #16824.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.7%; Score 38.8; DB 13; Length 2952;
Best Local Similarity 53.2%; Pred. No. 1.3;
RESULT 847
ID ABL25336 standard; DNA; 4285 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27481.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 38.8; DB 4; Length 4285;
Best Local Similarity 57.4%; Pred. No. 1.7;
RESULT 848
ID ABD32648 standard; cDNA; 5913 BP.
DE Mouse cancer-associated cDNA MR13-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.7%; Score 38.8; DB 13; Length 5913;
Best Local Similarity 49.0%; Pred. No. 2;
RESULT 849
ID ADB61924 standard; cDNA; 2462 BP.
DE Human cDNA encoding clone BNGH42007798.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 38.6; DB 10; Length 2462;
Best Local Similarity 65.9%; Pred. No. 1.4;
RESULT 850
ID ADH18905 standard; cDNA; 4000 BP.
DE Human cell adhesion and extracellular matrix CAECM-1 cDNA - SEQ 32.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.6; DB 12; Length 4000;
Best Local Similarity 65.9%; Pred. No. 1.8;
RESULT 851
ID ACM42224 standard; cDNA; 4045 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1099.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.6; DB 13; Length 4045;
Best Local Similarity 65.9%; Pred. No. 1.8;
RESULT 852
ID ACM42225 standard; cDNA; 4053 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1100.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.6; DB 13; Length 4053;
Best Local Similarity 65.9%; Pred. No. 1.8;
RESULT 853

ID AAD49595 standard; cDNA; 4080 BP.
DE Human cytoskeleton-associated protein, CSAP-6 cDNA.
PN WO200279404-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.6; DB 8; Length 4080;
Best Local Similarity 65.9%; Pred. No. 1.9;
RESULT 854
ID ABT16046 standard; DNA; 4131 BP.
DE NOVX related polynucleotide SEQ ID No 59.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.7%; Score 38.6; DB 8; Length 4131;
Best Local Similarity 65.9%; Pred. No. 1.9;
RESULT 855
ID AD041693 standard; cDNA; 4131 BP.
DE Novel human polypeptide NOV22a cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENNA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 3.7%; Score 38.6; DB 12; Length 4131;
Best Local Similarity 65.9%; Pred. No. 1.9;
RESULT 856
ID AAD49596 standard; cDNA; 4360 BP.
DE Human cytoskeleton-associated protein, CSAP-7 cDNA.
PN WO200279404-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.6; DB 8; Length 4360;
Best Local Similarity 65.9%; Pred. No. 1.9;
RESULT 857
ID ACN42223 standard; cDNA; 4633 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1098.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.6; DB 13; Length 4633;
Best Local Similarity 65.9%; Pred. No. 2;
RESULT 858
ID AAK51847 standard; cDNA; 4694 BP.
DE Human polynucleotide SEQ ID NO 392.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 3.7%; Score 38.6; DB 4; Length 4694;
Best Local Similarity 65.9%; Pred. No. 2;
RESULT 859
ID AAK51848 standard; cDNA; 4739 BP.
DE Human polynucleotide SEQ ID NO 393.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 38.6; DB 4; Length 4739;
Best Local Similarity 65.9%; Pred. No. 2;
RESULT 860
ID ACN42222 standard; cDNA; 4834 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1097.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.6; DB 13; Length 4834;
Best Local Similarity 65.9%; Pred. No. 2;
RESULT 861
ID ADQ18863 standard; DNA; 4955 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1682.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.7%; Score 38.6; DB 12; Length 4955;
Best Local Similarity 65.9%; Pred. No. 2.1;
RESULT 862
ID ADRI4752 standard; DNA; 5244 BP.
DE Nucleotide sequence of human MAPKX orthologue #10.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.7%; Score 38.6; DB 13; Length 5244;
Best Local Similarity 65.9%; Pred. No. 2.1;
RESULT 863
ID ADH82128 standard; DNA; 366 BP.
DE Enterococcus faecalis polynucleotide #13.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 3.7%; Score 38.4; DB 10; Length 366;
Best Local Similarity 51.1%; Pred. No. 0.56;
RESULT 864
ID ABD02016 standard; DNA; 366 BP.
DE Pseudomonas aeruginosa polynucleotide #620.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.7%; Score 38.4; DB 11; Length 366;
Best Local Similarity 51.1%; Pred. No. 0.56;
RESULT 865
ID ADH82126 standard; DNA; 591 BP.
DE Enterococcus faecalis polynucleotide #11.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 3.7%; Score 38.4; DB 10; Length 591;
Best Local Similarity 51.1%; Pred. No. 0.74;
RESULT 866
ID ABD02170 standard; DNA; 912 BP.
DE Pseudomonas aeruginosa polynucleotide #774.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.7%; Score 38.4; DB 11; Length 912;
Best Local Similarity 51.1%; Pred. No. 0.93;
RESULT 867
ID ABD02039 standard; DNA; 948 BP.
DE Pseudomonas aeruginosa polynucleotide #643.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.7%; Score 38.4; DB 11; Length 948;
Best Local Similarity 51.1%; Pred. No. 0.96;
RESULT 868
ID AAL49438 standard; DNA; 984 BP.
DE Cell adhesion molecule coding sequence SEQ ID NO: 1.
PN WO200264771-A1.
PD 22-AUG-2002.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 3.7%; Score 38.4; DB 6; Length 984;
Best Local Similarity 53.3%; Pred. No. 0.97;
RESULT 869
ID AD43022 standard; cDNA; 1281 BP.
DE Bacterial polynucleotide #17773.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.7%; Score 38.4; DB 13; Length 1281;
Best Local Similarity 47.5%; Pred. No. 1.1;
RESULT 870
ID AAL39652 standard; DNA; 1500 BP.
DE Human secreted protein DNA SEQ ID NO 96.
PN WO200238602-A2.
PD 16-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.4; DB 6; Length 1500;
Best Local Similarity 53.3%; Pred. No. 1.2;
RESULT 871
ID AD69626 standard; cDNA; 1513 BP.
DE Human REMAP cDNA - SEQ ID 55.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.4; DB 10; Length 1513;
Best Local Similarity 53.3%; Pred. No. 1.2;
RESULT 872
ID AAL49439 standard; DNA; 1523 BP.
DE Cell adhesion molecule related DNA #14.
PN WO200264771-A1.
PD 22-AUG-2002.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 3.7%; Score 38.4; DB 6; Length 1523;
Best Local Similarity 53.3%; Pred. No. 1.2;
RESULT 873
ID ADB63075 standard; cDNA; 2375 BP.
DE Human cDNA encoding clone SMINT20017310.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 38.4; DB 10; Length 2375;
Best Local Similarity 53.3%; Pred. No. 1.6;
RESULT 874
ID ADM02018 standard; cDNA; 2735 BP.
DE Human cDNA of the invention SEQ ID NO:703.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 38.4; DB 11; Length 2735;
Best Local Similarity 53.3%; Pred. No. 1.7;
RESULT 875
ID ABL13797 standard; cDNA; 4808 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35873.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 38.4; DB 4; Length 4808;
Best Local Similarity 58.9%; Pred. No. 2.3;
RESULT 876

ID AAD60168 standard; cDNA; 4890 BP.
DE Drosophila melanogaster VEGFR cDNA #2.
PN US6599717-B1.
PD 29-JUL-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.7%; Score 38.4; DB 10; Length 4890;
Best Local Similarity 58.9%; Pred. No. 2.4;
RESULT 877
ID AAD60170 standard; cDNA; 4943 BP.
DE Drosophila melanogaster VEGFR isolated mutant cDNA.
PN US6599717-B1.
PD 29-JUL-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.7%; Score 38.4; DB 10; Length 4943;
Best Local Similarity 58.9%; Pred. No. 2.4;
RESULT 878
ID AAD60169 standard; cDNA; 5170 BP.
DE Drosophila melanogaster VEGFR cDNA #3.
PN US6599717-B1.
PD 29-JUL-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.7%; Score 38.4; DB 10; Length 5170;
Best Local Similarity 58.9%; Pred. No. 2.4;
RESULT 879
ID ABL13796 standard; cDNA; 20311 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35870.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 38.4; DB 4; Length 20311;
Best Local Similarity 58.9%; Pred. No. 5.2;
RESULT 880
ID ABL25337 standard; DNA; 1242 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 38; DB 4; Length 1242;
Best Local Similarity 60.8%; Pred. No. 1.5;
RESULT 881
ID AAS2631 standard; DNA; 885 BP.
DE Eosinophil activating peptide gene 24.
PN WO200032630-A2.
PD 08-JUN-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 3.7%; Score 37.8; DB 3; Length 885;
Best Local Similarity 45.7%; Pred. No. 1.4;
RESULT 882
ID ABZ83196 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #355.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.7%; Score 37.8; DB 10; Length 1024;
Best Local Similarity 45.7%; Pred. No. 1.5;
RESULT 883
ID ABL20249 standard; DNA; 1605 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12220.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 37.8; DB 4; Length 1605;
Best Local Similarity 48.4%; Pred. No. 2;
RESULT 884
ID ADF61833 standard; DNA; 2631 BP.
DE Human glucose-6-phosphate dehydrogenase DNA.
PN WO2003088910-A2.
PD 30-OCT-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 3.7%; Score 37.8; DB 10; Length 2631;
Best Local Similarity 45.7%; Pred. No. 2.6;
RESULT 885
ID ADQ86257 standard; cDNA; 2631 BP.

DE Human tumour-associated antigenic target (TAT) cDNA sequence #3129.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.7%; Score 37.8; DB 12; Length 2631;
Best Local Similarity 45.7%; Pred. No. 2.6;
RESULT 886
ID ADQ87416 standard; cDNA; 2631 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4293.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.7%; Score 37.8; DB 12; Length 2631;
Best Local Similarity 45.7%; Pred. No. 2.6;
RESULT 887
ID ACN41102 standard; cDNA; 2631 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA327111, SEQ ID NO:6320.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 37.8; DB 13; Length 2631;
Best Local Similarity 45.7%; Pred. No. 2.6;
RESULT 888
ID ADQ22767 standard; DNA; 2680 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5587.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.7%; Score 37.8; DB 12; Length 2680;
Best Local Similarity 45.7%; Pred. No. 2.6;
RESULT 889
ID AAF21697 standard; DNA; 2803 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 84.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 37.8; DB 3; Length 2803;
Best Local Similarity 45.7%; Pred. No. 2.7;
RESULT 890
ID ABL20248 standard; DNA; 9680 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12217.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 37.8; DB 4; Length 9680;
Best Local Similarity 48.4%; Pred. No. 5.3;
RESULT 891
ID AAX35377 standard; DNA; 384 BP.
DE SEQ ID 52 of WO9916889.
PN WO9916889-A1.
PD 08-APR-1999.
PA (SEAR) SEARLE & CO G D.
Query Match 3.6%; Score 37.6; DB 2; Length 384;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 892
ID ADG48023 standard; DNA; 387 BP.
DE Human variant TTR (C10A/G83C) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 893
ID ADG48019 standard; DNA; 387 BP.
DE Human variant TTR (C10A) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.

PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 894
ID ADG48020 standard; DNA; 387 BP.
DE Human variant TTR (C10A/A37C) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 895
ID ADG48024 standard; DNA; 387 BP.
DE Human variant TTR (C10A/K15A/G83C) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 896
ID ADG48021 standard; DNA; 387 BP.
DE Human variant TTR (C10A/D38C) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 897
ID ADG48018 standard; DNA; 387 BP.
DE Human transthyretin (TTR) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 898
ID ADG68775 standard; cDNA; 387 BP.
DE Human mutant transthyretin (TTR) cDNA #1.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 899
ID ADG68779 standard; cDNA; 387 BP.
DE Human mutant transthyretin (TTR) cDNA #5.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 900
ID ADG68774 standard; cDNA; 387 BP.
DE Human transthyretin (TTR) cDNA.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 387;
Best Local Similarity 50.6%; Pred. No. 1;
RESULT 901
ID ADG68777 standard; cDNA; 387 BP.
DE Human mutant transthyretin (TTR) cDNA #3.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.

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Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 387;
RESULT 902
ID ADG68776 standard; cDNA; 387 BP.
DE Human mutant transthyretin (TTR) cDNA #2.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 387;
RESULT 903
ID ADG68780 standard; cDNA; 387 BP.
DE Human mutant transthyretin (TTR) cDNA #6.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 387;
RESULT 904
ID ADG48033 standard; DNA; 439 BP.
DE Human TTR (C10A/G83C)-bradykinin variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 439;
RESULT 905
ID ADG68789 standard; cDNA; 439 BP.
DE Human mutant transthyretin (TTR) cDNA #15.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 439;
RESULT 906
ID AB283385 standard; cDNA; 483 BP.
DE Toxicologically relevant human nucleotide sequence #544.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 10; Length 483;
RESULT 907
ID ADG48089 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/K15A/G83C) fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 908
ID ADG48027 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/D38C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 909
ID ADG48029 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/G83C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 910
ID ADG48091 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/K15A/A37C) fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 911
ID ADG48025 standard; DNA; 495 BP.
DE Human TMP-TTR fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 912
ID ADG48026 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/A37C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 913
ID ADG68785 standard; cDNA; 495 BP.
DE Human mutant transthyretin (TTR) cDNA #11.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 914
ID ADG68782 standard; cDNA; 495 BP.
DE Human mutant transthyretin (TTR) cDNA #8.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 915
ID ADG68781 standard; cDNA; 495 BP.
DE Human mutant transthyretin (TTR) cDNA #7.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 916
ID ADG68783 standard; cDNA; 495 BP.
DE Human mutant transthyretin (TTR) cDNA #9.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 917
ID ADG48084 standard; DNA; 510 BP.
DE Human TTR-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 495;
RESULT 918
ID ADG48084 standard; DNA; 510 BP.
DE Human TTR-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match
Best Local Similarity 3.6%; Score 37.6; DB 12; Length 510;
RESULT 919
ID ADG48084 standard; DNA; 510 BP.
DE Human TTR-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
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ID ADG48088 standard; DNA; 510 BP.
DE Human TTR (C10A/K15A/G83C)-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 510;
Best Local Similarity 50.6%; Pred. No. 1.2;
RESULT 919
ID ADG48086 standard; DNA; 510 BP.
DE Human TTR (C10A/K15A/A37C)-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 510;
Best Local Similarity 50.6%; Pred. No. 1.2;
RESULT 920
ID ADG48085 standard; DNA; 510 BP.
DE Human TTR (C10A/K15A)-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 510;
Best Local Similarity 50.6%; Pred. No. 1.2;
RESULT 921
ID ADE76836 standard; cDNA; 572 BP.
DE Human cDNA differentially expressed in a liver disorder #1.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 3.6%; Score 37.6; DB 12; Length 572;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 922
ID ADG48065 standard; DNA; 591 BP.
DE Human GLP-1-TTR (C10A/K15A/G83C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 591;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 923
ID ADG48064 standard; DNA; 594 BP.
DE Human GLP-1-TTR (C10A/G83C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 594;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 924
ID ABQ78304 standard; DNA; 615 BP.
DE Nucleotide sequence of transthyretin polypeptide.
PN WO200259621-A2.
PD 01-AUG-2002.
PA (FARB) BAYER CORP.
Query Match 3.6%; Score 37.6; DB 6; Length 615;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 925
ID ABQ78305 standard; DNA; 615 BP.
DE Nucleotide sequence of transthyretin polypeptide.
PN WO200259621-A2.
PD 01-AUG-2002.
PA (FARB) BAYER CORP.
Query Match 3.6%; Score 37.6; DB 6; Length 615;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 926
ID AAN60839 standard; cDNA; 631 BP.
DE Cloned pre-albumin DNA.
PN JP61052292-A.
PD 14-MAR-1986.
PA (MITH) MITSUI PHARM INC.
Query Match 3.6%; Score 37.6; DB 1; Length 631;
Best Local Similarity 50.6%; Pred. No. 1.3;
RESULT 927
ID AAN90103 standard; cDNA; 669 BP.
DE Human prealbumin cDNA.
PN JP01117790-A.
PD 10-MAY-1989.
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
Query Match 3.6%; Score 37.6; DB 1; Length 669;
Best Local Similarity 50.6%; Pred. No. 1.4;
RESULT 928
ID ADG48078 standard; DNA; 723 BP.
DE Human immunoglobulin CH2 domain-TTR (C10A) fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 723;
Best Local Similarity 50.6%; Pred. No. 1.5;
RESULT 929
ID ADG48072 standard; DNA; 735 BP.
DE Human TTR (C10A)-immunoglobulin CH2 domain fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 735;
Best Local Similarity 50.6%; Pred. No. 1.5;
RESULT 930
ID ADG48081 standard; DNA; 831 BP.
DE Human TMP-immunoglobulin CH2 domain-TTR (C10A) fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 831;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 931
ID ADG48031 standard; DNA; 843 BP.
DE Human IL-1ra-TTR (C10A) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 843;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 932
ID ADG48075 standard; DNA; 843 BP.
DE Human TTR (C10A)-CH2-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 843;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 933
ID ADG48073 standard; DNA; 843 BP.
DE Human TMP-TTR (C10A)-immunoglobulin CH2 domain fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 843;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 934
ID ADG68787 standard; cDNA; 843 BP.
DE Human mutant transthyretin (TTR) cDNA #13.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 843;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 935
ID ADG68787 standard; cDNA; 843 BP.
DE Human mutant transthyretin (TTR) cDNA #13.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 843;

Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 935
ID ADG48032 standard; DNA; 855 BP.
DE Human TTR (C10A)-IL-lra variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALKER/) WALKER K.
PA (XIONG/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 855;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 936
ID ADG68788 standard; cDNA; 855 BP.
DE Human mutant transthyretin (TTR) cDNA #14.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALKER/) WALKER K.
PA (XIONG/) XIONG F.
Query Match 3.6%; Score 37.6; DB 12; Length 855;
Best Local Similarity 50.6%; Pred. No. 1.6;
RESULT 937
ID ADS45904 standard; cDNA; 1017 BP.
DE Bacterial polynucleotide #647.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.6%; Score 37.6; DB 13; Length 1017;
Best Local Similarity 47.5%; Pred. No. 1.8;
RESULT 938
ID ADF83430 standard; DNA; 1370 BP.
DE Bread wheat phytase enzyme coding sequence #2.
PN WO200183763-A2.
PD 08-NOV-2001.
PA (RISO-) RISOE FORSKNINGSCENTER.
Query Match 3.6%; Score 37.6; DB 6; Length 1370;
Best Local Similarity 49.0%; Pred. No. 2.1;
RESULT 939
ID AD114335 standard; DNA; 5198 BP.
DE Human Neogenin nucleic acid.
PN WO2004003150-A2.
PD 08-JAN-2004.
PA (UYVA/) UNIV YALE.
Query Match 3.6%; Score 37.6; DB 12; Length 5198;
Best Local Similarity 48.6%; Pred. No. 4.3;
RESULT 940
ID ADQ62949 standard; cDNA; 1829 BP.
DE Novel human cDNA sequence #110.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 37.4; DB 12; Length 1829;
Best Local Similarity 53.0%; Pred. No. 2.8;
RESULT 941
ID AA161348 standard; cDNA; 2265 BP.
DE Human polynucleotide SEQ ID NO 5337.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 37.4; DB 4; Length 2265;
Best Local Similarity 53.0%; Pred. No. 3.2;
RESULT 942
ID AB115323 standard; cDNA; 2472 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40451.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 37.4; DB 4; Length 2472;
Best Local Similarity 57.1%; Pred. No. 3.3;
RESULT 943
ID ADM93822 standard; DNA; 2916 BP.
Query Match 3.6%; Score 37; DB 12; Length 4091;
DE Nucleotide sequence of tyrosine kinase-like orphan receptor 2.
PN WO2004048540-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.6%; Score 37; DB 12; Length 4091;
DE DNA encoding human NOV protein #21.
PN US2004009480-A1.
PD 15-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (BAUM/) BAUMGARTNER J C.
PA (BOLD/) BOLD OG F L.
PA (CASW/) CASMAN S J.
PA (EDIN/) EDINGER S R.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X S.
PA (HUAL/) HUALT T.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 3.6%; Score 37.4; DB 12; Length 2916;
Best Local Similarity 47.6%; Pred. No. 3.6;
RESULT 944
ID AAC84449 standard; cDNA; 3705 BP.
DE Nucleotide sequence of mddt cDNA clone ID No: 243096.6.
PN WO200075298-A2.
PD 14-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 37.4; DB 4; Length 3705;
Best Local Similarity 53.0%; Pred. No. 4.1;
RESULT 945
ID AAA30430 standard; DNA; 925 BP.
DE Human RaceACAM DNA sequence.
PN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.6%; Score 37; DB 3; Length 925;
Best Local Similarity 49.5%; Pred. No. 2.6;
RESULT 946
ID AD744452 standard; cDNA; 1857 BP.
DE Bacterial polynucleotide #19203.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.6%; Score 37; DB 13; Length 1857;
Best Local Similarity 49.2%; Pred. No. 3.8;
RESULT 947
ID ADL13892 standard; DNA; 2832 BP.
DE Osteoarthritis-associated polymorphic nucleotide #424.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 37; DB 10; Length 2832;
Best Local Similarity 47.6%; Pred. No. 4.8;
RESULT 948
ID ADP74597 standard; DNA; 4091 BP.
DE Nucleotide sequence of tyrosine kinase-like orphan receptor 2.
PN WO2004048540-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.6%; Score 37; DB 12; Length 4091;

Best Local Similarity 47.6%; Pred. No. 5.8;
RESULT 949
ID AAV70230 standard; DNA; 4092 BP.
DE Human receptor tyrosine kinase ROR-2 encoding DNA.
FN US5843749-A.
PD 01-DEC-1998.
PA (REGE-) REGENERON PHARM INC.
Query Match 3.6%; Score 37; DB 2; Length 4092;
Best Local Similarity 47.6%; Pred. No. 5.8;
RESULT 950
ID ADI13891 standard; DNA; 4092 BP.
DE Osteoarthritis-associated polymorphic nucleotide #423.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 37; DB 10; Length 4092;
Best Local Similarity 47.6%; Pred. No. 5.8;
RESULT 951
ID AD019268 standard; DNA; 4092 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2087.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 37; DB 12; Length 4092;
Best Local Similarity 47.6%; Pred. No. 5.8;
RESULT 952
ID AQ089065 standard; cDNA; 4092 BP.
DE Human urological disorder related protein 5410 encoding cDNA SEQ:17.
FN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.6%; Score 37; DB 13; Length 4092;
Best Local Similarity 47.6%; Pred. No. 5.8;
RESULT 953
ID ADQ23542 standard; DNA; 4132 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6362.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 37; DB 12; Length 4132;
Best Local Similarity 47.6%; Pred. No. 5.9;
RESULT 954
ID ABK84529 standard; cDNA; 7195 BP.
DE Human cDNA differentially expressed in granulocytic cells #1100.
FN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 37; DB 6; Length 7195;
Best Local Similarity 53.0%; Pred. No. 8;
RESULT 955
ID AAH48024 standard; DNA; 14041 BP.
DE Internal control B19c #1.
FN WO200146463-A2.
PD 28-JUN-2001.
PA (BAXT) BAXTER AG.
Query Match 3.6%; Score 37; DB 4; Length 14041;
Best Local Similarity 17.4%; Pred. No. 12;
RESULT 956
ID ABD11363 standard; DNA; 546 BP.
DE Pseudomonas aeruginosa polynucleotide #9967.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 36.8; DB 11; Length 546;
Best Local Similarity 50.0%; Pred. No. 2.2;
RESULT 957
ID ABD11580 standard; DNA; 1350 BP.
DE Pseudomonas aeruginosa polynucleotide #10184.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 36.8; DB 11; Length 1350;
Best Local Similarity 50.0%; Pred. No. 3.6;
RESULT 958
ID ABD11441 standard; DNA; 3639 BP.
DE Pseudomonas aeruginosa polynucleotide #10045.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 36.8; DB 11; Length 3639;
Best Local Similarity 50.0%; Pred. No. 6.3;
RESULT 959
ID ABD11188 standard; DNA; 3717 BP.
DE Pseudomonas aeruginosa polynucleotide #9792.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 36.8; DB 11; Length 3717;
Best Local Similarity 50.0%; Pred. No. 6.4;
RESULT 960
ID AAD60167 standard; cDNA; 5220 BP.
DE Drosophila melanogaster VEGFR cDNA #1.
FN US6595717-B1.
PD 29-JUL-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.6%; Score 36.8; DB 10; Length 5220;
Best Local Similarity 58.0%; Pred. No. 7.7;
RESULT 961
ID AAV89551 standard; cDNA; 397 BP.
DE EST clone CR1162.
FN WO9845436-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 3.5%; Score 36.4; DB 2; Length 397;
Best Local Similarity 49.5%; Pred. No. 2.5;
RESULT 962
ID AAH06394 standard; cDNA; 820 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:3229.
FN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 36.4; DB 4; Length 820;
Best Local Similarity 49.5%; Pred. No. 3.7;
RESULT 963
ID AAD04299 standard; cDNA; 1242 BP.
DE Human brain immunoglobulin superfamily receptor (Bigr) cDNA.
FN WO200129083-A1.
PD 26-APR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 3.5%; Score 36.4; DB 5; Length 1242;
Best Local Similarity 49.5%; Pred. No. 4.6;
RESULT 964
ID AAD04351 standard; cDNA; 1242 BP.
DE Alternative version of human Bigr cDNA.
FN WO200129083-A1.
PD 26-APR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 3.5%; Score 36.4; DB 5; Length 1242;
Best Local Similarity 49.5%; Pred. No. 4.6;
RESULT 965
ID ABT17389 standard; DNA; 1242 BP.
DE Human IG gene related nucleic acid SEQ ID No 15.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1242;
Best Local Similarity 49.5%; Pred. No. 4.6;
RESULT 966
ID ABT17386 standard; DNA; 1274 BP.
DE Human IG gene related nucleic acid SEQ ID No 12.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1274;
Best Local Similarity 49.5%; Pred. No. 4.7;
RESULT 967

ID ABLT17388 standard; DNA; 1299 BP.
DE Human IG gene related nucleic acid SEQ ID No 14.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC. 3.5%; Score 36.4; DB 8; Length 1299;
Query Match Similarity 49.5%; Pred. No. 4.7;
RESULT 968
ID ABLT17387 standard; DNA; 1376 BP.
DE Human IG gene related nucleic acid SEQ ID No 13.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC. 3.5%; Score 36.4; DB 8; Length 1376;
Query Match Similarity 49.5%; Pred. No. 4.9;
RESULT 970
ID ACX38048 standard; DNA; 1515 BP.
DE Prokaryotic essential gene #19705.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 3.5%; Score 36.4; DB 8; Length 1515;
Query Match Similarity 49.0%; Pred. No. 5.2;
RESULT 971
ID AAV84523 standard; DNA; 1542 BP.
DE Human secreted protein gene 113 clone HCE3Q10.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC. 3.5%; Score 36.4; DB 2; Length 1542;
Query Match Similarity 49.5%; Pred. No. 5.2;
RESULT 972
ID ABA83441 standard; cDNA; 1542 BP.
DE Human secreted protein related cDNA SEQ ID NO:1244.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 3.5%; Score 36.4; DB 4; Length 1542;
Query Match Similarity 49.5%; Pred. No. 5.2;
RESULT 973
ID ACH04807 standard; cDNA; 1542 BP.
DE Novel human secreted protein #113 cDNA.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 3.5%; Score 36.4; DB 9; Length 1542;
Query Match Similarity 49.5%; Pred. No. 5.2;
RESULT 974
ID ACD44617 standard; cDNA; 1542 BP.
DE Human cDNA from novel secreted protein gene 113.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 3.5%; Score 36.4; DB 9; Length 1542;
Query Match Similarity 49.5%; Pred. No. 5.2;
RESULT 975
ID AA208540 standard; cDNA; 1614 BP.
DE Human MBGP1 encoding cDNA.
PN EP939124-A2.
PD 01-SEP-1999.
PA (SMIX) SMITHKLINE BEECHAM PLC. 3.5%; Score 36.4; DB 2; Length 1614;
Query Match Similarity 49.5%; Pred. No. 5.3;
RESULT 976
ID AAX52229 standard; DNA; 1685 BP.

DE Protein PRO258 cDNA clone DNA35918-1174.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 2; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 977
ID ADC78403 standard; cDNA; 1685 BP.
DE Human PRO258 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 3; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 978
ID AAF72387 standard; cDNA; 1685 BP.
DE Human PRO258 cDNA.
PN WO2000104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 4; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 979
ID AAS21417 standard; cDNA; 1685 BP.
DE Human cDNA sequence encoding for PRO258 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 4; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 980
ID AAC97445 standard; cDNA; 1685 BP.
DE Human angiogenesis-associated protein PRO258 cDNA, SEQ ID NO:100.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 4; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 981
ID ABL88093 standard; cDNA; 1685 BP.
DE Human PRO258 cDNA sequence SEQ ID NO:43.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 6; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 982
ID ABL95582 standard; cDNA; 1685 BP.
DE Human angiogenesis related cDNA PRO258 SEQ ID NO: 43.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 6; Length 1685;
Query Match Similarity 49.5%; Pred. No. 5.5;
RESULT 983
ID AC60068 standard; cDNA; 1685 BP.
DE Human cDNA for secreted/transmembrane protein PRO258.
PN US2003003530-A1.

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 984
ID ACD07468 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 985
ID ACA03776 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 986
ID ABX71516 standard; cDNA; 1685 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO258.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 987
ID ACH06848 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane polypeptide PRO258 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 988
ID ABX89314 standard; cDNA; 1685 BP.
DE DNA encoding novel secreted and transmembrane protein PRO258.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 989
ID ACU41968 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 990
ID ABX96085 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 991
ID ACA05406 standard; cDNA; 1685 BP.
DE cDNA encoding human secreted protein PRO258.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 992
ID ACD20073 standard; cDNA; 1685 BP.
DE Human secreted / transmembrane polypeptide PRO258 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 993
ID ACA04197 standard; cDNA; 1685 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 347.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 994
ID ACA54876 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 8; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 995
ID ACD19711 standard; cDNA; 1685 BP.
DE Human secreted / transmembrane polypeptide PRO258 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 996
ID ADA5866 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 997
ID ADA76297 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 998
ID ADB29288 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 999
ID ADA18947 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1000
ID ADA61570 standard; cDNA; 1685 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1001
ID ADB19355 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1002
ID ADA97035 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1003
ID ADA96375 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1004
ID ADA97339 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1005
ID ADA97725 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1006
ID ADA18144 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1007
ID ACD66858 standard; cDNA; 1685 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO258.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1008
ID ADA67520 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1009
ID ADB30527 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1010
ID ADA85823 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1011
ID ADA97035 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1012
ID ADA97339 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1013
ID ADA87478 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1014
ID ADB16680 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1015
ID ACD83019 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #15.
PN US200304793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1016
ID ADA16119 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1017
ID ADA91772 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1018
ID ADB14835 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1019
ID ADB18796 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
RESULT 1020
ID ADA85823 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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RESULT 1020
ID ADA94011 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1021
ID ADB19907 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1022
ID ADB13219 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1023
ID ADB29975 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
FN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1024
ID ADA74473 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1025
ID ADA42264 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
FN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1026
ID ADB24706 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
FN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1027
ID ADA82230 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1028
ID ADA75193 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1029
ID ADB26792 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1030
ID ADA84719 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1031
ID ACD23197 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #15.
FN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1032
ID ADB29975 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
FN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1033
ID ADA80503 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1034
ID ADA75745 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1035
ID ADA46970 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1036
ID ADB25266 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
FN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1037
ID ADA93442 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1038
ID ADB26792 standard; cDNA; 1685 BP.
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DE cDNA encoding human PRO polypeptide #174.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1039
ID ADB31079 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1040
ID ADA61007 standard; cDNA; 1685 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1041
ID ADB24154 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1042
ID ADA96483 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1043
ID ADA81055 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1044
ID ADA95931 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1045
ID ADB26240 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1046
ID ADB21725 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1047
ID ADA77504 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003054351-A1.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1048
ID ADB18244 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1049
ID ADA86927 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1050
ID ADA16543 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1051
ID ADA12972 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1052
ID ADA41840 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1053
ID ADA8030 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1054
ID ADA46418 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1055
ID ADA17187 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 9; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1056
ID ADA42690 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003054351-A1.
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PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity 3.5%; Score 36.4; DB 9; Length 1685;
 Query Match 49.5%; Pred. No. 5.5;
 RESULT 1057
 ID ADB28448 standard; cDNA; 1685 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1058
 ID ADB29000 standard; cDNA; 1685 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1059
 ID ADA76952 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1060
 ID ADA88582 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1061
 ID ADA97587 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1062
 ID ADB27344 standard; cDNA; 1685 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1063
 ID ADB22277 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1064
 ID ACD23559 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #15.
 PN US2003064923-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1065
 ID ADA66968 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003068793-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;

Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1066
 ID ADB22829 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1067
 ID ADB23602 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide SEQ ID NO 347.
 PN US2003077712-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1068
 ID ADA92324 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1069
 ID ADB15387 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1070
 ID ADB38639 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1071
 ID ADB38087 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1072
 ID ADB66559 standard; cDNA; 1685 BP.
 DE Novel human secreted and transmembrane protein PRO258 cDNA.
 PN US2003082689-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1073
 ID ADB89639 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 9; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1074
 ID ADB90371 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 10; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;
 RESULT 1075
 ID ADB90371 standard; cDNA; 1685 BP.
 DE Human PRO polynucleotide #174.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.5%; Score 36.4; DB 10; Length 1685;
 Best Local Similarity 49.5%; Pred. No. 5.5;

RESULT 1075
ID ADB77609 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1076
ID ADB39472 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1077
ID ADB74745 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1078
ID ADB47095 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1079
ID ADB86702 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1080
ID ADB77307 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1081
ID ADB34464 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1082
ID ADB35568 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1083
ID ADB33912 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1084

ID ADB35016 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1085
ID ADB36120 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide SEQ ID NO 347.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1086
ID ADB46515 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1087
ID ADC28391 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1088
ID ADC39591 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1089
ID ADC40105 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1090
ID ADC18933 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1091
ID ADC34229 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1092
ID ADC29284 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 10; Length 1685;
Query Match Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1093
ID ADC28815 standard; cDNA; 1685 BP.

DE Human secreted/transmembrane protein cDNA, #17.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1094
ID ADC40700 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1095
ID ADC19357 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1096
ID ADC33805 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1097
ID ADC12875 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1098
ID ADC50388 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1099
ID ADC71935 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1100
ID ADC59914 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1101
ID ADC52921 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1102
ID ADC57275 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.

PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1103
ID ADC60466 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1104
ID ADC50941 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1105
ID ADC65468 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1106
ID ADC54566 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1107
ID ADC53527 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1108
ID ADC59050 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1109
ID ADC5928 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1110
ID ADC58498 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID347.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1111
ID ADC12327 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003082541-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1112
ID ADC03172 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1113
ID ADC90164 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1114
ID ADC69583 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1115
ID ADC48472 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1116
ID ADD10001 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1117
ID ADD04576 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1118
ID ADC80532 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1119
ID ADD11039 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1120
ID ADD10332 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #22.
PN US2003105011-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1121
ID ADC47920 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1122
ID ADD04882 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1123
ID ADC79980 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1124
ID ADD11292 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #22.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1125
ID ADD09449 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1126
ID ADD03888 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1127
ID ADD03464 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1128
ID ADD41162 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1129
ID ADD52301 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1130
ID ADD53041 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1131
ID ADD53593 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1132
ID ADD37085 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #22.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1133
ID ADD51749 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1134
ID ADD02548 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1135
ID ADD01982 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1136
ID ADD54164 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1137
ID ADD92481 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1138
ID ADD91377 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1139
ID ADE03991 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1140
ID ADE32288 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1141
ID ADE22220 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1142
ID ADD79444 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1143
ID ADE41980 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1144
ID ADE17797 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1145
ID ADD91929 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1146
ID ADE33392 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1147
ID ADE33944 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 10; Length 1685;
RESULT 1148
ID ADD91377 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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ID ABE32840 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1158
ID ABE42532 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1159
ID ADD80548 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1160
ID ADD89576 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1161
ID ABE40860 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1162
ID ABE292788 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1163
ID ADE92788 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1164
ID ADG21497 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1165
ID ADG23138 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1166
ID ADF97473 standard; cDNA; 1685 BP.

DE Human PRO polynucleotide #174.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1167
ID ADG80637 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1168
ID ADG79985 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1169
ID ADH59199 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1170
ID ADH55277 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1171
ID ADH55829 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1172
ID ADI37978 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1173
ID ADI64048 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1174
ID ADI64997 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1175
ID ADI63496 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087353-A1.

PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1176
ID ADH81910 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1177
ID ADH81358 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1178
ID ACA58964 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #15.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1179
ID ACD24026 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1180
ID ACA58361 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #15.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1181
ID ACA67167 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1182
ID ADJ26246 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 10; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1183
ID ADM62527 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 11; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1184
ID ADN15926 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087353-A1.

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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 11; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1185
ID ADN16555 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 11; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1186
ID ADN15374 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 11; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1187
ID ADN14822 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 11; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1188
ID ADC81084 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1189
ID ADE79161 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1190
ID ADD76532 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1191
ID ADD87896 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1192
ID ADD86300 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1193
ID ADE79585 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1194
ID ADE75748 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1195
ID ADE73261 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1196
ID ADE41293 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #22.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1197
ID ADE23324 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1198
ID ADE23876 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1199
ID ADE24519 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1200
ID ADD87344 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1201
ID ADE89210 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1202
ID ADE73796 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1203
ID ADE18349 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1204
ID ADE88658 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1205
ID ADE99350 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1206
ID ADE94678 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1207
ID ADE91089 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1208
ID ADE95230 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1209
ID ADE93340 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1210
ID ADF34921 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1211
ID ADE98469 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1212
ID ADE92236 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1213
ID ADE90537 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1214
ID ADE91684 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1215
ID ADE98896 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1216
ID ADG40366 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1217
ID ADF73760 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1218
ID ADG02263 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1219
ID ADG22049 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.5%; Score 36.4; DB 12; Length 1685;
RESULT 1220
ID ADG20119 standard; cDNA; 1685 BP.
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DE cDNA encoding human PRO polypeptide #174.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1221
ID ADF98025 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1222
ID ADG34242 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1223
ID ADF98596 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1224
ID ADG03427 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1225
ID ADF99148 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1226
ID ADG16733 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1227
ID ADG05192 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1228
ID ADG19459 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1229
ID ADF73336 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.

PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1230
ID ADG13296 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1231
ID ADG08353 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1232
ID ADG15523 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1233
ID ADF96921 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1234
ID ADG06106 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1235
ID ADG23690 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1236
ID ADG03979 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1237
ID ADG24880 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1238
ID ADG07177 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207350-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1239
ID ADG07729 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1240
ID ADG55224 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1241
ID ADG60888 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1242
ID ADG61992 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1243
ID ADG92179 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1244
ID ADG82193 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1245
ID ADG57432 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1246
ID ADG56880 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1247
ID ADG55776 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1248
ID ADG58536 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1249
ID ADG70902 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1250
ID ADG92806 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1251
ID ADG57984 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1252
ID ADG53568 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1253
ID ADG71454 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1254
ID ADG81641 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1255
ID ADH30603 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1256
ID ADH11970 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;

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Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1257
ID ADG52392 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1258
ID ADG54120 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1259
ID ADG81089 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1260
ID ADG56328 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1261
ID ADH12594 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1262
ID ADG61440 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1263
ID ADH28527 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1264
ID ADG54672 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1265
ID ADG59712 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1266
ID ADH20395 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1267
ID ADH43476 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #22.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1268
ID ADH07250 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1269
ID ADH59795 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1270
ID ADH06823 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2004005655-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1271
ID ADI81136 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1272
ID ADI18565 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 3.5%; Score 36.4; DB 12; Length 1685;
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1273
ID ADI65285 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003148419-A1.
PD 07-AUG-2003.
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PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1274
ID ADI37548 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1275
ID ADG09879 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1276
ID ADH97352 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1277
ID ADI15350 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1278
ID ADG09227 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1279
ID ADI65712 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1280
ID ADI14682 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1281
ID ADH60455 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1282
ID ADI18277 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1283
ID ADJ99512 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1284
ID ADL08705 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1285
ID ADM25050 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1286
ID ADJ63558 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
FN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1287
ID ADM29796 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cdna, #17.
FN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1288
ID ADJ77453 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #174.
FN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1289
ID ADR82821 standard; cDNA; 1685 BP.
DE Human PRO polynucleotide #22.
FN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1290
ID ADJ65575 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
FN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1291

ID ADM27711 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1292
ID ADM2435 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1293
ID ADO06118 standard; cDNA; 1685 BP.
DE Human-PRO polynucleotide #17.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1294
ID ADM28297 standard; cDNA; 1685 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1295
ID ADRI0970 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 12; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1296
ID ADRI7879 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATH J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1301
ID AAZ61418 standard; DNA; 1718 BP.
DE DNA encoding the short extracellular form of human B7-1 (CD80).
PN WO200008057-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP. 3.5%; Score 36.4; DB 3; Length 1718;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1302
ID AAZ50887 standard; DNA; 1718 BP.
DE Human LDCAM binding protein, B7L-1 short form encoding DNA.
PN WO200008158-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP. 3.5%; Score 36.4; DB 3; Length 1718;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1303
ID ACH87501 standard; DNA; 1739 BP.
DE Human genome derived single exon probe #20696.
PN US2003194704-A1.
PD 16-OCT-2003.

PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 13; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1298
ID ADI96331 standard; cDNA; 1685 BP.
DE Novel human secreted and transmembrane protein PRO258 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 13; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1299
ID ADT03555 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane protein cDNA, #17.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC. 3.5%; Score 36.4; DB 13; Length 1685;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1300
ID ADS74518 standard; cDNA; 1685 BP.
DE Human secreted/transmembrane cDNA #17.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATH J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1301
ID AAZ61418 standard; DNA; 1718 BP.
DE DNA encoding the short extracellular form of human B7-1 (CD80).
PN WO200008057-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP. 3.5%; Score 36.4; DB 3; Length 1718;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1302
ID AAZ50887 standard; DNA; 1718 BP.
DE Human LDCAM binding protein, B7L-1 short form encoding DNA.
PN WO200008158-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP. 3.5%; Score 36.4; DB 3; Length 1718;
Query Match
Best Local Similarity 49.5%; Pred. No. 5.5;
RESULT 1303
ID ACH87501 standard; DNA; 1739 BP.
DE Human genome derived single exon probe #20696.
PN US2003194704-A1.
PD 16-OCT-2003.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.5%; Score 36.4; DB 12; Length 1739;
Best Local Similarity 47.1%; Pred. No. 5.6;
RESULT 1304
ID AA261416 standard; DNA; 1820 BP.
DE DNA encoding the long extracellular form of human B7-1 (CD80).
PN WO200008057-A2.
PD 17-FEB-2000.
PA (IMWV) IMMUNEX CORP.
Query Match 3.5%; Score 36.4; DB 3; Length 1820;
Best Local Similarity 49.5%; Pred. No. 5.7;
RESULT 1305
ID AA250896 standard; DNA; 1820 BP.
DE Human LDCAM binding protein, B7L-1 long form encoding DNA.
PN WO200008159-A2.
PD 17-FEB-2000.
PA (IMWV) IMMUNEX CORP.
Query Match 3.5%; Score 36.4; DB 3; Length 1820;
Best Local Similarity 49.5%; Pred. No. 5.7;
RESULT 1306
ID AA30423 standard; cDNA; 2224 BP.
DE Human cDNA clone ACAM#6 nucleotide sequence.
PN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.5%; Score 36.4; DB 3; Length 2224;
Best Local Similarity 49.5%; Pred. No. 6.4;
RESULT 1307
ID AAH14434 standard; cDNA; 2463 BP.
DE Human cDNA sequence SEQ ID NO:11895.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 36.4; DB 4; Length 2463;
Best Local Similarity 49.5%; Pred. No. 6.8;
RESULT 1308
ID AAV63189 standard; cDNA; 2496 BP.
DE cDNA from clone cr1162_25 which encodes a secreted protein.
PN WO9844113-A1.
PD 08-OCT-1998.
PA (GENY) GENETICS INST INC.
Query Match 3.5%; Score 36.4; DB 2; Length 2496;
Best Local Similarity 49.5%; Pred. No. 6.8;
RESULT 1309
ID ABQ92039 standard; cDNA; 2496 BP.
DE Human polynucleotide SEQ ID NO 36.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SFAU/) SPAULDING V.
Query Match 3.5%; Score 36.4; DB 6; Length 2496;
Best Local Similarity 49.5%; Pred. No. 6.8;
RESULT 1310
ID AD103925 standard; DNA; 2496 BP.
DE Human B7-1 polypeptide encoding DNA.
PN WO2003105887-A1.
PD 24-DEC-2003.
PA (AWHP) WYETH.
Query Match 3.5%; Score 36.4; DB 12; Length 2496;
Best Local Similarity 49.5%; Pred. No. 6.8;
RESULT 1311
ID ABA83306 standard; cDNA; 2537 BP.
DE Human secreted protein gene 113 SEQ ID NO:123.
PN WO200162891-A2.
PD 30-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 36.4; DB 4; Length 2537;
Best Local Similarity 49.5%; Pred. No. 6.9;
RESULT 1312
ID AAA13652 standard; cDNA; 2543 BP.
DE Human Beat-like 1 (BL1) cDNA sequence.
PN CN1242376-A.
PD 26-JAN-2000.
PA (BASI-) BASIC MEDICAL SCI RES INST CHINESE ACAD.
Query Match 3.5%; Score 36.4; DB 3; Length 2543;
Best Local Similarity 49.5%; Pred. No. 6.9;
RESULT 1313
ID ACN43565 standard; cDNA; 2642 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2440.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 36.4; DB 13; Length 2642;
Best Local Similarity 49.5%; Pred. No. 7;
RESULT 1314
ID AAA30424 standard; cDNA; 2837 BP.
DE Human cDNA clone ACAM#4 nucleotide sequence.
PN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.5%; Score 36.4; DB 3; Length 2837;
Best Local Similarity 49.5%; Pred. No. 7.3;
RESULT 1315
ID ADA24421 standard; DNA; 3557 BP.
DE Human tumour suppressor gene, TSLL1.
PN US2003109016-A1.
PD 12-JUN-2003.
PA (PRES-) PRESIDENT NAT CANCER CENT.
PA (EMLB-) EML INC.
Query Match 3.5%; Score 36.4; DB 9; Length 3557;
Best Local Similarity 49.5%; Pred. No. 8.3;
RESULT 1316
ID AAS81244 standard; cDNA; 14934 BP.
DE DNA encoding novel human diagnostic protein #17048.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 36.4; DB 5; Length 14934;
Best Local Similarity 47.1%; Pred. No. 18;
RESULT 1317
ID AAS88024 standard; cDNA; 14934 BP.
DE DNA encoding novel human diagnostic protein #23828.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 36.4; DB 5; Length 14934;
Best Local Similarity 47.1%; Pred. No. 18;
RESULT 1318
ID AAS87217 standard; cDNA; 14948 BP.
DE DNA encoding novel human diagnostic protein #23021.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 36.4; DB 5; Length 14948;
Best Local Similarity 47.1%; Pred. No. 18;
RESULT 1319
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 36.4; DB 4; Length 68356;
Best Local Similarity 47.1%; Pred. No. 42;
RESULT 1320
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 36.4; DB 4; Length 68356;
Best Local Similarity 47.1%; Pred. No. 42;
RESULT 1321
ID ADQ59443 standard; DNA; 352938 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:79.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 36.4; DB 12; Length 110000;
Best Local Similarity 50.6%; Pred. No. 55;
RESULT 1322
Query Match 3.5%; Score 36.4; DB 12; Length 110000;
Best Local Similarity 50.6%; Pred. No. 55;
RESULT 1323
ID ADJ83982 standard; DNA; 321 BP.
DE HERV-K HML-2 subgroup CORF (Rec) optimised DNA.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 36.2; DB 12; Length 321;
Best Local Similarity 50.3%; Pred. No. 2.5;
RESULT 1324
ID ADJ83984 standard; DNA; 438 BP.
DE HERV-K HML-2 subgroup PCAP5 optimised DNA.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 36.2; DB 12; Length 438;
Best Local Similarity 50.3%; Pred. No. 3;
RESULT 1325
ID ADJ83906 standard; DNA; 2103 BP.
DE HERV-K HML-2 subgroup env (envelope) optimised DNA.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 36.2; DB 12; Length 2103;
Best Local Similarity 50.3%; Pred. No. 7.1;
RESULT 1326
ID ADJ83875 standard; DNA; 4657 BP.
DE HERV-K HML-2 subgroup-related vector pCMVkm2-CORFOpt HML-2 DNA.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 36.2; DB 12; Length 4657;
Best Local Similarity 50.3%; Pred. No. 11;
RESULT 1327
ID ADJ83876 standard; DNA; 4773 BP.
DE HERV-K HML-2 subgroup-related vector pCMVkm2-pCAP5opt HML-2 DNA.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 36.2; DB 12; Length 4773;
Best Local Similarity 50.3%; Pred. No. 11;
RESULT 1328
ID ABD33039 standard; DNA; 33294 BP.
DE Human cancer-associated genomic DNA HD22-025.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 36.2; DB 13; Length 33294;
Best Local Similarity 51.6%; Pred. No. 33;
RESULT 1329
ID ADG48022 standard; DNA; 387 BP.
DE Human variant TTR (C10A/A81C) DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 387;
Best Local Similarity 50.0%; Pred. No. 3.2;
RESULT 1330
ID ADG68778 standard; cDNA; 387 BP.

DE Human mutant transthyretin (TTR) cDNA #4.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 387;
Best Local Similarity 50.0%; Pred. No. 3.2;
RESULT 1331
ID ADG48030 standard; DNA; 489 BP.
DE Human PTH-TTR (C10A/K15A/G83C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 489;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1332
ID ADG48059 standard; DNA; 489 BP.
DE Human PTH-TTR (C10A/K15A/A81C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 489;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1333
ID ADG68786 standard; cDNA; 489 BP.
DE Human mutant transthyretin (TTR) cDNA #12.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 489;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1334
ID ADG48028 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/A81C) variant fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 495;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1335
ID ADG48090 standard; DNA; 495 BP.
DE Human TMP-TTR (C10A/K15A/A81C) fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 495;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1336
ID ADG68784 standard; cDNA; 495 BP.
DE Human mutant transthyretin (TTR) cDNA #10.
PN US2003191056-A1.
PD 09-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 495;
Best Local Similarity 50.0%; Pred. No. 3.7;
RESULT 1337
ID ADG48087 standard; DNA; 510 BP.
DE Human TTR (C10A/K15A/A81C)-TMP fusion DNA.
PN US2003195154-A1.
PD 16-OCT-2003.
PA (WALK/) WALKER K.
PA (XION/) XIONG F.
Query Match 3.5%; Score 36; DB 12; Length 510;
Best Local Similarity 50.0%; Pred. No. 3.8;
RESULT 1338
ID AAL03221 standard; DNA; 1348 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5909.

PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 35.8; DB 4; Length 1348;
Best Local Similarity 59.2%; Pred. No. 7.4;
RESULT 1339
ID ABK74382 standard; DNA; 1731 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #1673.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Query Match 3.5%; Score 35.8; DB 6; Length 1731;
Best Local Similarity 48.3%; Pred. No. 8.5;
RESULT 1340
ID ADG32035 standard; DNA; 2734 BP.
DE DNA encoding a mutant B_licheniformis secreted polypeptide SeqID 5.
PN WO2003093453-A2.
PD 13-NOV-2003.
PA (NOVO) NOVOZYMES AS.
Query Match 3.5%; Score 35.8; DB 12; Length 2734;
Best Local Similarity 48.3%; Pred. No. 11;
RESULT 1341
ID ACD03633 standard; cDNA; 2916 BP.
DE Novel human GPCR related protein NOV9b cDNA.
PN WO200299116-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.5%; Score 35.8; DB 8; Length 2916;
Best Local Similarity 47.2%; Pred. No. 11;
RESULT 1342
ID ADB53259 standard; DNA; 3170 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 35.8; DB 10; Length 3170;
Best Local Similarity 48.3%; Pred. No. 12;
RESULT 1343
ID AAV62739 standard; cDNA; 3997 BP.
DE Human neural cell adhesion molecule NrcAMvar cDNA.
PN WO9836062-A1.
PD 20-AUG-1998.
PA (SMTK) SMITHKLINE BEECHAM PLC.
Query Match 3.5%; Score 35.8; DB 2; Length 3997;
Best Local Similarity 65.8%; Pred. No. 14;
RESULT 1344
ID AAZ38152 standard; DNA; 4134 BP.
DE Human Nr-CAM gene sequence.
PN WO955380-A1.
PD 04-NOV-1999.
PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.
Query Match 3.5%; Score 35.8; DB 3; Length 4134;
Best Local Similarity 65.8%; Pred. No. 14;
RESULT 1345
ID ACN43499 standard; cDNA; 5084 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2374.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5084;
Best Local Similarity 65.8%; Pred. No. 15;
RESULT 1346
ID ACN41814 standard; cDNA; 5126 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:689.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5126;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1347
ID ACN41813 standard; cDNA; 5232 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:688.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5232;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1348
ID ACN43498 standard; cDNA; 5366 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2373.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5366;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1349
ID ACN41812 standard; cDNA; 5371 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:687.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5371;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1350
ID ACN41811 standard; cDNA; 5387 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:686.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5387;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1351
ID ACN43497 standard; cDNA; 5393 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2372.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5393;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1352
ID ACN43496 standard; cDNA; 5396 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2371.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5396;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1353
ID ACN43495 standard; cDNA; 5398 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2370.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 13; Length 5398;
Best Local Similarity 65.8%; Pred. No. 16;
RESULT 1354
ID ADN95537 standard; DNA; 6218 BP.
DE Human BEC/LEC-related gene sequence SeqID460.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 3.5%; Score 35.8; DB 11; Length 6218;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1355
ID ADQ20706 standard; DNA; 6218 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3526.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.5%; Score 35.8; DB 12; Length 6218;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1356
ID ADRI4186 standard; DNA; 6218 BP.
DE Human NF-kappaB pathway-associated gene SeqID187.

PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.5%; Score 35.8; DB 13; Length 6218;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1357
ID ADRI4795 standard; DNA; 6218 BP.
DE Nucleotide sequence of human MAPCAX orthologue #27.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.5%; Score 35.8; DB 13; Length 6218;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1358
ID ADQ24679 standard; DNA; 6234 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7499.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.5%; Score 35.8; DB 12; Length 6234;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1359
ID AAAG4155 standard; cDNA; 6253 BP.
DE Nucleotide sequence of secreted protein clone CO722_1.
PN WO2000050592-A1.
PD 31-AUG-2000.
PA (GENY) GENETICS INST INC.
Query Match 3.5%; Score 35.8; DB 3; Length 6253;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1360
ID AAV40887 standard; cDNA; 6254 BP.
DE Coding sequence of clone CO722_1.
PN WO9824905-A2.
PD 11-JUN-1998.
PA (GENY) GENETICS INST INC.
Query Match 3.5%; Score 35.8; DB 2; Length 6254;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1361
ID AAF98452 standard; cDNA; 6254 BP.
DE Human cDNA clone CO722_1 sequence SEQ ID 129.
PN WO200119988-A1.
PD 22-MAR-2001.
PA (GENY) GENETICS INST INC.
Query Match 3.5%; Score 35.8; DB 5; Length 6254;
Best Local Similarity 65.8%; Pred. No. 17;
RESULT 1362
ID ADE77114 standard; cDNA; 6384 BP.
DE Human cDNA differentially expressed in a liver disorder #206.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 3.5%; Score 35.8; DB 12; Length 6384;
Best Local Similarity 65.8%; Pred. No. 18;
RESULT 1363
ID ADLI2995 standard; cDNA; 6384 BP.
DE Human steroid-induced C3A liver cell cDNA #724.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 12; Length 6384;
Best Local Similarity 65.8%; Pred. No. 18;
RESULT 1364
ID ADJ87608 standard; DNA; 6385 BP.
DE Nervous system disease differentially expressed gene #10.
PN WO2003103474-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 35.8; DB 12; Length 6385;
Best Local Similarity 65.8%; Pred. No. 18;
RESULT 1365
ID AAA01952 standard; cDNA; 718 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1943.
PN WO9958675-A2.

PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.4%; Score 35.6; DB 3; Length 718;
Best Local Similarity 48.6%; Pred. No. 6;
RESULT 1366
ID ACA44307 standard; DNA; 1199 BP.
DE Prokaryotic essential gene #25964.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.4%; Score 35.6; DB 8; Length 1199;
Best Local Similarity 53.6%; Pred. No. 8;
RESULT 1367
ID AAF61080 standard; DNA; 1932 BP.
DE P. putida KT2440-associated DNA ORF09354.
PN DE19935088-A1.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUITA-) QUIAGEN GMBH.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Query Match 3.4%; Score 35.6; DB 4; Length 1932;
Best Local Similarity 53.6%; Pred. No. 10;
RESULT 1368
ID ADB08265 standard; DNA; 2298 BP.
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:2205.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 3.4%; Score 35.6; DB 9; Length 2298;
Best Local Similarity 60.2%; Pred. No. 12;
RESULT 1369
ID ADB08267 standard; DNA; 2298 BP.
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:2207.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 3.4%; Score 35.6; DB 9; Length 2298;
Best Local Similarity 60.2%; Pred. No. 12;
RESULT 1370
ID ABU15322 standard; cDNA; 4734 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40448.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 35.6; DB 4; Length 4734;
Best Local Similarity 57.0%; Pred. No. 17;
RESULT 1371
Query Match 3.4%; Score 35.6; DB 9; Length 110000;
Best Local Similarity 60.2%; Pred. No. 98;
RESULT 1372
ID ABD09108 standard; DNA; 840 BP.
DE Pseudomonas aeruginosa polynucleotide #7712.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35.4; DB 11; Length 840;
Best Local Similarity 44.7%; Pred. No. 7.6;
RESULT 1373
ID ABL24133 standard; DNA; 843 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23872.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 35.4; DB 4; Length 843;
Best Local Similarity 50.3%; Pred. No. 7.6;
RESULT 1374
ID ABD09246 standard; DNA; 1221 BP.
DE Pseudomonas aeruginosa polynucleotide #7850.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35.4; DB 11; Length 1221;
Best Local Similarity 44.7%; Pred. No. 9.4;
RESULT 1375
ID ACH95924 standard; DNA; 3324 BP.
DE Klebsiella pneumoniae polynucleotide seqid 1719.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35.4; DB 11; Length 3324;
Best Local Similarity 45.5%; Pred. No. 16;
RESULT 1376
ID AAA10595 standard; DNA; 6741 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 3.4%; Score 35.4; DB 3; Length 6741;
Best Local Similarity 19.0%; Pred. No. 24;
RESULT 1377
ID ABL20787 standard; DNA; 10242 BP.
DE Drosophila melanogaster genomic polynucleotide seq ID NO 13834.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 35.2; DB 4; Length 10242;
Best Local Similarity 49.0%; Pred. No. 35;
RESULT 1378
ID ABL20786 standard; DNA; 20978 BP.
DE Drosophila melanogaster genomic polynucleotide seq ID NO 13831.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 35.2; DB 4; Length 20978;
Best Local Similarity 49.0%; Pred. No. 52;
RESULT 1379
ID AAQ94572 standard; DNA; 879 BP.
DE Pseudomonas mendocina SD702 lipase gene.
PN WO9514783-A1.
PD 01-JUN-1995.
PA (SHOW) SHOWA DENKO KK.
Query Match 3.4%; Score 35; DB 2; Length 879;
Best Local Similarity 49.2%; Pred. No. 10;
RESULT 1380
ID ABD10093 standard; DNA; 1005 BP.
DE Pseudomonas aeruginosa polynucleotide #8697.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35; DB 11; Length 1005;
Best Local Similarity 47.9%; Pred. No. 11;
RESULT 1381
ID ACA36139 standard; DNA; 1731 BP.
DE Prokaryotic essential gene #17796.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.4%; Score 35; DB 8; Length 1731;
Best Local Similarity 56.5%; Pred. No. 15;
RESULT 1382
ID ACH99754 standard; DNA; 1749 BP.
DE Klebsiella pneumoniae polynucleotide seqid 5549.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35; DB 11; Length 1749;
Best Local Similarity 56.5%; Pred. No. 15;
RESULT 1383
ID ABD10478 standard; DNA; 2706 BP.
DE Pseudomonas aeruginosa polynucleotide #9082.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 35; DB 11; Length 2706;
Best Local Similarity 47.9%; Pred. No. 19;
RESULT 1384
ID ABL16074 standard; DNA; 3693 BP.
DE NOVX related polynucleotide seq ID NO 115.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.4%; Score 35; DB 8; Length 3693;
Best Local Similarity 49.8%; Pred. No. 23;
RESULT 1385
ID ADO41749 standard; cDNA; 3693 BP.
DE Novel human polypeptide NOV37b cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENNA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 3.4%; Score 35; DB 12; Length 3693;
Best Local Similarity 49.8%; Pred. No. 23;
RESULT 1386
ID ADQ23001 standard; DNA; 4053 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5821.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.4%; Score 35; DB 12; Length 4053;
Best Local Similarity 49.8%; Pred. No. 24;
RESULT 1387
ID ABD08895 standard; DNA; 1077 BP.
DE Pseudomonas aeruginosa polynucleotide #7489.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 34.8; DB 11; Length 1077;
Best Local Similarity 50.0%; Pred. No. 13;
RESULT 1388
ID ABL04261 standard; cDNA; 1110 BP.
DE Drosophila melanogaster expressed polynucleotide seq ID NO 7265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 34.8; DB 4; Length 1110;
Best Local Similarity 58.8%; Pred. No. 14;
RESULT 1389
ID AD745810 standard; cDNA; 1242 BP.

DE Bacterial polynucleotide #20561.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.4%; Score 34.8; DB 13; Length 1242;
Best Local Similarity 46.3%; Pred. No. 14;
RESULT 1390
ID ABD08604 standard; DNA; 2748 BP.
DE Pseudomonas aeruginosa polynucleotide #7208.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 34.8; DB 11; Length 2748;
Best Local Similarity 50.0%; Pred. No. 22;
RESULT 1391
ID AAI171055 standard; cDNA; 3357 BP.
DE Benign prostatic hyperplasia associated cDNA clone JTI156897.
PN WO200198456-A2.
PD 27-DEC-2001.
PA (GENE-) GENE LOGIC INC.
PA (NITSB) JAPAN TOBACCO INC.
Query Match 3.4%; Score 34.8; DB 6; Length 3357;
Best Local Similarity 50.9%; Pred. No. 25;
RESULT 1392
ID ABL04260 standard; cDNA; 3426 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 3.4%; Score 34.8; DB 4; Length 3426;
Best Local Similarity 58.8%; Pred. No. 25;
RESULT 1393
ID ABL14607 standard; cDNA; 4645 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38303.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 3.4%; Score 34.8; DB 4; Length 4645;
Best Local Similarity 62.8%; Pred. No. 30;
RESULT 1394
ID ADQ89651 standard; DNA; 4645 BP.
DE Antagonist of cell cycle progression nucleotide sequence #41.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 3.4%; Score 34.8; DB 13; Length 4645;
Best Local Similarity 62.8%; Pred. No. 30;
RESULT 1395
ID ABV99327 standard; DNA; 8554 BP.
DE Human NOVIA coding sequence.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.4%; Score 34.8; DB 6; Length 8554;
Best Local Similarity 50.9%; Pred. No. 42;
RESULT 1396
ID AAS28894 standard; DNA; 8895 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 256.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1397
ID AAS28888 standard; DNA; 8895 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 250.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.4%; Score 34.8; DB 4; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1398
ID ABA06851 standard; DNA; 8895 BP.
DE Human genomic DNA SEQ ID NO: 937.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1399
ID ABA06801 standard; DNA; 8895 BP.
DE Human genomic DNA SEQ ID NO: 887.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1400
ID ABV84188 standard; DNA; 8895 BP.
DE Human polynucleotide SEQ ID NO 937.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.4%; Score 34.8; DB 6; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1401
ID ABV84138 standard; DNA; 8895 BP.
DE Human polynucleotide SEQ ID NO 887.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.4%; Score 34.8; DB 6; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1402
ID ADB31735 standard; DNA; 8895 BP.
DE Human novel protein DNA SEQ ID NO 256.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 10; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1403
ID ADB31729 standard; DNA; 8895 BP.
DE Human novel protein DNA SEQ ID NO 250.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 10; Length 8895;
Best Local Similarity 50.9%; Pred. No. 43;
RESULT 1404
ID ABK90048 standard; DNA; 9109 BP.
DE DNA encoding predicted human adlcan-2 protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 3.4%; Score 34.8; DB 6; Length 9109;
Best Local Similarity 50.9%; Pred. No. 44;
RESULT 1405
ID ADL02249 standard; cDNA; 9109 BP.
DE Human OCP cDNA #9.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 3.4%; Score 34.8; DB 12; Length 9109;
Best Local Similarity 50.9%; Pred. No. 44;
RESULT 1406
ID AAS28884 standard; DNA; 9656 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 246.

PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1407
ID AAS28893 standard; DNA; 9656 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID No 255.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1408
ID ABA06800 standard; DNA; 9656 BP.
DE Human genomic DNA SEQ ID No: 886.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1409
ID ABA06847 standard; DNA; 9656 BP.
DE Human genomic DNA SEQ ID No: 933.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 4; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1410
ID ABV84137 standard; DNA; 9656 BP.
DE Human polynucleotide SEQ ID NO 886.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.4%; Score 34.8; DB 6; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1411
ID ABV84184 standard; DNA; 9656 BP.
DE Human polynucleotide SEQ ID NO 933.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.4%; Score 34.8; DB 6; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1412
ID ADS31734 standard; DNA; 9656 BP.
DE Human novel protein DNA SEQ ID NO 255.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 10; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1413
ID ADS31725 standard; DNA; 9656 BP.
DE Human novel protein DNA SEQ ID NO 246.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 34.8; DB 10; Length 9656;
Best Local Similarity 50.9%; Pred. No. 45;
RESULT 1414
ID ACC00398 standard; cDNA; 10569 BP.
DE Human cell adhesion and extracellular matrix protein, CAECM-7, DNA.
PN WO200302730-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.4%; Score 34.8; DB 8; Length 10569;
Best Local Similarity 50.9%; Pred. No. 47;

RESULT 1415
ID ABL14606 standard; cDNA; 20348 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38300.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 34.8; DB 4; Length 20348;
Best Local Similarity 62.8%; Pred. No. 68;
RESULT 1416
ID ACN45090 standard; DNA; 350764 BP.
DE Human genomic sequence hCG22125.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.4%; Score 34.8; DB 11; Length 110000;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1417
ID AAC70680 standard; DNA; 440 BP.
DE Single nucleotide polymorphism containing sequence #170.
PN WO200058519-A2.
PD 05-OCT-2000.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
Query Match 3.3%; Score 34.6; DB 3; Length 440;
Best Local Similarity 47.8%; Pred. No. 9.4;
RESULT 1418
ID ADK68389 standard; cDNA; 668 BP.
DE Amorphophallus konjac a-Lectin-encoding cDNA.
PN CN1384196-A.
PD 11-DEC-2002.
PA (FUDA-) FUDANDIEN BIOTECHNOLOGY CO LTD SHANGHAI.
Query Match 3.3%; Score 34.6; DB 10; Length 668;
Best Local Similarity 50.9%; Pred. No. 12;
RESULT 1419
ID ABA06474 standard; cDNA; 942 BP.
DE Human cDNA SEQ ID NO: 140.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.6; DB 4; Length 942;
Best Local Similarity 48.6%; Pred. No. 14;
RESULT 1420
ID ABV83811 standard; cDNA; 942 BP.
DE Human polynucleotide SEQ ID NO 140.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 34.6; DB 6; Length 942;
Best Local Similarity 48.6%; Pred. No. 14;
RESULT 1421
ID AAS28819 standard; cDNA; 1020 BP.
DE Human immunoglobulin encoding cDNA SEQ ID No 65.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.6; DB 4; Length 1020;
Best Local Similarity 48.6%; Pred. No. 15;
RESULT 1422
ID ADB31544 standard; cDNA; 1020 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 65.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.6; DB 10; Length 1020;
Best Local Similarity 48.6%; Pred. No. 15;
RESULT 1423
ID ACC59920 standard; cDNA; 1539 BP.
DE Human REMAP-33 encoding cDNA SEQ ID NO:69.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 3.3%; Score 34.6; DB 9; Length 1539;
Best Local Similarity 51.6%; Pred. No. 19;
RESULT 1424
ID ADQ21633 standard; DNA; 3613 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4453.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 34.6; DB 12; Length 3613;
Best Local Similarity 48.6%; Pred. No. 30;
RESULT 1425
ID AAC42222 standard; DNA; 3695 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34740.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 3.3%; Score 34.6; DB 3; Length 3695;
Best Local Similarity 58.1%; Pred. No. 31;
RESULT 1426
ID ADQ25448 standard; DNA; 4176 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8268.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 34.6; DB 12; Length 4176;
Best Local Similarity 48.6%; Pred. No. 33;
RESULT 1427
ID AAS28869 standard; cDNA; 573 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 115.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.4; DB 4; Length 573;
Best Local Similarity 48.0%; Pred. No. 13;
RESULT 1428
ID ABA06680 standard; cDNA; 573 BP.
DE Human cDNA SEQ ID NO: 346.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.4; DB 4; Length 573;
Best Local Similarity 48.0%; Pred. No. 13;
RESULT 1429
ID ABV84017 standard; cDNA; 573 BP.
DE Human polynucleotide SEQ ID NO 346.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 34.4; DB 6; Length 573;
Best Local Similarity 48.0%; Pred. No. 13;
RESULT 1430
ID ADB31594 standard; cDNA; 573 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 115.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 34.4; DB 10; Length 573;
Best Local Similarity 48.0%; Pred. No. 13;
RESULT 1431
ID AA75378 standard; DNA; 1179 BP.
DE Ralstonia eutropha nucleotide sequence #1.
PN WO200111014-A1.
PD 15-FEB-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (RIKE) RIKEN KK.
Query Match 3.3%; Score 34.4; DB 5; Length 1179;
Best Local Similarity 52.0%; Pred. No. 19;
RESULT 1432
ID ABX17282 standard; DNA; 1179 BP.
DE DNA encoding Poly3-hydroxybutanoate synthase associated protein #5.
PN JP2002199890-A.
PD 16-JUL-2002.

PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 3.3%; Score 34.4; DB 6; Length 1179;
Best Local Similarity 52.0%; Pred. No. 19;
RESULT 1433
ID AAR94263 standard; DNA; 1181 BP.
DE Beta-ketothiolase gene, phba.
PN EPI076095-A1.
PD 14-FEB-2001.
PA (RIKE) RIKEN KK.
Query Match 3.3%; Score 34.4; DB 4; Length 1181;
Best Local Similarity 52.0%; Pred. No. 19;
RESULT 1434
ID AAQ67910 standard; DNA; 1182 BP.
DE Alcaligenes eutrophus ketothiolase gene.
PN WO9412014-A1.
PD 09-JUN-1994.
PA (CETU) AGRACETUS INC.
Query Match 3.3%; Score 34.4; DB 2; Length 1182;
Best Local Similarity 52.0%; Pred. No. 19;
RESULT 1435
ID ADP83239 standard; DNA; 1182 BP.
DE PhaA without signal sequence DNA.
PN WO2004006657-A1.
PD 22-JAN-2004.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (UYQU) UNIV QUEENSLAND.
Query Match 3.3%; Score 34.4; DB 12; Length 1182;
Best Local Similarity 52.0%; Pred. No. 19;
RESULT 1436
ID ADP83241 standard; DNA; 1280 BP.
DE Modified PhaA without signal sequence DNA.
PN WO2004006657-A1.
PD 22-JAN-2004.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (UYQU) UNIV QUEENSLAND.
Query Match 3.3%; Score 34.4; DB 12; Length 1280;
Best Local Similarity 52.0%; Pred. No. 20;
RESULT 1437
ID ADF14870 standard; cDNA; 1360 BP.
DE Sunflower resistance gene analogue RS7-4 cDNA #2.
PN US6608240-B1.
PD 19-AUG-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 3.3%; Score 34.4; DB 10; Length 1360;
Best Local Similarity 53.8%; Pred. No. 20;
RESULT 1438
ID ADP83248 standard; DNA; 1428 BP.
DE Full length PhaA DNA.
PN WO2004006657-A1.
PD 22-JAN-2004.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (UYQU) UNIV QUEENSLAND.
Query Match 3.3%; Score 34.4; DB 12; Length 1428;
Best Local Similarity 52.0%; Pred. No. 21;
RESULT 1439
ID AAQ85641 standard; DNA; 1431 BP.
DE Acetyl-CoA-acyltransferase (3-ketothiolase) DNA.
PN WO9505472-A2.
PD 23-FEB-1995.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 3.3%; Score 34.4; DB 2; Length 1431;
Best Local Similarity 52.0%; Pred. No. 21;
RESULT 1440
ID ADP83250 standard; DNA; 1529 BP.
DE Modified full length PhaA DNA.
PN WO2004006657-A1.
PD 22-JAN-2004.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (UYQU) UNIV QUEENSLAND.
Query Match 3.3%; Score 34.4; DB 12; Length 1529;
Best Local Similarity 52.0%; Pred. No. 22;
RESULT 1441
ID AAN91209 standard; DNA; 2327 BP.

DE Beta-ketothiolase and acetyl-CoA reductase genes.
PN W08900202-A.
PD 12-JAN-1989.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.3%; Score 34.4; DB 1; Length 2327;
Best Local Similarity 52.0%; Pred. No. 27;
RESULT 1442
ID AAQ10501 standard; DNA; 2328 BP.
DE Clone pAer3 contg. thiolase and acetoacetyl CoA reductase genes.
PN W09100917-A.
PD 24-JAN-1991.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.3%; Score 34.4; DB 2; Length 2328;
Best Local Similarity 52.0%; Pred. No. 27;
RESULT 1443
ID AA231774 standard; DNA; 2328 BP.
DE Acetoacetyl-CoA reductase, phbB, coding sequence.
PN JP11276180-A.
PD 12-OCT-1999.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (NAKA) NAKASHITA H.
PA (YOSH) YOSHIOKA K.
Query Match 3.3%; Score 34.4; DB 2; Length 2328;
Best Local Similarity 52.0%; Pred. No. 27;
RESULT 1444
ID AAD03827 standard; DNA; 2328 BP.
DE Ralstonia eutropha 3-ketoacyl-CoA reductase DNA.
PN W0200123580-A2.
PD 05-APR-2001.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match 3.3%; Score 34.4; DB 4; Length 2328;
Best Local Similarity 52.0%; Pred. No. 27;
RESULT 1445
ID AAD07038 standard; DNA; 2328 BP.
DE Ralstonia eutropha 3-ketoacyl-CoA reductase DNA.
PN W0200123596-A2.
PD 05-APR-2001.
PA (PTON-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.3%; Score 34.4; DB 4; Length 2328;
Best Local Similarity 52.0%; Pred. No. 27;
RESULT 1446
ID ADF14868 standard; cDNA; 3456 BP.
DE Sunflower resistance gene analogue RS6-8 cDNA #2.
PN US6608240-B1.
PD 19-AUG-2003.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match 3.3%; Score 34.4; DB 10; Length 3456;
Best Local Similarity 53.8%; Pred. No. 34;
RESULT 1447
ID ACC84741 standard; DNA; 4193 BP.
DE R. eutropha PHA biosynthesis-related enzymes (PHAe) gene fragment.
PN W02003046159-A1.
PD 05-JUN-2003.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 3.3%; Score 34.4; DB 9; Length 4193;
Best Local Similarity 52.0%; Pred. No. 38;
RESULT 1448
ID AAQ36660 standard; DNA; 4980 BP.
DE A. eutrophus polyhydroxybutyrate (PHB) operon including PHB synthase gene, the 3-ketothiolase gene and the acetoacetyl-CoA reductase gene.
PN W03020187-A1.
PD 04-FEB-1993.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 3.3%; Score 34.4; DB 2; Length 4980;
Best Local Similarity 52.0%; Pred. No. 42;
RESULT 1449
ID AA178986 standard; DNA; 4984 BP.
DE Polyhydroxyalkanoate biosynthetic operon in pUC18.
PN W09804713-A1.
PD 05-FEB-1998.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.3%; Score 34.4; DB 2; Length 4984;

Best Local Similarity 52.0%; Pred. No. 42;
RESULT 1450
ID AAF84261 standard; DNA; 4984 BP.
DE phb operon.
PN EPI076095-A1.
PD 14-FEB-2001.
PA (RIKE) RIKEN KK.
Query Match 3.3%; Score 34.4; DB 4; Length 4984;
Best Local Similarity 52.0%; Pred. No. 42;
RESULT 1451
ID AAC62287 standard; cDNA; 7928 BP.
DE cDNA encoding a splice variant of a signal transduction polypeptide.
PN W0200063381-A1.
PD 26-OCT-2000.
PA (SCIO-) SCIOS INC.
Query Match 3.3%; Score 34.4; DB 5; Length 7928;
Best Local Similarity 45.5%; Pred. No. 54;
RESULT 1452
ID ABX11641 standard; cDNA; 8106 BP.
DE Human serine/threonine or protein kinase 59079, cDNA.
PN US2002168742-A1.
PD 14-NOV-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 34.4; DB 8; Length 8106;
Best Local Similarity 45.5%; Pred. No. 54;
RESULT 1453
ID ADQ22881 standard; DNA; 20489 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5701.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 34.4; DB 12; Length 20489;
Best Local Similarity 45.5%; Pred. No. 91;
RESULT 1454
ID ABX11642 standard; cDNA; 24120 BP.
DE Human serine/threonine or protein kinase 12599, cDNA.
PN US2002168742-A1.
PD 14-NOV-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 34.4; DB 8; Length 24120;
Best Local Similarity 45.5%; Pred. No. 99;
RESULT 1455
ID ACH39035 standard; cDNA; 458 BP.
DE Human foetal brain cDNA #402.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA) DRMANAC R T.
PA (LABA) LABAT I.
PA (STAC) STACHE-CRAIN B.
PA (DICK) DICKSON M C.
PA (JONE) JONES L W.
Query Match 3.3%; Score 34.2; DB 9; Length 458;
Best Local Similarity 47.0%; Pred. No. 13;
RESULT 1456
ID AAT30562 standard; cDNA; 640 BP.
DE Eukaryotic cell growth inhibiting factor cDNA clone pTB1671.
PN W09617933-A2.
PD 13-JUN-1996.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 3.3%; Score 34.2; DB 2; Length 640;
Best Local Similarity 58.3%; Pred. No. 15;
RESULT 1457
ID ADA69968 standard; DNA; 1353 BP.
DE Rice gene, SEQ ID 3291.
PN W02003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.3%; Score 34.2; DB 8; Length 1353;
Best Local Similarity 48.6%; Pred. No. 23;
RESULT 1458
ID AAA92302 standard; DNA; 31422 BP.
DE S. avermitilis avermectin aglycon synthase DNA aveAII SEQ ID NO:2.
PN W0200050605-A1.

PD 31-AUG-2000.
PA (KITA) KITASATO INST.
Query Match 3.3%; Score 34.2; DB 3; Length 31422;
Best Local Similarity 54.3%; Pred. No. 1.3e+02;
RESULT 1459
ID AAH79278 standard; DNA; 31422 BP.
DE Streptomyces avermitilis coding sequences SEQ ID NO: 2.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 3.3%; Score 34.2; DB 4; Length 31422;
Best Local Similarity 54.3%; Pred. No. 1.3e+02;
RESULT 1460
ID ADL08124 standard; DNA; 176080 BP.
DE Human gene associated with low HDL-C LRPAP1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.3%; Score 34.2; DB 12; Length 176080;
Best Local Similarity 46.8%; Pred. No. 3.4e+02;
RESULT 1461
ID ABL21947 standard; DNA; 648 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17314.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.3%; Score 34; DB 4; Length 648;
Best Local Similarity 54.9%; Pred. No. 18;
RESULT 1462
ID AAC68637 standard; cDNA; 1746 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 5.
PN WO200065055-A2.
PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1746;
Best Local Similarity 45.0%; Pred. No. 31;
RESULT 1463
ID AAC68640 standard; cDNA; 1746 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 11.
PN WO200065055-A2.
PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1746;
Best Local Similarity 45.0%; Pred. No. 31;
RESULT 1464
ID AAC68635 standard; cDNA; 1884 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 1.
PN WO200065055-A2.
PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1884;
Best Local Similarity 45.0%; Pred. No. 32;
RESULT 1465
ID AAC68639 standard; cDNA; 1884 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 9.
PN WO200065055-A2.
PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1884;
Best Local Similarity 45.0%; Pred. No. 32;
RESULT 1466
ID AAC68638 standard; cDNA; 1884 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 7.
PN WO200065055-A2.
PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1884;
Best Local Similarity 45.0%; Pred. No. 32;
RESULT 1467
ID AAC68636 standard; cDNA; 1884 BP.
DE Novel human transporter protein cDNA SEQ ID NO: 3.
PN WO200065055-A2.

PD 02-NOV-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.3%; Score 34; DB 3; Length 1884;
Best Local Similarity 45.0%; Pred. No. 32;
RESULT 1468
ID AAS64404 standard; cDNA; 2631 BP.
DE DNA encoding novel human diagnostic protein #208.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 34; DB 5; Length 2631;
Best Local Similarity 53.8%; Pred. No. 39;
RESULT 1469
ID ABNS9863 standard; cDNA; 2878 BP.
DE Novel human coding sequence SEQ ID NO: 274.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 34; DB 6; Length 2878;
Best Local Similarity 45.0%; Pred. No. 41;
RESULT 1470
ID AAC76422 standard; cDNA; 2900 BP.
DE Human OREF ORF1977 polynucleotide sequence SEQ ID NO:3953.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 3.3%; Score 34; DB 3; Length 2900;
Best Local Similarity 45.0%; Pred. No. 41;
RESULT 1471
ID AAA93125 standard; cDNA; 2927 BP.
DE Human secreted protein coding sequence SEQ ID NO: 49.
PN WO200049134-A1.
PD 24-AUG-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 3.3%; Score 34; DB 3; Length 2927;
Best Local Similarity 45.0%; Pred. No. 41;
RESULT 1472
ID ABL21946 standard; DNA; 3470 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17311.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.3%; Score 34; DB 4; Length 3470;
Best Local Similarity 54.9%; Pred. No. 45;
RESULT 1473
ID AAI67897 standard; DNA; 4341 BP.
DE Nucleotide sequence of codon optimised sequence Id No. 3.
PN EP1156112-A1.
PD 21-NOV-2001.
PA (GENE-) GENEART GMBH.
Query Match 3.3%; Score 34; DB 6; Length 4341;
Best Local Similarity 51.3%; Pred. No. 51;
RESULT 1474
ID AAI67896 standard; DNA; 4343 BP.
DE Nucleotide sequence of optimised GagPol HIV-1IIB.
PN EP1156112-A1.
PD 21-NOV-2001.
PA (GENE-) GENEART GMBH.
Query Match 3.3%; Score 34; DB 6; Length 4343;
Best Local Similarity 51.3%; Pred. No. 51;
RESULT 1475
ID ABS67999 standard; cDNA; 4376 BP.
DE DNA encoding IE B-domain-deleted-Factor VIII (FVIII).
PN WO200264799-A2.
PD 22-AUG-2002.
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
Query Match 3.3%; Score 34; DB 6; Length 4376;
Best Local Similarity 47.2%; Pred. No. 51;
RESULT 1476
ID ABS68000 standard; cDNA; 4384 BP.
DE DNA encoding 5Arg B-domain-deleted-Factor VIII (FVIII).
PN WO200264799-A2.
PD 22-AUG-2002.

PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
Query Match 3.3%; Score 34; DB 6; Length 4384;
Best Local Similarity 47.2%; Pred. No. 52;
RESULT 1477
ID ACN44332 standard; DNA; 114633 BP.
DE Mouse genomic sequence MCG17870.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 34; DB 11; Length 114633;
Best Local Similarity 61.1%; Pred. No. 3.1e+02;
RESULT 1478
ID ADP43517 standard; DNA; 347001 BP.
DE Human MAD1-like 1 DNA #7.
PN US2004115650-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 34; DB 12; Length 347001;
Best Local Similarity 49.4%; Pred. No. 5.7e+02;
RESULT 1479
ID ACH82331 standard; DNA; 315 BP.
DE Human genome derived single exon probe #15526.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.3%; Score 33.8; DB 12; Length 315;
Best Local Similarity 56.9%; Pred. No. 14;
RESULT 1480
ID ABA54256 standard; DNA; 461 BP.
DE Human foetal liver single exon nucleic acid probe #2561.
PN WO200357277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.3%; Score 33.8; DB 4; Length 461;
Best Local Similarity 56.9%; Pred. No. 17;
RESULT 1481
ID ABA43797 standard; DNA; 461 BP.
DE Human breast cell single exon nucleic acid probe #2492.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.3%; Score 33.8; DB 4; Length 461;
Best Local Similarity 56.9%; Pred. No. 17;
RESULT 1482
ID ABA24007 standard; DNA; 461 BP.
DE Probe #2473 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.3%; Score 33.8; DB 4; Length 461;
Best Local Similarity 56.9%; Pred. No. 17;
RESULT 1483
ID ABS27557 standard; DNA; 461 BP.
DE Human liver single exon probe, SEQ ID NO 2547.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.3%; Score 33.8; DB 4; Length 461;
Best Local Similarity 56.9%; Pred. No. 17;
RESULT 1484
ID AAI02459 standard; DNA; 461 BP.
DE Probe #2450 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.3%; Score 33.8; DB 5; Length 461;
Best Local Similarity 56.9%; Pred. No. 17;
RESULT 1485
ID ACH68631 standard; DNA; 566 BP.
DE Human genome derived single exon probe #1826.
PN US2003194704-A1.

PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.3%; Score 33.8; DB 12; Length 566;
Best Local Similarity 56.9%; Pred. No. 19;
RESULT 1486
ID ADS57570 standard; cDNA; 772 BP.
DE Bacterial polynucleotide #9557.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.3%; Score 33.8; DB 13; Length 772;
Best Local Similarity 51.0%; Pred. No. 23;
RESULT 1487
ID ADE52373 standard; cDNA; 1029 BP.
DE Mouse C5L2 receptor encoding cDNA.
PN WO2003100439-A2.
PD 04-DEC-2003.
PA (UYSH-) UNIV SHEFFIELD.
Query Match 3.3%; Score 33.8; DB 12; Length 1029;
Best Local Similarity 48.2%; Pred. No. 27;
RESULT 1488
ID ADO30229 standard; cDNA; 1032 BP.
DE Mouse GPCR GPR77 polynucleotide, SEQ ID NO:1332.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 3.3%; Score 33.8; DB 12; Length 1032;
Best Local Similarity 48.2%; Pred. No. 27;
RESULT 1489
ID AAA30433 standard; cDNA; 1122 BP.
DE Human ACAM#6 PCR product.
PN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.3%; Score 33.8; DB 3; Length 1122;
Best Local Similarity 54.4%; Pred. No. 28;
RESULT 1490
ID AAT29035 standard; cDNA; 1321 BP.
DE Endoglucanase (60 kDa Family 5 cellulase) cDNA sequence.
PN WO9611262-A1.
PD 18-APR-1996.
PA (NOVO) NOVO-NORDISK AS.
Query Match 3.3%; Score 33.8; DB 2; Length 1321;
Best Local Similarity 49.2%; Pred. No. 31;
RESULT 1491
ID ABD12458 standard; DNA; 1416 BP.
DE Pseudomonas aeruginosa polynucleotide #11062.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.3%; Score 33.8; DB 11; Length 1416;
Best Local Similarity 47.4%; Pred. No. 32;
RESULT 1492
ID AAS26547 standard; cDNA; 1646 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 726.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 33.8; DB 4; Length 1646;
Best Local Similarity 58.4%; Pred. No. 35;
RESULT 1493
ID ABX73888 standard; DNA; 1646 BP.
DE Human novel polynucleotide #716.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.
Query Match 3.3%; Score 33.8; DB 8; Length 1646;
Best Local Similarity 58.4%; Pred. No. 35;
RESULT 1494
ID AAA30440 standard; cDNA; 1694 BP.
DE Human cDNA sequence encoding ACAM4/IgG4-Fc fusion protein.
FN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.3%; Score 33.8; DB 3; Length 1694;
Best Local Similarity 54.4%; Pred. No. 35;
RESULT 1495
ID ABD12590 standard; DNA; 1761 BP.
DE Pseudomonas aeruginosa polynucleotide #11194.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.3%; Score 33.8; DB 11; Length 1761;
Best Local Similarity 47.4%; Pred. No. 36;
RESULT 1496
ID ADS56267 standard; cDNA; 1770 BP.
DE Bacterial polynucleotide #8254.
FN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.3%; Score 33.8; DB 13; Length 1770;
Best Local Similarity 48.2%; Pred. No. 36;
RESULT 1497
ID AAA30436 standard; cDNA; 1796 BP.
DE Human cDNA sequence encoding ACAM6/IgG4-Fc fusion protein.
FN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.3%; Score 33.8; DB 3; Length 1796;
Best Local Similarity 54.4%; Pred. No. 36;
RESULT 1498
ID AAA30439 standard; cDNA; 1900 BP.
DE Human cDNA sequence encoding ACAM4/IgG1-Fc fusion protein.
FN WO200032633-A1.
PD 08-JUN-2000.
PA (ICOS-) ICOS CORP.
Query Match 3.3%; Score 33.8; DB 3; Length 1900;
Best Local Similarity 54.4%; Pred. No. 37;
RESULT 1499
ID ADB53599 standard; DNA; 2196 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4141.
FN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 33.8; DB 10; Length 2196;
Best Local Similarity 54.4%; Pred. No. 41;
RESULT 1500
ID AAT86704 standard; DNA; 3147 BP.
DE DNA encoding thermostable esterase TspA E101.
FN WO9725058-A1.
PD 17-JUL-1997.
PA (THER-) THERMOGEN INC.
Query Match 3.3%; Score 33.8; DB 2; Length 3147;
Best Local Similarity 50.3%; Pred. No. 49;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2005, 03:13:42 ; Search time 187.627 Seconds
(without alignments)
9026.128 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 atgaacaaccatccagccaaa.....acctgcttctcaatttga 1035

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents_NA.*

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5: /cgm2_6/ptodata/1/ina/ECTUS_COMB.seq.*
6: /cgm2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1032	99.7	1032	4	US-09-700-397-1
3	939	90.7	939	4	US-09-700-397-5
4	342	33.0	1238	2	US-08-414-657D-3
5	342	33.0	1238	3	US-09-135-080-3
6	340.6	32.9	924	2	US-08-414-657D-7
7	340.6	32.9	977	2	US-08-414-657D-1
8	340.6	32.9	977	3	US-09-135-080-1
9	340.6	32.9	1014	2	US-08-414-657D-5
10	340.6	32.9	1014	3	US-09-135-080-7
11	340.6	32.9	1195	4	US-09-976-594-403
12	338.6	32.7	861	2	US-08-414-657D-9
13	338.6	32.7	912	2	US-08-414-657D-6
14	337.4	32.6	945	2	US-08-414-657D-8
15	333.8	32.3	861	2	US-08-414-657D-10
16	316.2	30.6	333	4	US-09-513-999C-23289
17	303.6	29.3	756	2	US-08-414-657D-11
18	298.2	28.8	756	2	US-08-414-657D-12
19	279	27.0	1030	4	US-09-949-016-4587
20	193.6	18.7	352	4	US-09-513-999C-2775
21	105.6	10.2	913	4	US-09-774-528-410
22	100	9.7	219	2	US-08-414-657D-11
23	95.2	9.2	219	2	US-08-414-657D-12
24	78.6	7.6	113538	4	US-09-949-016-16329
25	77.8	7.5	177	2	US-08-414-657D-13
26	77.8	7.5	177	2	US-08-414-657D-14
27	76.8	7.4	601	4	US-09-949-016-163724

c

28	65.6	6.3	198	2	US-08-414-657D-15	Sequence 15, Appl
29	63.4	6.1	198	2	US-08-414-657D-16	Sequence 16, Appl
30	45.4	4.4	7218	1	US-08-232-463-14	Sequence 14, Appl
31	42.4	4.1	4548	4	US-09-571-479C-5	Sequence 5, Appl
32	41.2	4.0	2599	4	US-09-949-016-4676	Sequence 4676, Ap
33	41.2	4.0	2633	4	US-09-023-655-950	Sequence 950, App
34	41.2	4.0	5807	4	US-09-976-594-245	Sequence 245, App
35	40.2	3.9	5506	4	US-09-976-594-530	Sequence 530, App
36	39	3.8	3450	4	US-09-902-540-9001	Sequence 9001, Ap
37	39	3.8	7305	4	US-09-902-540-961	Sequence 961, App
38	38.4	3.7	366	4	US-09-252-991A-620	Sequence 620, App
39	38.4	3.7	366	4	US-09-134-000C-13	Sequence 13, Appl
40	38.4	3.7	591	4	US-09-134-000C-11	Sequence 11, Appl
41	38.4	3.7	912	4	US-09-252-991A-774	Sequence 774, App
42	38.4	3.7	948	4	US-09-252-991A-643	Sequence 643, App
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44	38.4	3.7	4943	4	US-09-677-046A-7	Sequence 7, Appl
45	38.4	3.7	5170	4	US-09-677-046A-5	Sequence 5, Appl
46	38.4	3.7	41798	4	US-09-949-016-16058	Sequence 16058, A
47	37.6	3.6	572	4	US-09-919-039-1	Sequence 1, Appl
48	37.6	3.6	615	4	US-09-949-016-2355	Sequence 2355, Ap
49	37.2	3.6	474	4	US-09-621-976-18033	Sequence 18033, A
50	37	3.6	1884	4	US-09-902-540-3055	Sequence 3055, Ap
51	37	3.6	4092	2	US-08-469-537A-106	Sequence 106, App
52	37	3.6	6713	4	US-09-902-540-793	Sequence 793, App
53	36.8	3.6	546	4	US-09-252-991A-9967	Sequence 9967, Ap
54	36.8	3.6	1350	4	US-09-252-991A-10184	Sequence 10184, A
55	36.8	3.6	3639	4	US-09-252-991A-10045	Sequence 10045, A
56	36.8	3.6	3717	4	US-09-252-991A-9792	Sequence 9792, A
57	36.8	3.6	5220	4	US-09-677-046A-1	Sequence 1, Appl
58	36.4	3.5	1542	4	US-09-205-258-123	Sequence 123, App
59	36.4	3.5	1685	4	US-09-907-794A-83	Sequence 83, Appl
60	36.4	3.5	1685	4	US-09-905-125A-83	Sequence 83, Appl
61	36.4	3.5	1685	4	US-09-902-775A-83	Sequence 83, Appl
62	36.4	3.5	1685	4	US-09-905-700-83	Sequence 83, Appl
63	36.4	3.5	1685	4	US-09-903-603A-83	Sequence 83, Appl
64	36.4	3.5	1685	4	US-09-904-920A-83	Sequence 84, Appl
65	36.4	3.5	1685	4	US-09-909-064-83	Sequence 83, Appl
66	36.4	3.5	1685	4	US-09-905-381A-83	Sequence 83, Appl
67	36.4	3.5	1685	4	US-09-906-618-83	Sequence 83, Appl
68	36.4	3.5	1718	4	US-09-778-510-5	Sequence 5, Appl
69	36.4	3.5	1820	4	US-09-778-510-1	Sequence 1, Appl
70	36.2	3.5	801	4	US-09-902-540-2454	Sequence 2454, Ap
71	36.2	3.5	2631	4	US-09-949-016-4987	Sequence 4987, Ap
72	36.2	3.5	11620	4	US-09-902-540-1010	Sequence 1010, Ap
73	35.8	3.5	601	4	US-09-949-016-31698	Sequence 31698, A
74	35.8	3.5	601	4	US-09-949-016-199396	Sequence 199396,
75	35.8	3.5	5905	4	US-09-949-016-5625	Sequence 5625, Ap
76	35.8	3.5	6218	4	US-09-949-016-706	Sequence 706, App
77	35.8	3.5	6384	4	US-09-976-594-724	Sequence 724, App
78	35.8	3.5	6384	4	US-09-919-039-279	Sequence 279, App
79	35.8	3.5	102520	4	US-09-949-016-17367	Sequence 17367, A
80	35.8	3.5	102526	4	US-09-949-016-12448	Sequence 12448, A
81	35.8	3.5	119032	4	US-09-949-016-12160	Sequence 12160, A
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86	35	3.4	1005	4	US-09-252-991A-8697	Sequence 8697, Ap
87	35	3.4	1749	4	US-09-489-039A-5549	Sequence 5549, Ap
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91	34.6	3.3	309	4	US-09-902-540-7628	Sequence 7628, Ap
92	34.6	3.3	5308	4	US-09-902-540-750	Sequence 750, App
93	34.4	3.3	1181	4	US-09-635-132-3	Sequence 3, Appl
94	34.4	3.3	1182	1	US-08-241-943-23	Sequence 23, Appl
95	34.4	3.3	1360	4	US-09-602-472A-14	Sequence 14, Appl
96	34.4	3.3	1431	1	US-08-254-357-1	Sequence 1, Appl
97	34.4	3.3	2327	6	5229279-5	Patent No. 5229279
98	34.4	3.3	2327	6	5512669-5	Patent No. 5512669
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101	34.4	3.3	2328	4	US-09-672-749-11	Sequence 11, Appl	c 174	32.6	3.1	59252	4	US-09-949-016-15374	Sequence 15374, A
102	34.4	3.3	3456	4	US-09-602-472A-12	Sequence 12, Appl	175	32.4	3.1	399	4	US-09-621-976-8976	Sequence 8976, Ap
103	34.4	3.3	4983	1	US-08-472-358-1	Sequence 1, Appl	176	32.4	3.1	879	4	US-09-489-039A-4233	Sequence 4233, Ap
104	34.4	3.3	4983	5	PCT-US92-05786A-1	Sequence 1, Appl	177	32.4	3.1	1173	2	US-08-614-156B-2	Sequence 2, Appl
105	34.4	3.3	4984	1	US-08-687-806-1	Sequence 1, Appl	178	32.4	3.1	1173	4	US-09-949-016-80	Sequence 80, Appl
106	34.4	3.3	4984	4	US-09-635-132-1	Sequence 1, Appl	179	32.4	3.1	1173	4	US-09-949-016-2243	Sequence 2243, Ap
107	34.4	3.3	12738	4	US-09-754-112A-1	Sequence 1, Appl	c 180	32.4	3.1	1410	4	US-09-252-991A-10013	Sequence 10013, A
108	34	3.3	1141	4	US-09-806-708B-22	Sequence 22, Appl	181	32.4	3.1	1426	4	US-09-638-649-2	Sequence 2, Appl
109	34	3.3	1746	4	US-09-556-916-5	Sequence 5, Appl	182	32.4	3.1	1426	4	US-09-638-648-2	Sequence 2, Appl
110	34	3.3	1746	4	US-09-556-916-11	Sequence 11, Appl	183	32.4	3.1	1533	4	US-09-252-991A-10092	Sequence 10092, A
111	34	3.3	1884	4	US-09-556-916-1	Sequence 1, Appl	184	32.4	3.1	1750	4	US-09-949-016-2361	Sequence 2361, Ap
112	34	3.3	1884	4	US-09-556-916-3	Sequence 3, Appl	185	32.4	3.1	1826	4	US-09-220-132-78	Sequence 78, Appl
113	34	3.3	1884	4	US-09-556-916-7	Sequence 7, Appl	186	32.4	3.1	1862	1	US-07-864-475A-1	Sequence 1, Appl
114	34	3.3	1884	4	US-09-556-916-9	Sequence 9, Appl	187	32.4	3.1	1862	2	US-08-468-249A-1	Sequence 1, Appl
115	34	3.3	2286	4	US-09-556-916-2290	Sequence 2290, Ap	188	32.4	3.1	1863	1	US-07-864-475A-2	Sequence 2, Appl
116	34	3.3	2900	4	US-09-949-016-969	Sequence 969, App	189	32.4	3.1	1863	2	US-08-468-249A-2	Sequence 2, Appl
117	33.8	3.3	601	4	US-09-949-016-50665	Sequence 50665, A	190	32.4	3.1	1917	4	US-09-252-991A-10026	Sequence 10026, A
118	33.8	3.3	1321	2	US-08-809-763-6	Sequence 6, Appl	191	32.4	3.1	2298	4	US-09-252-991A-12254	Sequence 12254, A
119	33.8	3.3	1321	3	US-08-956-253-6	Sequence 6, Appl	c 192	32.4	3.1	2346	4	US-09-252-991A-12355	Sequence 12355, A
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121	33.8	3.3	1761	4	US-09-252-991A-11194	Sequence 11194, A	194	32.4	3.1	2934	3	US-08-206-942-52	Sequence 52, Appl
122	33.8	3.3	3147	2	US-08-781-802-7	Sequence 7, Appl	195	32.4	3.1	2952	3	US-09-206-942-50	Sequence 50, Appl
123	33.8	3.3	3147	3	US-08-694-078-7	Sequence 7, Appl	196	32.4	3.1	3015	3	US-09-206-942-56	Sequence 56, Appl
124	33.8	3.3	3147	3	US-09-058-260-7	Sequence 7, Appl	197	32.4	3.1	3018	3	US-09-206-942-40	Sequence 40, Appl
125	33.8	3.3	6814	3	US-09-484-970B-66	Sequence 66, Appl	198	32.4	3.1	3033	3	US-09-206-942-54	Sequence 54, Appl
126	33.8	3.3	10925	4	US-09-949-016-13210	Sequence 13210, A	199	32.4	3.1	3036	3	US-09-206-942-38	Sequence 38, Appl
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128	33.6	3.2	1176	3	US-08-911-853-34	Sequence 34, Appl	201	32.4	3.1	5173	4	US-09-949-016-13985	Sequence 13985, A
129	33.6	3.2	1176	3	US-09-479-409-34	Sequence 34, Appl	202	32.4	3.1	5641	4	US-09-902-540-767	Sequence 767, App
130	33.6	3.2	1176	3	US-09-479-453-34	Sequence 34, Appl	203	32.4	3.1	18031	4	US-09-902-540-1180	Sequence 1180, Ap
131	33.6	3.2	17612	3	US-08-911-853-29	Sequence 29, Appl	204	32.4	3.1	18094	4	US-09-949-016-13179	Sequence 13179, A
132	33.6	3.2	17612	3	US-09-479-409-29	Sequence 29, Appl	c 205	32.4	3.1	54444	4	US-09-949-016-17344	Sequence 17344, A
133	33.6	3.2	17612	3	US-09-479-433-29	Sequence 29, Appl	206	32.4	3.1	66065	4	US-09-949-016-13292	Sequence 13292, A
134	33.6	3.2	767677	4	US-09-949-016-12147	Sequence 12147, A	c 207	32.4	3.1	139552	4	US-09-949-016-15300	Sequence 15300, A
135	33.6	3.2	767677	4	US-09-949-016-17361	Sequence 17361, A	208	32.4	3.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
136	33.4	3.2	1509	1	US-08-115-052-1	Sequence 1, Appl	209	32.4	3.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
137	33.4	3.2	2856	4	US-09-902-540-3022	Sequence 3022, Ap	210	32.2	3.1	1062	4	US-09-902-540-4962	Sequence 4962, Ap
138	33.4	3.2	3542	4	US-09-902-540-642	Sequence 642, App	211	32.2	3.1	1438	4	US-08-755-235-1	Sequence 1, Appl
139	33.2	3.2	362	4	US-09-270-767-14941	Sequence 14941, A	c 212	32.2	3.1	1479	4	US-09-902-540-7414	Sequence 7414, Ap
140	33.2	3.2	1033	2	US-08-414-657D-19	Sequence 19, Appl	213	32.2	3.1	1721	1	US-07-828-980A-1	Sequence 1, Appl
141	33.2	3.2	1851	4	US-08-414-657D-20	Sequence 20, Appl	214	32.2	3.1	2294	4	US-09-270-767-10469	Sequence 10469, A
142	33.2	3.2	1851	3	US-09-135-080-5	Sequence 5, Appl	c 215	32.2	3.1	5245	4	US-09-902-540-714	Sequence 714, App
143	33.2	3.2	3551	4	US-09-620-312D-760	Sequence 760, App	216	32.2	3.1	13299	4	US-09-902-540-968	Sequence 968, App
144	33.2	3.2	360470	4	US-09-949-016-13173	Sequence 13173, A	c 217	32.2	3.1	27219	4	US-09-902-540-1244	Sequence 1244, Ap
145	33	3.2	642	4	US-09-902-540-9027	Sequence 9027, Ap	218	32	3.1	474	4	US-09-902-540-8781	Sequence 8781, Ap
146	33	3.2	1194	4	US-09-489-039A-5294	Sequence 5294, Ap	c 219	32	3.1	601	4	US-09-949-016-125997	Sequence 125997, A
147	33	3.2	1693	3	US-09-320-878-23	Sequence 23, Appl	220	32	3.1	601	4	US-09-949-016-172806	Sequence 172806, A
148	33	3.2	1693	4	US-09-141-908-19	Sequence 19, Appl	221	32	3.1	601	4	US-09-949-016-172807	Sequence 172807, A
149	33	3.2	1693	4	US-09-657-440-23	Sequence 23, Appl	222	32	3.1	1062	4	US-09-902-540-3810	Sequence 3810, Ap
150	33	3.2	3027	2	US-08-680-326-23	Sequence 23, Appl	223	32	3.1	1080	4	US-09-902-540-9563	Sequence 9563, Ap
151	33	3.2	10085	4	US-09-902-540-964	Sequence 964, App	224	32	3.1	1293	2	US-08-924-440-1	Sequence 1, Appl
152	32.8	3.2	1026	4	US-09-902-540-4176	Sequence 4176, Ap	225	32	3.1	1795	4	US-09-902-540-3151	Sequence 3151, Ap
153	32.8	3.2	1168	3	US-09-484-970B-89	Sequence 89, Appl	226	32	3.1	3943	3	US-08-506-296B-27	Sequence 27, Appl
154	32.8	3.2	3318	4	US-09-949-016-14450	Sequence 4450, Ap	227	32	3.1	4078	4	US-09-016-434-1120	Sequence 1120, Ap
155	32.8	3.2	3360	1	US-08-408-093-5	Sequence 5, Appl	228	32	3.1	4202	4	US-09-620-312D-1040	Sequence 1040, Ap
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157	32.8	3.2	3360	1	US-08-714-901-5	Sequence 5, Appl	c 230	32	3.1	7170	4	US-09-902-540-933	Sequence 933, App
158	32.8	3.2	3360	4	US-08-040-741-5	Sequence 5, Appl	231	32	3.1	9165	4	US-09-902-540-1050	Sequence 1050, Ap
159	32.8	3.2	23201	4	US-09-902-540-1208	Sequence 1208, Ap	232	32	3.1	9165	4	US-09-902-540-1087	Sequence 1087, Ap
160	32.6	3.1	601	4	US-09-949-016-128265	Sequence 128265, A	c 233	32	3.1	14823	4	US-09-902-540-1143	Sequence 1143, Ap
161	32.6	3.1	601	4	US-09-949-016-128266	Sequence 128266, A	234	32	3.1	19598	4	US-09-902-540-1143	Sequence 1143, Ap
162	32.6	3.1	978	4	US-09-252-991A-1439	Sequence 1439, Ap	235	32	3.1	21010	4	US-09-902-540-1188	Sequence 1188, Ap
163	32.6	3.1	1839	4	US-09-252-991A-1273	Sequence 1273, Ap	236	32	3.1	27219	4	US-09-902-540-1244	Sequence 1244, Ap
164	32.6	3.1	1980	4	US-09-252-991A-1333	Sequence 1333, Ap	c 237	32	3.1	74790	4	US-09-949-016-13613	Sequence 13613, A
165	32.6	3.1	2181	4	US-09-252-991A-9840	Sequence 9840, Ap	238	32	3.1	76281	4	US-09-949-016-152708	Sequence 152708, A
166	32.6	3.1	2331	4	US-09-252-991A-10146	Sequence 10146, A	c 239	32	3.1	86273	4	US-09-949-016-15273	Sequence 15273, A
167	32.6	3.1	4026	4	US-09-252-991A-10214	Sequence 10214, A	240	32	3.1	86439	4	US-09-949-016-11945	Sequence 11945, A
168	32.6	3.1	4608	3	US-09-041-886-24	Sequence 24, Appl	241	32	3.1	86440	4	US-09-949-016-16990	Sequence 16990, A
169	32.6	3.1	4608	5	PCT-US94-05277-1	Sequence 1, Appl	c 242	32	3.1	99828	4	US-09-949-016-16630	Sequence 16630, A
170	32.6	3.1	4848	3	US-08-955-957A-1	Sequence 1, Appl	c 243	31.8	3.1	601	4	US-09-949-016-157961	Sequence 157961, A
171	32.6	3.1	4848	3	US-08-955-957A-4	Sequence 4, Appl	c 244	31.8	3.1	939	4	US-09-252-991A-2586	Sequence 2586, Ap
172	32.6	3.1	4848	3	US-08-955-957A-6	Sequence 6, Appl	c 245	31.8	3.1	1233	4	US-09-252-991A-2330	Sequence 2330, Ap
173	32.6	3.1	59252	4	US-09-949-016-12150	Sequence 12150, A	246	31.8	3.1	1847	4	US-09-949-016-5449	Sequence 5449, Ap

247	31.8	3.1	4111	4	US-09-375-248-1	Sequence 1, Appli	Sequence 1, Appli	320	31.2	3.0	1388	4	US-09-902-540-8495	Sequence 8495, Ap
248	31.8	3.1	4195	3	US-08-340-011-1	Sequence 1, Appli	Sequence 1, Appli	321	31.2	3.0	1638	4	US-09-902-540-6292	Sequence 6292, Ap
249	31.8	3.1	4195	3	US-08-901-710-1	Sequence 1, Appli	Sequence 1, Appli	c 322	31.2	3.0	1746	4	US-09-252-991A-10643	Sequence 10643, A
250	31.8	3.1	4195	4	US-09-169-079-1	Sequence 1, Appli	Sequence 1, Appli	323	31.2	3.0	2418	4	US-09-949-016-1694	Sequence 1694, Ap
251	31.8	3.1	4416	3	US-08-795-430-1	Sequence 1, Appli	Sequence 1, Appli	324	31.2	3.0	2979	4	US-09-252-991A-10524	Sequence 10524, A
252	31.8	3.1	4416	3	US-09-355-700-1	Sequence 1, Appli	Sequence 1, Appli	c 325	31.2	3.0	3626	4	US-09-902-540-444	Sequence 444, App
253	31.8	3.1	4416	3	US-08-601-132-36	Sequence 36, Appli	Sequence 36, Appli	c 326	31.2	3.0	3991	3	US-08-506-296B-3	Sequence 3, Appli
254	31.8	3.1	4416	4	US-08-671-573B-36	Sequence 36, Appli	Sequence 36, Appli	c 327	31.2	3.0	4843	3	US-08-986-485-1	Sequence 1, Appli
255	31.8	3.1	4416	4	US-09-631-092B-36	Sequence 36, Appli	Sequence 36, Appli	c 328	31.2	3.0	7538	4	US-09-902-540-894	Sequence 894, App
256	31.8	3.1	4416	4	US-09-534-376A-1	Sequence 1, Appli	Sequence 1, Appli	c 329	31.2	3.0	13332	4	US-09-902-540-1047	Sequence 1047, Ap
257	31.8	3.1	4425	1	US-08-222-616-31	Sequence 31, Appli	Sequence 31, Appli	330	31.2	3.0	30001	1	US-08-125-468-1	Sequence 1, Appli
258	31.8	3.1	4425	3	US-08-446-648-31	Sequence 31, Appli	Sequence 31, Appli	331	31.2	3.0	30001	2	US-08-474-933-1	Sequence 1, Appli
259	31.8	3.1	4425	4	US-09-023-655-889	Sequence 889, App	Sequence 889, App	332	31.2	3.0	45469	4	US-09-949-016-13398	Sequence 13398, A
260	31.8	3.1	4425	3	US-09-982-610-31	Sequence 31, Appli	Sequence 31, Appli	333	31.2	3.0	68580	4	US-09-949-016-15844	Sequence 15844, A
261	31.8	3.1	4425	5	PCT-US95-04228-31	Sequence 31, Appli	Sequence 31, Appli	c 334	31.2	3.0	385136	4	US-09-949-016-16073	Sequence 16073, A
262	31.8	3.1	4716	4	US-09-902-540-3779	Sequence 3779, Ap	Sequence 3779, Ap	335	31	3.0	352	3	US-09-060-756-478	Sequence 478, App
263	31.8	3.1	4795	1	US-08-340-011-3	Sequence 3, Appli	Sequence 3, Appli	336	31	3.0	352	4	US-09-670-314-478	Sequence 478, App
264	31.8	3.1	4795	3	US-08-901-710-3	Sequence 3, Appli	Sequence 3, Appli	c 337	31	3.0	501	4	US-09-252-991A-11149	Sequence 11149, A
265	31.8	3.1	4795	4	US-09-169-079-3	Sequence 3, Appli	Sequence 3, Appli	338	31	3.0	861	4	US-09-489-039A-1499	Sequence 1499, Ap
266	31.8	3.1	9108	3	US-08-446-648-45	Sequence 45, Appli	Sequence 45, Appli	339	31	3.0	888	4	US-09-902-540-9355	Sequence 9355, Ap
267	31.8	3.1	9108	4	US-09-982-610-45	Sequence 45, Appli	Sequence 45, Appli	340	31	3.0	1020	4	US-09-489-039A-1488	Sequence 1488, Ap
268	31.8	3.1	9108	5	PCT-US95-04228-45	Sequence 45, Appli	Sequence 45, Appli	341	31	3.0	1140	3	US-09-023-173-4	Sequence 4, Appli
269	31.8	3.1	20721	4	US-09-949-016-16257	Sequence 16257, A	Sequence 16257, A	342	31	3.0	1301	2	US-08-641-314C-1	Sequence 1, Appli
270	31.8	3.1	23233	4	US-09-902-540-1184	Sequence 1184, Ap	Sequence 1184, Ap	343	31	3.0	1401	4	US-09-252-991A-10908	Sequence 10908, A
271	31.8	3.1	34094	4	US-09-292-034-1	Sequence 1, Appli	Sequence 1, Appli	344	31	3.0	1440	4	US-09-252-991A-11041	Sequence 11041, A
272	31.6	3.1	601	4	US-09-949-016-32897	Sequence 32897, A	Sequence 32897, A	c 345	31	3.0	1788	4	US-09-252-991A-16032	Sequence 4632, Ap
273	31.6	3.1	601	4	US-09-949-016-67210	Sequence 67210, A	Sequence 67210, A	346	31	3.0	1965	4	US-09-902-540-8991	Sequence 8991, Ap
274	31.6	3.1	984	4	US-09-489-039A-3507	Sequence 3507, Ap	Sequence 3507, Ap	347	31	3.0	2250	4	US-09-252-991A-4181	Sequence 4181, Ap
275	31.6	3.1	1147	4	US-09-270-767-11931	Sequence 11931, A	Sequence 11931, A	348	31	3.0	2949	3	US-09-412-554A-3	Sequence 3, Appli
276	31.6	3.1	1317	4	US-09-252-991A-187	Sequence 187, App	Sequence 187, App	c 349	31	3.0	3102	4	US-09-252-991A-4429	Sequence 4429, Ap
277	31.6	3.1	1320	4	US-09-724-797-85	Sequence 85, App	Sequence 85, App	350	31	3.0	4131	1	US-08-485-588-4	Sequence 4, Appli
278	31.6	3.1	1509	4	US-09-949-016-1983	Sequence 1983, Ap	Sequence 1983, Ap	351	31	3.0	4131	2	US-08-484-565-4	Sequence 4, Appli
279	31.6	3.1	1519	4	US-09-949-016-769	Sequence 769, App	Sequence 769, App	352	31	3.0	4131	2	US-08-480-751-4	Sequence 4, Appli
280	31.6	3.1	1742	3	US-09-383-586-23	Sequence 23, Appli	Sequence 23, Appli	353	31	3.0	4131	2	US-08-943-986-4	Sequence 4, Appli
281	31.6	3.1	1742	4	US-09-823-038A-23	Sequence 23, Appli	Sequence 23, Appli	354	31	3.0	4131	3	US-08-353-784-4	Sequence 4, Appli
282	31.6	3.1	1967	3	US-09-383-586-22	Sequence 22, Appli	Sequence 22, Appli	355	31	3.0	4131	3	US-08-484-719B-4	Sequence 4, Appli
283	31.6	3.1	1967	4	US-09-823-038A-22	Sequence 22, Appli	Sequence 22, Appli	356	31	3.0	4131	3	US-08-484-159-4	Sequence 4, Appli
284	31.6	3.1	2127	4	US-09-902-540-3949	Sequence 3949, Ap	Sequence 3949, Ap	357	31	3.0	9996	4	US-09-902-540-999	Sequence 999, App
285	31.6	3.1	21295	4	US-09-902-540-1194	Sequence 1194, Ap	Sequence 1194, Ap	c 358	31	3.0	16992	4	US-09-902-540-960	Sequence 960, App
286	31.6	3.1	58108	4	US-09-949-016-13383	Sequence 13383, A	Sequence 13383, A	359	30.8	3.0	601	4	US-09-949-016-66074	Sequence 66074, A
287	31.6	3.1	100463	4	US-09-949-016-12511	Sequence 12511, A	Sequence 12511, A	c 360	30.8	3.0	601	4	US-09-949-016-125667	Sequence 125667, A
288	31.6	3.1	100468	4	US-09-949-016-13725	Sequence 13725, A	Sequence 13725, A	c 361	30.8	3.0	601	4	US-09-949-016-154964	Sequence 154964, A
289	31.4	3.0	390	3	US-09-222-575-90	Sequence 90, Appli	Sequence 90, Appli	362	30.8	3.0	1443	4	US-09-902-540-5072	Sequence 5072, Ap
290	31.4	3.0	390	4	US-09-389-681-90	Sequence 90, Appli	Sequence 90, Appli	c 363	30.8	3.0	1734	4	US-09-248-796A-6383	Sequence 6383, Ap
291	31.4	3.0	390	4	US-09-620-405B-90	Sequence 90, Appli	Sequence 90, Appli	c 364	30.8	3.0	1829	4	US-09-902-540-6486	Sequence 6486, Ap
292	31.4	3.0	390	4	US-09-339-338-90	Sequence 90, Appli	Sequence 90, Appli	c 365	30.8	3.0	2016	4	US-09-902-540-4303	Sequence 4303, Ap
293	31.4	3.0	390	4	US-09-433-826B-90	Sequence 90, Appli	Sequence 90, Appli	366	30.8	3.0	2106	4	US-09-270-767-11012	Sequence 11012, A
294	31.4	3.0	390	4	US-09-604-287A-90	Sequence 90, Appli	Sequence 90, Appli	367	30.8	3.0	2577	4	US-09-952-060-1	Sequence 1, Appli
295	31.4	3.0	390	4	US-09-285-480-90	Sequence 90, Appli	Sequence 90, Appli	c 368	30.8	3.0	2650	4	US-09-952-060-5	Sequence 5, Appli
296	31.4	3.0	390	4	US-09-834-759-90	Sequence 90, Appli	Sequence 90, Appli	c 369	30.8	3.0	3916	4	US-09-902-540-463	Sequence 463, App
297	31.4	3.0	390	4	US-09-590-751A-90	Sequence 90, Appli	Sequence 90, Appli	c 370	30.8	3.0	4404	3	US-09-523-656-37	Sequence 37, Appli
298	31.4	3.0	390	4	US-09-551-621-90	Sequence 90, Appli	Sequence 90, Appli	371	30.8	3.0	4451	3	US-08-717-294-42	Sequence 42, Appli
299	31.4	3.0	435	4	US-09-621-976-1501	Sequence 1501, Ap	Sequence 1501, Ap	c 372	30.8	3.0	5310	4	US-09-620-312D-623	Sequence 623, App
300	31.4	3.0	609	4	US-09-902-540-6153	Sequence 6153, Ap	Sequence 6153, Ap	c 373	30.8	3.0	12335	4	US-09-949-016-13686	Sequence 13686, A
301	31.4	3.0	741	4	US-09-252-991A-7414	Sequence 7414, Ap	Sequence 7414, Ap	374	30.8	3.0	12299	4	US-09-949-016-13014	Sequence 13014, A
302	31.4	3.0	870	4	US-09-252-991A-6138	Sequence 6138, Ap	Sequence 6138, Ap	c 375	30.8	3.0	23807	4	US-09-902-540-1214	Sequence 1214, Ap
303	31.4	3.0	1398	4	US-09-252-991A-6413	Sequence 6413, Ap	Sequence 6413, Ap	c 376	30.8	3.0	28194	4	US-09-902-540-1250	Sequence 1250, Ap
304	31.4	3.0	1807	4	US-09-902-540-299	Sequence 299, App	Sequence 299, App	c 377	30.8	3.0	36675	4	US-08-311-731A-135	Sequence 135, App
305	31.4	3.0	1890	4	US-09-252-991A-6330	Sequence 6330, Ap	Sequence 6330, Ap	c 378	30.8	3.0	56616	4	US-09-949-016-12462	Sequence 12462, A
306	31.4	3.0	4233	4	US-09-602-628-9	Sequence 9, Appli	Sequence 9, Appli	c 379	30.8	3.0	56616	4	US-09-949-016-17085	Sequence 17085, A
307	31.4	3.0	5622	4	US-09-949-016-3732	Sequence 3732, Ap	Sequence 3732, Ap	c 380	30.8	3.0	138282	4	US-09-949-016-15307	Sequence 15307, A
308	31.4	3.0	5983	3	US-08-264-578-1	Sequence 1, Appli	Sequence 1, Appli	c 381	30.8	3.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
309	31.4	3.0	6240	4	US-09-949-016-137	Sequence 127, App	Sequence 127, App	c 382	30.8	3.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
310	31.4	3.0	87629	4	US-09-949-016-15262	Sequence 15262, A	Sequence 15262, A	c 383	30.6	3.0	429	4	US-09-252-991A-5365	Sequence 5365, Ap
311	31.4	3.0	87629	4	US-09-949-016-15263	Sequence 15263, A	Sequence 15263, A	c 384	30.6	3.0	510	4	US-09-902-540-9064	Sequence 9064, Ap
312	31.4	3.0	87629	4	US-09-949-016-15264	Sequence 15264, A	Sequence 15264, A	c 385	30.6	3.0	843	4	US-09-252-991A-10321	Sequence 10321, A
313	31.4	3.0	87629	4	US-09-949-016-15265	Sequence 15265, A	Sequence 15265, A	c 386	30.6	3.0	1043	4	US-09-495-052-44	Sequence 44, Appli
314	31.4	3.0	96878	4	US-09-949-016-12551	Sequence 12551, A	Sequence 12551, A	c 387	30.6	3.0	1164	4	US-09-252-991A-4913	Sequence 4913, Ap
315	31.4	3.0	194714	4	US-09-949-016-11869	Sequence 11869, A	Sequence 11869, A	c 388	30.6	3.0	1344	4	US-09-252-991A-5239	Sequence 5239, Ap
316	31.4	3.0	196714	4	US-09-949-016-15474	Sequence 15474, A	Sequence 15474, A	c 389	30.6	3.0	1349	1	US-08-451-777A-5	Sequence 4, Appli
317	31.2	3.0	384	4	US-09-252-991A-10331	Sequence 10331, A	Sequence 10331, A	c 390	30.6	3.0	1349	1	US-08-451-777A-5	Sequence 5, Appli
318	31.2	3.0	505	4	US-09-621-976-15639	Sequence 15639, A	Sequence 15639, A	c 391	30.6	3.0	1349	1	US-08-451-777A-6	Sequence 6, Appli
319	31.2	3.0	1176	4	US-09-902-540-6438	Sequence 6438, Ap	Sequence 6438, Ap	c 392	30.6	3.0	1349	2	US-08-451-777A-4	Sequence 4, Appli

C 393	30.6	3.0	1349	2	US-08-451-778A-5	Sequence 5, Appli	466	30.4	2.9	197337	4	US-09-949-016-14376	Sequence 14376, A
C 394	30.6	3.0	1349	2	US-08-451-778A-6	Sequence 6, Appli	467	30.4	2.9	234288	4	US-09-949-016-17272	Sequence 17272, A
C 395	30.6	3.0	1349	2	US-08-998-208-4	Sequence 4, Appli	468	30.2	2.9	289	3	US-09-007-005-17	Sequence 17, Appl
C 396	30.6	3.0	1349	2	US-08-998-208-5	Sequence 5, Appli	469	30.2	2.9	289	3	US-09-244-796-17	Sequence 17, Appl
C 397	30.6	3.0	1349	2	US-08-998-208-6	Sequence 6, Appli	470	30.2	2.9	474	4	US-09-252-991A-15418	Sequence 15418, A
C 398	30.6	3.0	1349	5	PCT-US94-10825-4	Sequence 4, Appli	471	30.2	2.9	536	4	US-09-569-611C-2	Sequence 2, Appli
C 399	30.6	3.0	1349	5	PCT-US95-06743-4	Sequence 4, Appli	472	30.2	2.9	996	4	US-09-569-611C-2	Sequence 8034, Ap
C 400	30.6	3.0	1349	5	PCT-US95-06743-5	Sequence 5, Appli	473	30.2	2.9	1002	4	US-09-902-540-8034	Sequence 11872, Ap
C 401	30.6	3.0	1349	5	PCT-US95-06743-6	Sequence 6, Appli	474	30.2	2.9	1017	4	US-09-252-991A-11872	Sequence 13557, A
C 402	30.6	3.0	1386	4	US-09-949-016-3585	Sequence 3585, Ap	475	30.2	2.9	1108	3	US-09-289-349-8	Sequence 8, Appli
C 403	30.6	3.0	1395	4	US-09-489-039A-2450	Sequence 2450, Ap	476	30.2	2.9	1459	4	US-09-569-611C-4	Sequence 4, Appli
C 404	30.6	3.0	1488	4	US-09-252-991A-4918	Sequence 4918, Ap	477	30.2	2.9	1464	4	US-09-252-991A-11508	Sequence 11508, A
C 405	30.6	3.0	1519	3	US-08-913-462-38	Sequence 38, Appl	478	30.2	2.9	1476	3	US-08-753-007A-7	Sequence 7, Appli
C 406	30.6	3.0	1566	4	US-09-902-540-3888	Sequence 3888, Ap	479	30.2	2.9	1476	3	US-09-338-496-7	Sequence 7, Appli
C 407	30.6	3.0	1728	4	US-09-252-991A-13641	Sequence 13641, A	480	30.2	2.9	1616	4	US-09-270-767-2247	Sequence 2247, Ap
C 408	30.6	3.0	1794	4	US-09-252-991A-5181	Sequence 5181, Ap	481	30.2	2.9	1616	4	US-09-270-767-17529	Sequence 17529, A
C 409	30.6	3.0	2327	4	US-09-976-594-1064	Sequence 1064, Ap	482	30.2	2.9	1629	4	US-09-252-991A-11733	Sequence 11733, A
C 410	30.6	3.0	2329	3	US-08-961-083-85	Sequence 85, Appl	483	30.2	2.9	1884	3	US-08-753-007A-5	Sequence 5, Appli
C 411	30.6	3.0	2329	4	US-09-536-784-85	Sequence 85, Appl	484	30.2	2.9	1884	3	US-09-398-496-5	Sequence 5, Appli
C 412	30.6	3.0	2547	4	US-08-252-991A-5294	Sequence 5294, Ap	485	30.2	2.9	2081	4	US-09-949-016-3203	Sequence 3203, Ap
C 413	30.6	3.0	3640	2	US-08-627-873-6	Sequence 6, Appli	486	30.2	2.9	2099	4	US-09-949-016-5169	Sequence 5169, Ap
C 414	30.6	3.0	4406	1	US-08-369-043-1	Sequence 1, Appli	487	30.2	2.9	2105	4	US-09-949-016-3204	Sequence 3204, Ap
C 415	30.6	3.0	5175	2	US-08-843-530B-3	Sequence 3, Appli	488	30.2	2.9	2123	4	US-09-949-016-3202	Sequence 3202, Ap
C 416	30.6	3.0	5175	3	US-09-636-728-3	Sequence 3, Appli	489	30.2	2.9	2157	4	US-09-569-611C-3	Sequence 3, Appli
C 417	30.6	3.0	5697	2	US-08-843-530B-5	Sequence 5, Appli	490	30.2	2.9	2229	4	US-09-252-991A-15478	Sequence 15478, A
C 418	30.6	3.0	5697	4	US-08-636-728-4	Sequence 4, Appli	491	30.2	2.9	2268	3	US-08-753-007A-31	Sequence 31, Appl
C 419	30.6	3.0	5824	4	US-09-620-312D-72	Sequence 72, Appl	492	30.2	2.9	2268	3	US-09-338-496-31	Sequence 31, Appl
C 420	30.6	3.0	6545	2	US-08-843-530B-1	Sequence 1, Appli	493	30.2	2.9	2675	1	US-08-070-165F-5	Sequence 5, Appli
C 421	30.6	3.0	6545	4	US-09-636-728-1	Sequence 1, Appli	494	30.2	2.9	2675	1	US-08-885-418-5	Sequence 5, Appli
C 422	30.6	3.0	14027	4	US-09-902-540-1023	Sequence 1023, Ap	495	30.2	2.9	2681	2	US-08-070-165F-9	Sequence 9, Appli
C 423	30.6	3.0	15363	3	US-08-961-527-139	Sequence 139, App	496	30.2	2.9	2681	2	US-08-885-418-9	Sequence 9, Appli
C 424	30.6	3.0	21706	4	US-08-949-016-16256	Sequence 16256, A	497	30.2	2.9	715	4	US-09-902-540-818	Sequence 818, App
C 425	30.6	3.0	2326	4	US-09-949-016-16153	Sequence 16153, A	498	30.2	2.9	9098	4	US-09-358-082A-28	Sequence 28, Appl
C 426	30.6	3.0	2326	4	US-09-949-016-15356	Sequence 15356, A	499	30.2	2.9	9098	4	US-09-358-082A-28	Sequence 28, Appl
C 427	30.6	3.0	32495	4	US-09-949-016-14952	Sequence 14952, A	500	30.2	2.9	9838	4	US-09-949-016-13011	Sequence 13011, A
C 428	30.6	3.0	3937	4	US-09-949-016-16147	Sequence 16147, A	501	30.2	2.9	22121	4	US-09-949-016-14359	Sequence 14359, A
C 429	30.6	3.0	52661	4	US-09-949-016-17191	Sequence 17191, A	502	30.2	2.9	22121	4	US-09-949-016-14909	Sequence 14909, A
C 430	30.6	3.0	83178	4	US-08-949-016-14606	Sequence 14606, A	503	30.2	2.9	27707	4	US-09-902-540-1226	Sequence 1226, Ap
C 431	30.4	2.9	237	4	US-09-902-540-4617	Sequence 4617, Ap	504	30.2	2.9	35629	4	US-09-949-016-15786	Sequence 15786, A
C 432	30.4	2.9	601	4	US-09-949-016-25296	Sequence 25296, A	505	30.2	2.9	121473	4	US-09-949-016-15330	Sequence 15330, A
C 433	30.4	2.9	735	4	US-09-949-016-124255	Sequence 124255, A	506	30.2	2.9	121473	4	US-09-949-016-15330	Sequence 15330, A
C 434	30.4	2.9	735	4	US-09-270-767-13925	Sequence 13925, A	507	30.2	2.9	134987	4	US-09-949-016-15349	Sequence 15349, A
C 435	30.4	2.9	738	4	US-09-252-991A-13874	Sequence 13874, A	508	30.2	2.9	134987	4	US-09-949-016-15349	Sequence 15349, A
C 436	30.4	2.9	1143	4	US-09-489-039A-2373	Sequence 2373, Ap	509	30.2	2.9	134987	4	US-09-949-016-15350	Sequence 15350, A
C 437	30.4	2.9	1215	4	US-09-489-039A-1776	Sequence 1776, Ap	510	30.2	2.9	134987	4	US-09-949-016-15507	Sequence 15507, A
C 438	30.4	2.9	1323	4	US-08-023-655-813	Sequence 813, App	511	30.2	2.9	134987	4	US-09-949-016-15508	Sequence 15508, A
C 439	30.4	2.9	1560	2	US-08-794-795-5	Sequence 5, Appli	512	30.2	2.9	136917	4	US-09-949-016-15509	Sequence 15509, A
C 440	30.4	2.9	1560	3	US-09-249-200-5	Sequence 5, Appli	513	30.2	2.9	187169	4	US-09-949-016-12776	Sequence 12776, A
C 441	30.4	2.9	1581	4	US-09-902-540-9170	Sequence 9170, Ap	514	30.2	2.9	191569	4	US-09-949-016-15940	Sequence 15940, A
C 442	30.4	2.9	1703	2	US-08-794-795-1	Sequence 1, Appli	515	30.2	2.9	191569	4	US-09-949-016-15940	Sequence 15940, A
C 443	30.4	2.9	1703	3	US-09-249-200-1	Sequence 1, Appli	516	30.2	2.9	254405	4	US-09-949-016-14381	Sequence 14381, A
C 444	30.4	2.9	2299	4	US-09-475-515-81	Sequence 81, Appl	517	30.2	2.9	340380	4	US-09-949-016-14179	Sequence 14179, A
C 445	30.4	2.9	2300	4	US-09-475-515-83	Sequence 83, Appl	518	30	2.9	390	4	US-09-252-991A-286	Sequence 286, App
C 446	30.4	2.9	2305	4	US-09-475-515-80	Sequence 80, Appl	519	30	2.9	402	1	US-08-370-975B-4	Sequence 4, Appli
C 447	30.4	2.9	2306	4	US-09-475-515-82	Sequence 82, Appl	520	30	2.9	439	4	US-09-270-767-1558	Sequence 1558, Ap
C 448	30.4	2.9	2312	4	US-09-475-515-84	Sequence 84, Appl	521	30	2.9	439	4	US-09-270-767-16840	Sequence 16840, A
C 449	30.4	2.9	3093	4	US-09-949-016-4183	Sequence 4183, Ap	522	30	2.9	510	4	US-09-902-540-6947	Sequence 6947, Ap
C 450	30.4	2.9	3334	4	US-09-668-119-2	Sequence 2, Appli	523	30	2.9	510	4	US-09-252-991A-15509	Sequence 15509, A
C 451	30.4	2.9	3334	4	US-09-949-016-1149	Sequence 1149, Ap	524	30	2.9	576	4	US-09-270-767-2049	Sequence 2049, Ap
C 452	30.4	2.9	3661	4	US-09-893-371A-3	Sequence 3, Appli	525	30	2.9	576	4	US-09-270-767-17331	Sequence 17331, A
C 453	30.4	2.9	3855	4	US-08-426-630-30	Sequence 30, Appl	526	30	2.9	601	4	US-09-949-016-63454	Sequence 63454, A
C 454	30.4	2.9	4188	4	US-09-252-991A-13774	Sequence 13774, A	527	30	2.9	601	4	US-09-902-540-3016	Sequence 3016, Ap
C 455	30.4	2.9	4319	4	US-09-475-515-6	Sequence 6, Appli	528	30	2.9	717	4	US-09-252-991A-6816	Sequence 6816, Ap
C 456	30.4	2.9	8211	4	US-09-252-991A-13656	Sequence 13656, A	529	30	2.9	813	4	US-09-252-991A-271	Sequence 271, App
C 457	30.4	2.9	11612	4	US-09-902-540-981	Sequence 981, App	530	30	2.9	1191	4	US-09-902-540-6833	Sequence 6833, Ap
C 458	30.4	2.9	18472	4	US-09-949-016-12891	Sequence 12891, A	531	30	2.9	1329	4	US-09-252-991A-15277	Sequence 15277
C 459	30.4	2.9	18478	4	US-09-949-016-15925	Sequence 15925, A	532	30	2.9	1383	4	US-09-248-796A-203	Sequence 203, App
C 460	30.4	2.9	27490	4	US-09-902-540-1227	Sequence 1227, Ap	533	30	2.9	1551	4	US-09-252-991A-15327	Sequence 15327, A
C 461	30.4	2.9	40586	4	US-09-949-016-16965	Sequence 16965, A	534	30	2.9	1587	4	US-09-252-991A-5980	Sequence 5980, Ap
C 462	30.4	2.9	143644	4	US-09-949-016-15238	Sequence 15238, A	535	30	2.9	1617	4	US-09-902-540-5384	Sequence 5384, Ap
C 463	30.4	2.9	147840	4	US-09-949-016-15238	Sequence 15238, A	536	30	2.9	1617	4	US-09-252-991A-5890	Sequence 5890, Ap
C 464	30.4	2.9	187848	4	US-09-949-016-12111	Sequence 12111, A	537	30	2.9	1853	1	US-08-553-110-2	Sequence 2, Appli
C 465	30.4	2.9	197336	4	US-09-949-016-12881	Sequence 12881, A	538	30	2.9	1953	4	US-09-252-991A-6975	Sequence 6975, Ap

539	30	2.9	2085	4	US-09-252-991A-5910	Sequence 5910, Ap	612	29.8	2.9	1788	4	US-09-252-991A-898	Sequence 898, App
540	30	2.9	2103	4	US-09-489-847-40	Sequence 40, Appl	613	29.8	2.9	1836	1	US-09-252-991A-4587	Sequence 4587, Ap
541	30	2.9	2274	4	US-09-902-540-4081	Sequence 4081, Ap	c 614	29.8	2.9	1908	1	US-08-460-934-8	Sequence 8, Appl1
542	30	2.9	2856	4	US-09-252-991A-6767	Sequence 6767, Ap	c 615	29.8	2.9	1908	2	US-08-782-118-8	Sequence 8, Appl1
543	30	2.9	2887	3	US-08-983-502-14	Sequence 14, Appl	616	29.8	2.9	1983	4	US-09-489-039A-1386	Sequence 1386, Ap
544	30	2.9	2887	4	US-09-516-747-14	Sequence 14, Appl	c 617	29.8	2.9	2178	4	US-09-252-991A-7630	Sequence 2, Appl1
545	30	2.9	2887	5	PCT-US96-10521-14	Sequence 14, Appl	618	29.8	2.9	2277	1	US-08-676-967-2	Sequence 2, Appl1
546	30	2.9	2955	4	US-09-620-312D-676	Sequence 676, App	619	29.8	2.9	2277	1	US-08-676-967-2	Sequence 2, Appl1
547	30	2.9	3039	4	US-09-620-312D-675	Sequence 675, App	620	29.8	2.9	2277	2	US-09-098-487-2	Sequence 2, Appl1
548	30	2.9	3147	4	US-09-614-221A-368	Sequence 368, App	621	29.8	2.9	2277	2	US-09-098-487-2	Sequence 2, Appl1
549	30	2.9	3891	4	US-09-902-540-601	Sequence 601, App	622	29.8	2.9	2901	4	US-09-902-540-5195	Sequence 5195, Ap
550	30	2.9	4168	4	US-09-266-225D-17	Sequence 17, Appl	c 622	29.8	2.9	2901	4	US-09-342-325C-43	Sequence 43, Appl
551	30	2.9	4196	4	US-09-774-528-236	Sequence 236, App	c 623	29.8	2.9	3030	4	US-09-252-991A-7921	Sequence 7921, Ap
552	30	2.9	4279	3	US-09-041-886-22	Sequence 22, Appl	c 624	29.8	2.9	3070	4	US-09-902-540-593	Sequence 593, App
553	30	2.9	5184	4	US-09-845-583A-9	Sequence 9, Appl1	625	29.8	2.9	3262	2	US-08-678-039A-41	Sequence 41, Appl
554	30	2.9	5184	4	US-09-561-709B-4	Sequence 4, Appl1	626	29.8	2.9	3332	4	US-09-949-016-5575	Sequence 5575, Ap
555	30	2.9	5559	1	US-08-287-442-3	Sequence 3, Appl1	627	29.8	2.9	3332	4	US-09-949-016-5576	Sequence 5576, Ap
556	30	2.9	5559	1	US-08-459-701-3	Sequence 3, Appl1	c 628	29.8	2.9	3521	3	US-08-961-527-118	Sequence 118, App
557	30	2.9	5559	1	US-08-460-298-3	Sequence 3, Appl1	629	29.8	2.9	5538	2	US-08-231-153A-55	Sequence 55, Appl
558	30	2.9	5559	1	US-08-460-298-3	Sequence 3, Appl1	630	29.8	2.9	5538	2	US-08-486-273A-55	Sequence 55, Appl
559	30	2.9	5559	5	PCT-US93-06300A-3	Sequence 3, Appl1	631	29.8	2.9	5538	3	US-08-940-086A-55	Sequence 55, Appl
560	30	2.9	9497	4	US-09-902-540-1054	Sequence 1054, Ap	632	29.8	2.9	5538	3	US-08-940-035A-55	Sequence 55, Appl
561	30	2.9	10763	1	US-08-761-258-1	Sequence 1, Appl1	633	29.8	2.9	5538	3	US-08-935-105A-55	Sequence 55, Appl
562	30	2.9	10763	2	US-08-977-306-1	Sequence 1, Appl1	634	29.8	2.9	5538	3	US-09-648-797-55	Sequence 55, Appl
563	30	2.9	11579	4	US-09-902-540-1052	Sequence 1052, Ap	635	29.8	2.9	5538	4	US-09-386-123-55	Sequence 55, Appl
564	30	2.9	18008	4	US-09-949-016-13291	Sequence 13291, A	636	29.8	2.9	5538	4	US-10-038-937-55	Sequence 55, Appl
565	30	2.9	24602	4	US-09-902-540-1202	Sequence 1202, Ap	637	29.8	2.9	7080	4	US-09-949-016-16896	Sequence 16896, A
566	30	2.9	25992	4	US-09-949-016-17425	Sequence 17425, A	638	29.8	2.9	15312	4	US-09-902-540-1115	Sequence 1115, Ap
567	30	2.9	26764	1	US-08-370-975B-1	Sequence 1, Appl1	c 639	29.8	2.9	17245	4	US-09-902-540-1073	Sequence 1073, Ap
568	30	2.9	29350	4	US-09-949-016-11963	Sequence 11963, A	640	29.8	2.9	18632	4	US-09-949-016-16574	Sequence 16574, A
569	30	2.9	29350	4	US-09-949-016-17160	Sequence 17160, A	c 641	29.8	2.9	34199	4	US-09-902-540-1255	Sequence 1255, Ap
570	30	2.9	34552	4	US-09-902-540-1262	Sequence 1262, A	642	29.8	2.9	43280	2	US-08-804-227C-1	Sequence 2, Appl1
571	30	2.9	115963	4	US-09-949-016-13298	Sequence 13298, A	c 643	29.8	2.9	71989	3	US-09-443-501A-2	Sequence 2, Appl1
572	30	2.9	144322	4	US-09-949-016-15316	Sequence 15316, A	644	29.8	2.9	100928	4	US-09-949-016-16926	Sequence 16926, A
573	30	2.9	149971	4	US-09-949-016-13590	Sequence 13590, A	645	29.6	2.9	237	4	US-09-902-540-5527	Sequence 5527, Ap
574	30	2.9	321022	4	US-09-949-016-11852	Sequence 11852, A	646	29.6	2.9	282	2	US-08-440-725A-4	Sequence 4, Appl1
575	30	2.9	321022	4	US-09-949-016-14166	Sequence 14166, A	647	29.6	2.9	282	5	PCT-US95-15991-4	Sequence 4, Appl1
576	29.8	2.9	180	4	US-09-270-767-5775	Sequence 77575, Ap	648	29.6	2.9	334	2	US-08-440-725A-4	Sequence 7, Appl1
577	29.8	2.9	273	4	US-09-583-110-1264	Sequence 1264, Ap	649	29.6	2.9	334	5	PCT-US95-15991-7	Sequence 7, Appl1
578	29.8	2.9	273	4	US-09-107-433-2569	Sequence 2569, Ap	650	29.6	2.9	379	3	US-09-060-756-482	Sequence 482, App
579	29.8	2.9	288	4	US-09-902-540-6916	Sequence 6916, Ap	651	29.6	2.9	379	4	US-09-670-314-482	Sequence 482, App
580	29.8	2.9	408	4	US-09-902-540-2536	Sequence 2536, Ap	c 652	29.6	2.9	489	4	US-09-621-976-126	Sequence 126, App
581	29.8	2.9	444	4	US-09-902-540-2536	Sequence 2536, Ap	653	29.6	2.9	492	4	US-09-902-540-7845	Sequence 7845, Ap
582	29.8	2.9	501	4	US-09-252-991A-11328	Sequence 11328, A	654	29.6	2.9	510	4	US-09-252-991A-4285	Sequence 4285, Ap
583	29.8	2.9	501	4	US-09-252-991A-11294	Sequence 11294, A	655	29.6	2.9	601	4	US-09-949-016-119990	Sequence 119990, A
584	29.8	2.9	858	4	US-09-902-540-9273	Sequence 9273, Ap	656	29.6	2.9	601	4	US-09-949-016-119991	Sequence 119991, A
585	29.8	2.9	915	4	US-09-489-039A-4735	Sequence 4735, Ap	657	29.6	2.9	601	4	US-09-949-001-349	Sequence 349, App
586	29.8	2.9	957	2	US-08-633-148-3	Sequence 3, Appl1	658	29.6	2.9	734	1	US-08-471-570-11	Sequence 11, Appl
587	29.8	2.9	963	4	US-09-252-991A-4485	Sequence 4485, Ap	c 659	29.6	2.9	798	4	US-09-902-540-3431	Sequence 3431, Ap
588	29.8	2.9	1023	2	US-08-633-148-1	Sequence 1, Appl1	c 660	29.6	2.9	843	4	US-09-621-976-16851	Sequence 16851, A
589	29.8	2.9	1110	4	US-09-252-991A-7852	Sequence 7852, Ap	c 661	29.6	2.9	999	4	US-09-252-991A-9602	Sequence 9602, Ap
590	29.8	2.9	1125	4	US-09-583-110-1263	Sequence 1263, Ap	662	29.6	2.9	1011	4	US-09-252-991A-9655	Sequence 9655, Ap
591	29.8	2.9	1215	4	US-09-949-016-5154	Sequence 5154, Ap	663	29.6	2.9	1077	4	US-09-170-496D-39	Sequence 39, Appl
592	29.8	2.9	1245	4	US-09-107-433-2382	Sequence 2382, Ap	664	29.6	2.9	1077	4	US-09-170-496D-185	Sequence 185, App
593	29.8	2.9	1391	4	US-09-638-649-4	Sequence 4, Appl1	665	29.6	2.9	1079	1	US-08-471-570-13	Sequence 13, Appl
594	29.8	2.9	1391	4	US-09-638-648-4	Sequence 4, Appl1	666	29.6	2.9	1110	3	US-09-336-536-27	Sequence 27, Appl
595	29.8	2.9	1405	4	US-08-755-235-3	Sequence 3, Appl1	667	29.6	2.9	1289	4	US-09-745-842-1	Sequence 1, Appl1
596	29.8	2.9	1419	4	US-09-252-991A-1062	Sequence 1062, Ap	668	29.6	2.9	1335	3	US-09-450-790A-18	Sequence 18, Appl
597	29.8	2.9	1423	4	US-09-823-038A-46	Sequence 46, Appl	c 669	29.6	2.9	1353	4	US-09-489-039A-1917	Sequence 1917, Ap
598	29.8	2.9	1428	4	US-09-252-991A-4267	Sequence 4267, Ap	670	29.6	2.9	1353	4	US-09-252-991A-9695	Sequence 9695, Ap
599	29.8	2.9	1431	4	US-09-252-991A-990	Sequence 990, App	671	29.6	2.9	1379	4	US-09-826-509-450	Sequence 450, App
600	29.8	2.9	1503	4	US-09-311-021-137	Sequence 137, App	672	29.6	2.9	1387	2	US-08-979-424-2	Sequence 2, Appl1
601	29.8	2.9	1644	1	US-07-903-047-7	Sequence 7, Appl1	673	29.6	2.9	1406	1	US-08-745-269-1	Sequence 1, Appl1
602	29.8	2.9	1644	3	US-09-111-752-13	Sequence 13, Appl	674	29.6	2.9	1406	2	US-08-157-185-1	Sequence 1, Appl1
603	29.8	2.9	1644	3	US-08-380-061B-15	Sequence 15, Appl	675	29.6	2.9	1406	3	US-08-281-526B-1	Sequence 1, Appl1
604	29.8	2.9	1644	3	US-08-487-183A-13	Sequence 13, Appl	676	29.6	2.9	1406	3	US-09-450-797-1	Sequence 1, Appl1
605	29.8	2.9	1644	4	US-09-581-241A-3	Sequence 3, Appl1	677	29.6	2.9	1406	3	US-09-450-790A-1	Sequence 1, Appl1
606	29.8	2.9	1644	4	US-09-581-241A-5	Sequence 5, Appl1	678	29.6	2.9	1406	3	US-09-332-837-1	Sequence 1, Appl1
607	29.8	2.9	1644	3	US-09-581-241A-7	Sequence 7, Appl1	679	29.6	2.9	1406	4	US-09-016-434-1362	Sequence 1362, Ap
608	29.8	2.9	1681	3	US-09-434-288-7	Sequence 7, Appl1	680	29.6	2.9	1406	5	PCT-US93-10553-1	Sequence 1, Appl1
609	29.8	2.9	1692	3	US-08-276-968A-21	Sequence 21, Appl	681	29.6	2.9	1417	2	US-08-428-243-8	Sequence 8, Appl1
610	29.8	2.9	1704	1	US-08-460-934-5	Sequence 5, Appl1	682	29.6	2.9	1417	5	PCT-US93-10301-8	Sequence 8, Appl1
611	29.8	2.9	1704	2	US-08-782-118-5	Sequence 5, Appl1	c 683	29.6	2.9	1542	4	US-09-949-016-4417	Sequence 4417, Ap
							684	29.6	2.9	1603	1	US-08-471-570-3	Sequence 3, Appl1

685	29.6	2.9	1737	4	US-09-489-039A-1985	Sequence 1985, Ap	758	29.4	2.8	1225	2	US-08-674-149A-1	Sequence 1, Appli
686	29.6	2.9	1763	4	US-09-270-767-13228	Sequence 13228, A	C 759	29.4	2.8	1248	4	US-09-252-991A-10656	Sequence 10656, A
687	29.6	2.9	1813	4	US-09-907-794A-38	Sequence 38, Appl	760	29.4	2.8	1287	4	US-03-902-540-2736	Sequence 2736, Ap
688	29.6	2.9	1813	4	US-09-903-125A-38	Sequence 38, Appl	761	29.4	2.8	1310	4	US-03-799-451-325	Sequence 325, App
689	29.6	2.9	1813	4	US-09-902-775A-38	Sequence 38, Appl	C 762	29.4	2.8	1422	4	US-09-252-991A-10550	Sequence 10550, A
690	29.6	2.9	1813	4	US-09-906-700-38	Sequence 38, Appl	763	29.4	2.8	1574	4	US-09-270-767-12428	Sequence 12428, A
691	29.6	2.9	1813	4	US-09-903-603A-38	Sequence 38, Appl	C 764	29.4	2.8	1701	4	US-09-774-528-162	Sequence 162, App
692	29.6	2.9	1813	4	US-09-904-920A-38	Sequence 38, Appl	C 765	29.4	2.8	2136	1	US-08-655-836-1	Sequence 1, Appli
693	29.6	2.9	1813	4	US-09-904-920A-38	Sequence 38, Appl	C 766	29.4	2.8	2136	2	US-08-020-753-1	Sequence 1, Appli
694	29.6	2.9	1813	4	US-09-905-381A-38	Sequence 38, Appl	C 767	29.4	2.8	2202	1	US-08-655-836-2	Sequence 2, Appli
695	29.6	2.9	1813	4	US-09-906-618-38	Sequence 38, Appl	C 768	29.4	2.8	2202	2	US-09-020-753-2	Sequence 2, Appli
696	29.6	2.9	1815	3	US-09-041-545-1	Sequence 1, Appli	769	29.4	2.8	2358	3	US-09-022-983-1	Sequence 1, Appli
697	29.6	2.9	1815	3	US-09-327-925-1	Sequence 1, Appli	770	29.4	2.8	2360	3	US-09-490-692-10	Sequence 10, Appl
698	29.6	2.9	1831	3	US-09-484-970B-84	Sequence 84, Appl	C 771	29.4	2.8	2364	1	US-08-655-836-3	Sequence 3, Appli
699	29.6	2.9	1869	3	US-09-336-536-26	Sequence 26, Appl	C 772	29.4	2.8	2364	2	US-08-020-753-3	Sequence 3, Appli
700	29.6	2.9	1954	1	US-08-471-570-5	Sequence 5, Appli	C 773	29.4	2.8	2948	4	US-09-865-621A-6	Sequence 6, Appli
701	29.6	2.9	2079	4	US-09-949-016-3171	Sequence 3171, Ap	C 774	29.4	2.8	3234	4	US-09-614-221A-259	Sequence 259, App
702	29.6	2.9	2079	4	US-09-949-016-3172	Sequence 3172, Ap	775	29.4	2.8	3427	4	US-09-865-621A-8	Sequence 8, Appli
703	29.6	2.9	2079	4	US-09-949-016-3173	Sequence 3173, Ap	776	29.4	2.8	3518	4	US-09-865-621A-5	Sequence 5, Appli
704	29.6	2.9	2079	4	US-09-949-016-3174	Sequence 3174, Ap	777	29.4	2.8	3884	4	US-09-562-930-10	Sequence 10, Appl
705	29.6	2.9	2079	4	US-09-949-016-3175	Sequence 3175, Ap	778	29.4	2.8	3979	4	US-03-865-621A-4	Sequence 4, Appli
706	29.6	2.9	2079	4	US-09-949-016-3176	Sequence 3176, Ap	779	29.4	2.8	4095	4	US-09-252-991A-10309	Sequence 10309, A
707	29.6	2.9	2079	4	US-09-949-016-3177	Sequence 3177, Ap	780	29.4	2.8	4810	4	US-09-865-621A-3	Sequence 3, Appli
708	29.6	2.9	2079	4	US-09-949-016-3178	Sequence 3178, Ap	781	29.4	2.8	4980	4	US-09-792-540-574	Sequence 574, App
709	29.6	2.9	2079	4	US-09-949-016-3179	Sequence 3179, Ap	782	29.4	2.8	5043	4	US-09-902-540-1129	Sequence 8, Appli
710	29.6	2.9	2079	4	US-09-949-016-3180	Sequence 3180, Ap	783	29.4	2.8	5163	4	US-09-865-621A-7	Sequence 7, Appli
C 711	29.6	2.9	2127	1	US-08-464-340A-1	Sequence 1, Appli	784	29.4	2.8	5509	4	US-03-865-621A-1	Sequence 1, Appli
C 712	29.6	2.9	2127	5	PCT-US94-08449A-1	Sequence 1, Appli	C 785	29.4	2.8	9301	3	US-09-449-218D-18	Sequence 18, Appl
C 713	29.6	2.9	2190	3	US-09-015-188-1	Sequence 1, Appli	C 786	29.4	2.8	9301	4	US-09-668-529A-18	Sequence 18, Appl
C 714	29.6	2.9	2310	1	US-08-471-570-9	Sequence 9, Appli	C 787	29.4	2.8	9301	4	US-09-668-037A-18	Sequence 18, Appl
715	29.6	2.9	2328	3	US-09-513-838-5	Sequence 5, Appli	C 788	29.4	2.8	9301	4	US-09-668-021-18	Sequence 18, Appl
716	29.6	2.9	2676	1	US-08-471-570-7	Sequence 7, Appli	C 789	29.4	2.8	14519	4	US-09-949-016-15611	Sequence 15611, A
717	29.6	2.9	3416	2	US-08-451-822A-15	Sequence 15, Appl	C 790	29.4	2.8	14519	4	US-09-949-016-15612	Sequence 15612, A
718	29.6	2.9	3416	3	US-08-323-430-15	Sequence 15, Appl	791	29.4	2.8	15689	4	US-09-902-540-1129	Sequence 1129, Ap
719	29.6	2.9	3549	4	US-09-826-509-586	Sequence 586, App	792	29.4	2.8	16365	4	US-09-949-016-13436	Sequence 13436, A
C 720	29.6	2.9	5589	4	US-09-902-540-784	Sequence 784, App	793	29.4	2.8	48763	4	US-09-916-204-3	Sequence 3, Appli
721	29.6	2.9	9039	4	US-09-902-540-983	Sequence 983, App	794	29.4	2.8	48763	4	US-10-282-048-3	Sequence 3, Appli
C 722	29.6	2.9	10304	4	US-09-949-016-16159	Sequence 16159, A	795	29.4	2.8	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 723	29.6	2.9	15661	4	US-09-949-016-13161	Sequence 13161, A	796	29.4	2.8	54452	4	US-09-949-016-12642	Sequence 12642, A
C 724	29.6	2.9	18192	4	US-09-949-016-1162	Sequence 1162, Ap	797	29.4	2.8	54452	4	US-09-949-016-13003	Sequence 13003, A
C 725	29.6	2.9	19861	4	US-09-949-016-14498	Sequence 14498, A	798	29.4	2.8	57811	4	US-09-949-016-13192	Sequence 13192, A
C 726	29.6	2.9	41768	4	US-09-902-540-1266	Sequence 1266, Ap	C 799	29.4	2.8	66175	4	US-09-949-016-12293	Sequence 12293, A
727	29.6	2.9	110266	4	US-09-949-016-14913	Sequence 14913, A	800	29.4	2.8	92139	4	US-09-918-686-1	Sequence 1, Appli
728	29.6	2.9	110266	4	US-09-949-016-14914	Sequence 14914, A	C 801	29.4	2.8	162914	4	US-09-949-016-15578	Sequence 15578, A
729	29.6	2.9	110266	4	US-09-949-016-14915	Sequence 14915, A	C 802	29.4	2.8	168575	3	US-03-426-290-1	Sequence 1, Appli
730	29.6	2.9	110266	4	US-09-949-016-14916	Sequence 14916, A	C 803	29.4	2.8	168971	4	US-09-949-016-13807	Sequence 13807, A
731	29.6	2.9	110266	4	US-09-949-016-14917	Sequence 14917, A	804	29.4	2.8	174493	4	US-09-804-471A-3	Sequence 3, Appli
732	29.6	2.9	110266	4	US-09-949-016-14918	Sequence 14918, A	C 805	29.4	2.8	236474	4	US-10-238-709-3	Sequence 3, Appli
733	29.6	2.9	110266	4	US-09-949-016-14919	Sequence 14919, A	C 806	29.4	2.8	236474	4	US-09-949-016-13418	Sequence 13418, A
734	29.6	2.9	110266	4	US-09-949-016-14920	Sequence 14920, A	C 807	29.2	2.8	263	4	US-09-313-294A-701	Sequence 701, App
735	29.6	2.9	110266	4	US-09-949-016-14921	Sequence 14921, A	C 808	29.2	2.8	273	2	US-08-997-080-142	Sequence 142, App
736	29.6	2.9	110266	4	US-09-949-016-14922	Sequence 14922, A	809	29.2	2.8	273	2	US-08-997-362-142	Sequence 142, App
C 737	29.6	2.9	114426	4	US-09-949-016-15078	Sequence 15078, A	810	29.2	2.8	273	3	US-09-095-855-142	Sequence 142, App
C 738	29.6	2.9	238815	4	US-09-949-016-16274	Sequence 16274, A	811	29.2	2.8	273	3	US-09-324-542-142	Sequence 142, App
C 739	29.6	2.9	312470	4	US-09-949-016-16274	Sequence 16274, A	812	29.2	2.8	273	3	US-09-205-426-142	Sequence 142, App
740	29.6	2.9	312957	4	US-09-949-001-31	Sequence 14043, A	813	29.2	2.8	358	4	US-09-513-999C-211	Sequence 211, App
741	29.6	2.9	312972	4	US-09-949-001-34	Sequence 34, Appl	814	29.2	2.8	366	4	US-09-252-991A-7382	Sequence 7382, Ap
C 742	29.6	2.9	336024	4	US-09-949-016-12373	Sequence 12373, A	C 815	29.2	2.8	420	4	US-09-252-991A-13290	Sequence 13290, A
743	29.4	2.8	255	4	US-09-513-999C-11125	Sequence 11125, A	816	29.2	2.8	450	4	US-09-902-540-6512	Sequence 6512, Ap
744	29.4	2.8	270	1	US-08-127-954-53	Sequence 53, Appl	817	29.2	2.8	504	4	US-09-270-767-2253	Sequence 2253, Ap
745	29.4	2.8	270	1	US-08-127-954-84	Sequence 84, Appl	818	29.2	2.8	504	4	US-09-270-767-17535	Sequence 17535, A
C 746	29.4	2.8	277	4	US-09-513-998C-34506	Sequence 34506, A	819	29.2	2.8	549	4	US-09-252-991A-5743	Sequence 5743, Ap
C 747	29.4	2.8	418	4	US-09-621-976-10709	Sequence 10709, A	820	29.2	2.8	601	4	US-09-949-016-176542	Sequence 176542, A
748	29.4	2.8	493	4	US-09-270-767-7655	Sequence 7655, Ap	821	29.2	2.8	624	4	US-09-252-991A-12674	Sequence 12674, A
749	29.4	2.8	493	4	US-09-270-767-22937	Sequence 22937, A	822	29.2	2.8	650	3	US-09-095-855-195	Sequence 195, App
C 750	29.4	2.8	601	4	US-09-949-016-57614	Sequence 57614, A	823	29.2	2.8	650	3	US-09-205-426-195	Sequence 195, App
C 751	29.4	2.8	601	4	US-09-949-016-57615	Sequence 57615, A	824	29.2	2.8	695	4	US-09-252-991A-1963	Sequence 1963, Ap
C 752	29.4	2.8	714	4	US-09-252-991A-3085	Sequence 3085, Ap	825	29.2	2.8	785	4	US-09-252-991A-14084	Sequence 14084, A
753	29.4	2.8	771	4	US-09-252-991A-2794	Sequence 2794, Ap	C 826	29.2	2.8	798	4	US-09-252-991A-2555	Sequence 2555, Ap
754	29.4	2.8	919	4	US-09-270-767-6882	Sequence 6882, Ap	827	29.2	2.8	801	4	US-09-252-991A-7458	Sequence 7458, Ap
755	29.4	2.8	919	4	US-09-270-767-22164	Sequence 22164, A	828	29.2	2.8	828	4	US-09-266-965-35	Sequence 35, Appl
C 756	29.4	2.8	975	4	US-09-489-039A-791	Sequence 791, App	829	29.2	2.8	1119	4	US-09-252-991A-7780	Sequence 7780, Ap
757	29.4	2.8	993	4	US-09-252-991A-2886	Sequence 2886, Ap	C 830	29.2	2.8	1134	4	US-09-902-540-6062	Sequence 6062, Ap

831	29.2	2.8	1146	4	US-09-252-991A-12818	Sequence 12818, A	c 904	29	2.8	601	4	US-09-949-016-30812	Sequence 30812, A
832	29.2	2.8	1221	4	US-09-252-991A-8402	Sequence 8402, Ap	905	29	2.8	601	4	US-09-949-016-89310	Sequence 89310, A
c 833	29.2	2.8	1353	4	US-09-252-991A-8442	Sequence 8442, Ap	906	29	2.8	601	4	US-09-949-016-89311	Sequence 89311, A
834	29.2	2.8	1386	4	US-09-949-016-3582	Sequence 3582, Ap	c 907	29	2.8	601	4	US-09-949-016-111578	Sequence 111578, A
c 835	29.2	2.8	1551	4	US-09-252-991A-2474	Sequence 2474, Ap	c 908	29	2.8	601	4	US-09-949-016-111579	Sequence 111579, A
836	29.2	2.8	1560	4	US-09-252-991A-2199	Sequence 2199, Ap	c 909	29	2.8	601	4	US-09-949-016-111580	Sequence 111580, A
c 837	29.2	2.8	1707	3	US-09-453-195A-1	Sequence 1, Appli	c 910	29	2.8	601	4	US-09-949-016-111726	Sequence 111726, A
c 838	29.2	2.8	1719	4	US-09-252-991A-7307	Sequence 7307, Ap	c 911	29	2.8	601	4	US-09-949-016-111727	Sequence 111727, A
839	29.2	2.8	1725	4	US-09-252-991A-830	Sequence 830, Ap	c 912	29	2.8	601	4	US-09-949-016-111728	Sequence 111728, A
840	29.2	2.8	1731	4	US-09-902-540-6944	Sequence 6944, Ap	c 913	29	2.8	601	4	US-09-949-016-111872	Sequence 111872, A
c 841	29.2	2.8	1776	4	US-09-252-991A-8333	Sequence 8333, Ap	c 914	29	2.8	601	4	US-09-949-016-111873	Sequence 111873, A
c 842	29.2	2.8	1845	4	US-09-252-991A-13124	Sequence 13124, A	c 915	29	2.8	601	4	US-09-949-016-111874	Sequence 111874, A
c 843	29.2	2.8	1887	4	US-09-252-991A-7920	Sequence 7920, Ap	c 916	29	2.8	601	4	US-09-949-016-112017	Sequence 112017, A
844	29.2	2.8	1911	4	US-09-252-991A-14136	Sequence 14136, A	c 917	29	2.8	601	4	US-09-949-016-112018	Sequence 112018, A
c 845	29.2	2.8	2125	4	US-09-485-529-14	Sequence 14, Appl	c 918	29	2.8	601	4	US-09-949-016-112019	Sequence 112019, A
c 846	29.2	2.8	2148	4	US-09-902-540-5682	Sequence 5682, Ap	c 919	29	2.8	601	4	US-09-949-016-131853	Sequence 131853, A
c 847	29.2	2.8	2163	4	US-09-252-991A-2047	Sequence 2047, Ap	c 920	29	2.8	601	4	US-09-949-016-138352	Sequence 138352, A
c 848	29.2	2.8	2190	4	US-09-252-991A-5685	Sequence 5685, Ap	c 921	29	2.8	601	4	US-09-949-016-138353	Sequence 138353, A
c 849	29.2	2.8	2214	4	US-09-902-540-9189	Sequence 9189, Ap	c 922	29	2.8	601	4	US-09-949-016-144439	Sequence 144439, A
c 850	29.2	2.8	2577	4	US-09-952-060-3	Sequence 3, Appli	c 923	29	2.8	601	4	US-09-949-016-147073	Sequence 147073, A
851	29.2	2.8	2580	4	US-09-774-528-327	Sequence 327, Ap	c 924	29	2.8	615	3	US-08-998-416-644	Sequence 644, App
c 852	29.2	2.8	2581	4	US-09-902-540-472	Sequence 472, Ap	c 925	29	2.8	750	4	US-09-902-540-8892	Sequence 8892, Ap
c 853	29.2	2.8	2598	4	US-09-816-094-1	Sequence 1, Appli	c 926	29	2.8	832	4	US-09-621-976-2813	Sequence 2813, Ap
c 854	29.2	2.8	2598	4	US-10-233-613-1	Sequence 1, Appli	c 927	29	2.8	840	4	US-03-252-991A-10789	Sequence 10789, A
c 855	29.2	2.8	2598	4	US-10-639-429-1	Sequence 1, Appli	c 928	29	2.8	1008	1	US-07-904-073-1	Sequence 1, Appli
c 856	29.2	2.8	2650	4	US-09-952-060-7	Sequence 7, Appli	c 929	29	2.8	1008	1	US-07-904-073-1	Sequence 1, Appli
c 857	29.2	2.8	2901	4	US-09-902-540-6866	Sequence 6866, Ap	c 930	29	2.8	1176	4	US-09-252-991A-3745	Sequence 3745, Ap
c 858	29.2	2.8	2903	4	US-09-949-016-5033	Sequence 5033, Ap	c 931	29	2.8	1265	4	US-09-614-912-195	Sequence 195, App
c 859	29.2	2.8	3396	3	US-08-974-549A-640	Sequence 640, App	c 932	29	2.8	1278	4	US-09-252-991A-738	Sequence 738, App
c 860	29.2	2.8	3396	4	US-09-721-456-640	Sequence 640, App	c 933	29	2.8	1278	4	US-09-489-039A-2413	Sequence 2413, Ap
c 861	29.2	2.8	3546	4	US-09-252-991A-1909	Sequence 1909, Ap	c 934	29	2.8	1341	4	US-09-902-540-8826	Sequence 8826, Ap
c 862	29.2	2.8	3597	4	US-09-634-238-105	Sequence 105, App	c 935	29	2.8	1359	4	US-09-252-991A-705	Sequence 705, App
c 863	29.2	2.8	3784	4	US-09-902-540-580	Sequence 580, App	c 936	29	2.8	1507	3	US-08-969-815-1	Sequence 1, Appli
c 864	29.2	2.8	4053	4	US-09-952-060-34	Sequence 34, Appl	c 937	29	2.8	1507	3	US-09-120-025-1	Sequence 1, Appli
c 865	29.2	2.8	4334	2	US-08-670-707A-38	Sequence 38, Appl	c 938	29	2.8	1507	3	US-09-710-481-1	Sequence 1, Appli
c 866	29.2	2.8	4334	3	US-09-037-601-38	Sequence 38, Appl	c 939	29	2.8	1507	4	US-09-533-875-1	Sequence 1, Appli
c 867	29.2	2.8	4334	3	US-09-315-179-38	Sequence 38, Appl	c 940	29	2.8	1507	4	US-09-768-670-1	Sequence 1, Appli
c 868	29.2	2.8	4587	4	US-09-902-540-600	Sequence 600, App	c 941	29	2.8	1587	4	US-09-796-266-1	Sequence 1, Appli
c 869	29.2	2.8	4647	4	US-09-252-991A-5730	Sequence 5730, Ap	c 942	29	2.8	1587	4	US-09-252-991A-676	Sequence 676, App
c 870	29.2	2.8	5720	4	US-09-800-729-18	Sequence 18, Appl	c 943	29	2.8	1620	4	US-09-252-991A-10368	Sequence 10368, A
c 871	29.2	2.8	6402	2	US-08-670-707A-36	Sequence 36, Appl	c 944	29	2.8	1638	4	US-09-902-540-7509	Sequence 7509, Ap
c 872	29.2	2.8	6402	3	US-09-037-601-36	Sequence 36, Appl	c 945	29	2.8	1656	4	US-09-252-991A-3787	Sequence 3787, Ap
c 873	29.2	2.8	6402	3	US-09-315-179-36	Sequence 36, Appl	c 946	29	2.8	1770	2	US-08-381-603-1	Sequence 1, Appli
c 874	29.2	2.8	6402	3	US-09-523-656-29	Sequence 29, Appl	c 947	29	2.8	1770	3	US-08-924-376-1	Sequence 1, Appli
c 875	29.2	2.8	7301	4	US-09-816-094-3	Sequence 3, Appli	c 948	29	2.8	1770	3	US-08-685-212-1	Sequence 1, Appli
c 876	29.2	2.8	7301	4	US-10-233-613-3	Sequence 3, Appli	c 949	29	2.8	1770	3	US-08-466-932A-1	Sequence 1, Appli
c 877	29.2	2.8	7301	4	US-10-639-429-3	Sequence 3, Appli	c 950	29	2.8	1770	5	PCT-US94-02414-1	Sequence 1, Appli
c 878	29.2	2.8	9076	4	US-09-949-016-12246	Sequence 12246, A	c 951	29	2.8	1770	5	PCT-US96-08899-1	Sequence 1, Appli
c 879	29.2	2.8	9077	4	US-09-949-016-16364	Sequence 16364, A	c 952	29	2.8	1833	4	US-09-252-991A-3728	Sequence 3728, Ap
c 880	29.2	2.8	11695	4	US-09-902-540-1045	Sequence 1045, Ap	c 953	29	2.8	1920	4	US-09-902-540-6398	Sequence 6398, Ap
c 881	29.2	2.8	12695	4	US-09-949-016-16775	Sequence 16775, A	c 954	29	2.8	1921	4	US-09-902-540-428	Sequence 428, App
c 882	29.2	2.8	13489	4	US-09-949-016-15911	Sequence 15911, A	c 955	29	2.8	1938	4	US-09-252-991A-8682	Sequence 8682, Ap
c 883	29.2	2.8	15923	4	US-09-902-540-1095	Sequence 1095, Ap	c 956	29	2.8	1971	4	US-09-252-991A-8564	Sequence 8564, Ap
c 884	29.2	2.8	16572	4	US-09-949-016-12409	Sequence 12409, A	c 957	29	2.8	2253	4	US-09-902-540-3708	Sequence 3708, Ap
c 885	29.2	2.8	16578	4	US-09-949-016-14680	Sequence 14680, A	c 958	29	2.8	2550	4	US-09-902-540-8526	Sequence 8526, Ap
c 886	29.2	2.8	22773	4	US-09-990-613A-6	Sequence 6, Appli	c 959	29	2.8	2622	4	US-09-949-016-4151	Sequence 4151, Ap
c 887	29.2	2.8	31199	4	US-09-949-016-16516	Sequence 16516, A	c 960	29	2.8	2657	2	US-08-424-881-1	Sequence 1, Appli
c 888	29.2	2.8	38519	4	US-09-952-060-28	Sequence 28, Appl	c 961	29	2.8	2657	2	US-08-874-763-1	Sequence 1, Appli
c 889	29.2	2.8	45716	3	US-08-965-048-5	Sequence 5, Appli	c 962	29	2.8	2657	3	US-09-370-867-1	Sequence 1, Appli
c 890	29.2	2.8	45989	3	US-08-965-048-6	Sequence 6, Appli	c 963	29	2.8	2657	3	US-09-729-472-1	Sequence 1, Appli
c 891	29.2	2.8	49225	4	US-09-902-540-1269	Sequence 1269, Ap	c 964	29	2.8	2657	3	US-09-729-499-1	Sequence 1, Appli
c 892	29.2	2.8	50725	4	US-09-902-540-1271	Sequence 1271, Ap	c 965	29	2.8	2659	4	US-09-902-540-4695	Sequence 4695, Ap
c 893	29.2	2.8	52992	4	US-09-949-016-16105	Sequence 16105, A	c 966	29	2.8	2733	4	US-09-313-942-37	Sequence 37, Appl
c 894	29.2	2.8	53500	4	US-09-266-965-76	Sequence 76, Appl	c 967	29	2.8	2750	4	US-09-976-594-376	Sequence 376, App
c 895	29.2	2.8	88950	4	US-09-949-016-17150	Sequence 17150, A	c 968	29	2.8	2985	4	US-09-902-540-9108	Sequence 9108, Ap
c 896	29.2	2.8	108310	4	US-09-949-016-16366	Sequence 16366, A	c 969	29	2.8	3011	1	US-07-821-716-1	Sequence 1, Appli
c 897	29.2	2.8	197875	4	US-09-949-016-15425	Sequence 15425, A	c 970	29	2.8	3011	4	US-08-406-824A-5	Sequence 5, Appli
c 898	29.2	2.8	235064	4	US-09-949-016-15390	Sequence 15390, A	c 971	29	2.8	3045	4	US-09-252-991A-14767	Sequence 14767, A
c 899	29	2.8	480	4	US-09-902-540-3465	Sequence 3465, Ap	c 972	29	2.8	3078	4	US-09-489-039A-922	Sequence 922, App
c 900	29	2.8	601	4	US-09-902-540-18703	Sequence 18703, A	c 973	29	2.8	3192	4	US-09-902-540-4843	Sequence 4843, Ap
c 901	29	2.8	601	4	US-09-949-016-18704	Sequence 18704, A	c 974	29	2.8	4079	4	US-09-016-434-1219	Sequence 1219, Ap
c 902	29	2.8	601	4	US-09-949-016-18705	Sequence 18705, A	c 975	29	2.8	4907	4	US-09-949-016-2701	Sequence 2701, Ap
c 903	29	2.8	601	4	US-09-949-016-30811	Sequence 30811, A	c 976	29	2.8	4910	4	US-09-023-655-1125	Sequence 1125, Ap

977	29	2.8	4910	4	US-09-814-915A-75	Sequence 75, Appl	1050	28.8	2.8	1273	4	US-09-778-510-3	Sequence 3, Appl
978	29	2.8	4910	4	US-09-949-016-129	Sequence 129, Appl	1051	28.8	2.8	1395	4	US-09-252-991A-16537	Sequence 16537, A
c 979	29	2.8	5165	4	US-09-902-540-729	Sequence 729, Appl	1052	28.8	2.8	1444	4	US-09-773-877B-23	Sequence 23, Appl
980	29	2.8	5173	4	US-09-949-016-1194	Sequence 1194, Ap	c1053	28.8	2.8	1467	4	US-09-252-991A-4853	Sequence 4853, Ap
981	29	2.8	5281	4	US-09-949-016-113	Sequence 13, Appl	c1054	28.8	2.8	1512	4	US-09-902-540-3874	Sequence 3874, A
982	29	2.8	7225	4	US-09-902-540-876	Sequence 876, Appl	c1055	28.8	2.8	1665	4	US-09-252-991A-16061	Sequence 16061, A
983	29	2.8	8264	4	US-09-949-016-15457	Sequence 15457, A	c1056	28.8	2.8	1806	4	US-09-902-540-3815	Sequence 3815, Ap
984	29	2.8	8765	4	US-09-902-540-939	Sequence 939, Appl	1057	28.8	2.8	1858	2	US-08-359-705B-7	Sequence 7, Appl
985	29	2.8	8820	4	US-09-902-540-974	Sequence 974, Appl	1058	28.8	2.8	1858	2	US-08-286-846A-7	Sequence 7, Appl
986	29	2.8	9053	4	US-09-976-594-306	Sequence 306, Appl	1059	28.8	2.8	1858	3	US-08-457-880A-7	Sequence 7, Appl
987	29	2.8	9097	4	US-09-902-540-947	Sequence 947, Appl	1060	28.8	2.8	1858	3	US-08-444-622A-7	Sequence 7, Appl
c 988	29	2.8	9321	4	US-09-902-540-998	Sequence 898, Appl	1061	28.8	2.8	1858	3	US-08-942-562-7	Sequence 7, Appl
989	29	2.8	12685	4	US-09-479-467A-3	Sequence 3, Appl	1062	28.8	2.8	1858	3	US-09-156-923-7	Sequence 7, Appl
990	29	2.8	16541	4	US-09-902-540-1165	Sequence 1165, Ap	1063	28.8	2.8	1887	4	US-09-252-991A-5560	Sequence 5560, Ap
991	29	2.8	18471	4	US-09-949-016-14228	Sequence 14228, A	c1064	28.8	2.8	1964	4	US-09-774-528-308	Sequence 308, App
992	29	2.8	21758	4	US-09-902-540-1238	Sequence 1238, Ap	1065	28.8	2.8	1984	4	US-09-949-016-758	Sequence 758, App
c 993	29	2.8	28958	4	US-09-902-540-1231	Sequence 1231, Ap	1066	28.8	2.8	1986	4	US-09-252-991A-4888	Sequence 4888, Ap
994	29	2.8	29935	4	US-09-949-016-11871	Sequence 11871, A	1067	28.8	2.8	2032	4	US-09-023-655-1483	Sequence 1483, Ap
995	29	2.8	29936	4	US-09-949-016-14443	Sequence 14443, A	1068	28.8	2.8	2040	2	US-08-031-538-10	Sequence 10, Appl
996	29	2.8	34422	4	US-09-949-016-12701	Sequence 12701, A	1069	28.8	2.8	2051	4	US-09-949-016-1712	Sequence 1712, Ap
997	29	2.8	34422	4	US-09-949-016-16075	Sequence 16075, A	c1070	28.8	2.8	2115	4	US-09-489-039A-6214	Sequence 6214, Ap
c 998	29	2.8	38119	4	US-09-949-016-17503	Sequence 17503, A	1071	28.8	2.8	2184	4	US-09-252-991A-9529	Sequence 9529, Ap
999	29	2.8	42246	4	US-09-949-016-17008	Sequence 17008, A	c1072	28.8	2.8	2346	4	US-09-252-991A-9636	Sequence 9636, Ap
1000	29	2.8	44789	4	US-09-949-016-13909	Sequence 13909, A	c1073	28.8	2.8	2358	4	US-09-902-540-2632	Sequence 2632, Ap
1001	29	2.8	48794	4	US-09-949-016-15637	Sequence 15637, A	c1074	28.8	2.8	2620	1	US-08-459-194-1	Sequence 1, Appl
1002	29	2.8	50453	4	US-09-949-016-16642	Sequence 16642, A	c1075	28.8	2.8	2620	3	US-07-968-953-1	Sequence 1, Appl
1003	29	2.8	50797	4	US-09-949-016-16346	Sequence 16346, A	c1076	28.8	2.8	2620	3	US-09-047-645-1	Sequence 1, Appl
1004	29	2.8	50797	4	US-09-949-016-16347	Sequence 16347, A	c1077	28.8	2.8	2657	2	US-08-424-881-1	Sequence 1, Appl
c1005	29	2.8	51242	4	US-09-949-016-12486	Sequence 12486, A	c1078	28.8	2.8	2657	2	US-08-874-763-1	Sequence 1, Appl
1006	29	2.8	59123	4	US-09-949-016-12177	Sequence 12177, A	c1079	28.8	2.8	2657	3	US-09-370-867-1	Sequence 1, Appl
c1007	29	2.8	94873	4	US-09-949-016-14277	Sequence 14277, A	c1080	28.8	2.8	2657	3	US-09-729-472-1	Sequence 1, Appl
1008	29	2.8	95255	4	US-09-949-016-17067	Sequence 17067, A	c1081	28.8	2.8	2657	2	US-09-729-499-1	Sequence 5, Appl
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1010	29	2.8	113876	4	US-09-949-016-14829	Sequence 14829, A	1083	28.8	2.8	2715	2	US-08-286-846A-5	Sequence 5, Appl
1011	29	2.8	115508	4	US-09-949-016-11800	Sequence 11800, A	1084	28.8	2.8	2715	3	US-08-444-622A-5	Sequence 5, Appl
1012	29	2.8	115508	4	US-09-949-016-14826	Sequence 14826, A	1085	28.8	2.8	2715	3	US-08-942-562-5	Sequence 5, Appl
1013	29	2.8	115508	4	US-09-949-016-14827	Sequence 14827, A	1086	28.8	2.8	2715	3	US-09-156-923-5	Sequence 5, Appl
1014	29	2.8	133613	4	US-09-949-016-15824	Sequence 15824, A	1087	28.8	2.8	2715	3	US-09-976-594-376	Sequence 376, App
c1015	29	2.8	238775	4	US-09-949-016-16435	Sequence 16435, A	c1088	28.8	2.8	2750	4	US-09-949-016-5225	Sequence 5225, Ap
c1016	29	2.8	374159	4	US-09-949-016-15868	Sequence 15868, A	c1089	28.8	2.8	2909	4	US-08-286-305A-8	Sequence 8, Appl
c1017	29	2.8	784019	4	US-09-949-016-14033	Sequence 14033, A	1090	28.8	2.8	2940	1	US-08-441-104A-8	Sequence 8, Appl
c1018	29	2.8	828152	4	US-09-949-016-12777	Sequence 12777, A	1091	28.8	2.8	2940	2	US-08-440-816A-8	Sequence 8, Appl
1019	28.8	2.8	225	3	US-08-985-492-11	Sequence 11, Appl	1092	28.8	2.8	2940	3	US-09-417-381A-8	Sequence 8, Appl
1020	28.8	2.8	265	4	US-09-513-999C-33279	Sequence 33279, A	1093	28.8	2.8	2940	3	US-09-724-797-81	Sequence 81, Appl
1021	28.8	2.8	480	2	US-08-642-406A-25	Sequence 25, Appl	1094	28.8	2.8	3033	3	US-09-189-462-5	Sequence 5, Appl
1022	28.8	2.8	480	3	US-09-199-534-25	Sequence 25, Appl	1095	28.8	2.8	4792	4	US-09-863-040-5	Sequence 5, Appl
c1024	28.8	2.8	519	4	US-09-270-767-14180	Sequence 14180, A	c1097	28.8	2.8	6927	4	US-09-949-016-17316	Sequence 17316, A
1025	28.8	2.8	579	4	US-09-252-991A-16342	Sequence 16342, A	c1098	28.8	2.8	12299	4	US-09-902-540-1056	Sequence 1056, Ap
1026	28.8	2.8	601	4	US-09-949-016-128664	Sequence 128664, A	c1099	28.8	2.8	13434	4	US-09-902-540-1003	Sequence 1003, Ap
c1027	28.8	2.8	601	4	US-09-949-016-162163	Sequence 162163, A	1100	28.8	2.8	14239	4	US-09-949-016-16811	Sequence 16811, A
c1028	28.8	2.8	601	4	US-09-949-016-162165	Sequence 162165, A	c1101	28.8	2.8	17173	4	US-09-902-540-1122	Sequence 1122, Ap
c1029	28.8	2.8	601	4	US-09-949-016-196805	Sequence 196805, A	c1102	28.8	2.8	21010	4	US-09-902-540-1188	Sequence 1188, Ap
1030	28.8	2.8	627	4	US-09-902-540-7323	Sequence 7323, Ap	c1103	28.8	2.8	21143	4	US-09-902-540-1191	Sequence 1191, Ap
1031	28.8	2.8	699	4	US-09-489-039A-2955	Sequence 2955, A	1104	28.8	2.8	26533	4	US-09-902-540-1199	Sequence 1199, Ap
1032	28.8	2.8	732	4	US-09-252-991A-11347	Sequence 11347, A	c1105	28.8	2.8	28958	1	US-08-258-261B-6	Sequence 6, Appl
1033	28.8	2.8	734	3	US-09-382-184-14	Sequence 14, Appl	c1106	28.8	2.8	28958	1	US-08-456-837-6	Sequence 6, Appl
c1034	28.8	2.8	819	4	US-09-489-039A-6248	Sequence 6248, Ap	c1107	28.8	2.8	28958	1	US-08-457-342-6	Sequence 6, Appl
c1035	28.8	2.8	846	4	US-09-902-540-4318	Sequence 4318, Ap	c1108	28.8	2.8	28958	1	US-08-457-646A-6	Sequence 6, Appl
c1036	28.8	2.8	913	4	US-09-509-712B-34	Sequence 34, Appl	c1109	28.8	2.8	28958	1	US-08-458-076A-6	Sequence 6, Appl
1037	28.8	2.8	924	4	US-09-252-991A-4864	Sequence 4864, Ap	c1110	28.8	2.8	28958	1	US-08-764-233A-4	Sequence 4, Appl
c1038	28.8	2.8	939	4	US-09-252-991A-5634	Sequence 5634, Ap	c1111	28.8	2.8	28958	1	US-08-457-335A-6	Sequence 6, Appl
1039	28.8	2.8	948	4	US-09-489-039A-2926	Sequence 2926, Ap	c1112	28.8	2.8	28958	1	US-08-729-214-6	Sequence 6, Appl
c1040	28.8	2.8	957	4	US-09-252-991A-5665	Sequence 5665, Ap	c1113	28.8	2.8	28958	3	US-09-028-534-6	Sequence 6, Appl
1041	28.8	2.8	984	4	US-09-248-796A-3305	Sequence 3305, Ap	c1114	28.8	2.8	37319	4	US-09-949-016-13164	Sequence 13164, A
c1042	28.8	2.8	984	4	US-09-902-540-4015	Sequence 4015, Ap	c1115	28.8	2.8	49377	1	US-08-764-233A-1	Sequence 1, Appl
1043	28.8	2.8	1092	1	US-08-400-422-1	Sequence 1, Appl	c1116	28.8	2.8	51273	4	US-09-949-016-13018	Sequence 13018, A
c1044	28.8	2.8	1125	2	US-08-997-080-153	Sequence 153, Appl	c1117	28.8	2.8	60788	4	US-09-949-016-16789	Sequence 16789, A
c1045	28.8	2.8	1125	2	US-08-997-362-153	Sequence 153, Appl	c1118	28.8	2.8	64291	4	US-09-949-016-16278	Sequence 16278, A
c1046	28.8	2.8	1125	3	US-09-095-855-153	Sequence 153, Appl	c1119	28.8	2.8	71645	4	US-09-949-016-12126	Sequence 12126, A
c1047	28.8	2.8	1125	3	US-09-324-542-153	Sequence 153, App	1120	28.8	2.8	71651	4	US-09-949-016-17258	Sequence 17258, A
c1048	28.8	2.8	1125	3	US-09-205-426-153	Sequence 153, App	c1121	28.8	2.8	95750	4	US-09-949-016-11926	Sequence 11926, A
1049	28.8	2.8	1203	4	US-09-252-991A-9574	Sequence 9574, Ap	c1122	28.8	2.8	117410	4	US-09-949-016-12262	Sequence 12262, A

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c1124	28.8	2.8	285986	4	US-09-949-016-12287	Sequence 12287, A	1197	28.6	2.8	17606	3	US-08-943-731-4	Sequence 4, Appli
c1125	28.8	2.8	288031	4	US-09-949-016-14864	Sequence 14864, A	1198	28.6	2.8	20017	4	US-09-943-016-17147	Sequence 17147, A
1126	28.6	2.8	262	4	US-09-854-133-619	Sequence 619, App	c1199	28.6	2.8	21330	4	US-09-902-540-1209	Sequence 1209, Ap
1127	28.6	2.8	319	3	US-09-423-233-6	Sequence 6, Appli	c1200	28.6	2.8	26136	4	US-09-949-016-13640	Sequence 13640, A
c1128	28.6	2.8	419	4	US-09-513-999C-23336	Sequence 23336, A	1201	28.6	2.8	37769	4	US-08-311-731A-23	Sequence 23, Appl
1129	28.6	2.8	432	4	US-09-513-999C-210	Sequence 210, App	1202	28.6	2.8	41768	4	US-09-902-540-1266	Sequence 1266, Ap
1130	28.6	2.8	445	4	US-09-621-976-10333	Sequence 10333, A	c1203	28.6	2.8	46902	4	US-09-949-016-13844	Sequence 13844, A
1131	28.6	2.8	465	4	US-09-489-039A-2449	Sequence 2449, Ap	c1204	28.6	2.8	68452	4	US-09-949-016-13305	Sequence 13305, A
c1132	28.6	2.8	481	4	US-09-270-767-11110	Sequence 11110, A	c1205	28.6	2.8	96739	4	US-09-949-016-15606	Sequence 15606, A
c1133	28.6	2.8	486	4	US-09-252-991A-13452	Sequence 13452, A	c1206	28.6	2.8	98701	4	US-09-949-016-15898	Sequence 15898, A
c1134	28.6	2.8	585	4	US-09-902-540-5518	Sequence 5518, Ap	c1207	28.6	2.8	98701	4	US-09-949-016-15899	Sequence 15899, A
c1135	28.6	2.8	601	4	US-09-949-016-65193	Sequence 65193, A	c1208	28.6	2.8	123980	4	US-09-949-016-12544	Sequence 12544, A
c1136	28.6	2.8	601	4	US-09-949-016-71301	Sequence 71301, A	c1209	28.6	2.8	189560	4	US-09-949-016-17202	Sequence 17202, A
c1137	28.6	2.8	601	4	US-09-949-016-188953	Sequence 188953, A	1210	28.6	2.8	194933	4	US-09-949-016-14172	Sequence 14172, A
c1138	28.6	2.8	601	4	US-09-949-016-130928	Sequence 130928, A	c1211	28.6	2.8	239527	4	US-09-949-016-15980	Sequence 15980, A
c1139	28.6	2.8	606	4	US-09-902-540-6157	Sequence 6157, Ap	1212	28.6	2.8	325791	4	US-09-768-185A-1	Sequence 1, Appli
c1140	28.6	2.8	608	4	US-09-902-540-3	Sequence 3, Appli	1213	28.6	2.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
1141	28.6	2.8	767	4	US-09-799-451-132	Sequence 132, App	1214	28.6	2.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c1142	28.6	2.8	849	4	US-09-270-767-11509	Sequence 11509, A	1215	28.4	2.7	364	4	US-09-621-976-17202	Sequence 17202, A
1143	28.6	2.8	906	2	US-08-656-906-24	Sequence 24, Appl	c1216	28.4	2.7	394	4	US-09-513-999C-34127	Sequence 34127, A
1144	28.6	2.8	906	3	US-09-217-847-24	Sequence 24, Appl	c1217	28.4	2.7	394	4	US-09-471-276-537	Sequence 537, App
c1145	28.6	2.8	968	4	US-09-864-866-46	Sequence 46, Appl	1218	28.4	2.7	399	4	US-09-252-991A-11223	Sequence 11223, A
1146	28.6	2.8	968	4	US-09-902-540-6625	Sequence 6625, Ap	1219	28.4	2.7	404	4	US-09-621-976-935	Sequence 935, App
c1147	28.6	2.8	1038	4	US-09-489-039A-1898	Sequence 1898, Ap	1220	28.4	2.7	416	4	US-09-485-529-18	Sequence 18, Appl
1148	28.6	2.8	1209	4	US-08-482-385A-1	Sequence 1, Appli	c1221	28.4	2.7	601	4	US-09-949-016-42963	Sequence 42963, A
c1149	28.6	2.8	1209	4	US-09-252-991A-13551	Sequence 13551, A	c1222	28.4	2.7	601	4	US-09-949-016-162164	Sequence 162164, A
c1150	28.6	2.8	1218	1	US-08-351-473B-6	Sequence 6, Appli	1223	28.4	2.7	647	4	US-10-101-464A-317	Sequence 317, App
1151	28.6	2.8	1219	4	US-08-981-700A-3	Sequence 3, Appli	1224	28.4	2.7	651	4	US-09-489-039A-2367	Sequence 2367, Ap
c1152	28.6	2.8	1230	4	US-09-252-991A-13890	Sequence 13890, A	1225	28.4	2.7	654	4	US-09-252-991A-16482	Sequence 16482, A
c1153	28.6	2.8	1239	4	US-09-252-991A-13787	Sequence 13787, A	1226	28.4	2.7	660	4	US-09-252-991A-5866	Sequence 5866, Ap
c1154	28.6	2.8	1299	3	US-09-472-971-2	Sequence 2, Appli	1227	28.4	2.7	786	4	US-09-252-991A-13761	Sequence 13761, A
1155	28.6	2.8	1344	4	US-09-252-991A-13647	Sequence 13647, A	1228	28.4	2.7	786	4	US-09-252-991A-2696	Sequence 2696, Ap
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1157	28.6	2.8	1353	4	US-09-270-767-24429	Sequence 24429, A	c1230	28.4	2.7	1026	4	US-09-902-540-9683	Sequence 9683, Ap
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c1163	28.6	2.8	1777	3	US-09-058-260-25	Sequence 25, Appl	1236	28.4	2.7	1335	2	US-08-659-984A-4	Sequence 4, Appli
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1170	28.6	2.8	2229	4	US-09-902-540-4193	Sequence 4193, Ap	1243	28.4	2.7	1416	3	US-09-479-453-3	Sequence 3, Appli
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1319	28.2	2.7	391	4	US-09-433-826B-228	Sequence 228, App	1392	28.2	2.7	1833	4	US-09-635-359B-6	Sequence 6, Appli
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c1328	28.2	2.7	462	4	US-09-270-767-17601	Sequence 17601, A	c1401	28.2	2.7	1883	3	US-09-291-692-3	Sequence 3, Appli
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1433 28.2 2.7 2856 4 US-09-630-940B-135 Sequence 135, App
1434 28.2 2.7 2856 4 US-09-285-479-135 Sequence 135, App
1435 28.2 2.7 2970 4 US-09-252-991A-15898 Sequence 15898, A
1436 28.2 2.7 2970 4 US-09-081-385-4 Sequence 4, Appl
1437 28.2 2.7 2998 4 US-09-081-385-149 Sequence 149, App
1438 28.2 2.7 2998 4 US-09-252-991A-6008 Sequence 6008, Ap
1439 28.2 2.7 3378 4 US-09-252-991A-2158 Sequence 2158, Ap
1440 28.2 2.7 3486 4 US-09-252-991A-6301 Sequence 6301, Ap
1441 28.2 2.7 3741 4 US-09-252-991A-6569 Sequence 6569, Ap
1442 28.2 2.7 3966 4 US-09-949-016-2932 Sequence 2932, Ap
1443 28.2 2.7 3978 4 US-09-949-016-1797 Sequence 1797, Ap
1444 28.2 2.7 4486 4 US-09-902-540-677 Sequence 677, App
1445 28.2 2.7 4549 4 US-09-774-528-153 Sequence 153, App
1446 28.2 2.7 4979 4 US-09-949-016-238 Sequence 238, App
1447 28.2 2.7 5781 4 US-09-902-540-711 Sequence 711, App
1448 28.2 2.7 6515 4 US-09-569-975-13 Sequence 13, Appl
1449 28.2 2.7 6603 4 US-09-902-540-796 Sequence 796, App
1450 28.2 2.7 7235 4 US-08-786-531B-6 Sequence 6, Appl
1451 28.2 2.7 7541 4 US-09-637-048C-4 Sequence 4, Appl
1452 28.2 2.7 7541 4 US-10-435-835-4 Sequence 4, Appl
1453 28.2 2.7 10301 4 US-09-902-540-985 Sequence 985, App
1454 28.2 2.7 10391 4 US-09-902-540-958 Sequence 958, App
1455 28.2 2.7 10878 4 US-09-911-842A-1 Sequence 1, Appl
1456 28.2 2.7 11254 4 US-09-902-540-1040 Sequence 1040, Ap
1457 28.2 2.7 12028 4 US-09-902-540-1071 Sequence 1071, Ap
1458 28.2 2.7 12739 4 US-09-902-540-1011 Sequence 1011, Ap
1459 28.2 2.7 13019 4 US-09-902-540-1171 Sequence 1171, Ap
1460 28.2 2.7 19567 4 US-09-949-016-15340 Sequence 15340, A
1461 28.2 2.7 21143 4 US-09-902-540-1191 Sequence 1191, Ap
1462 28.2 2.7 26841 4 US-09-949-016-15893 Sequence 15893, A
1463 28.2 2.7 26896 4 US-09-949-016-16800 Sequence 16800, A
1464 28.2 2.7 27578 4 US-09-949-016-12167 Sequence 12167, A
1465 28.2 2.7 27579 4 US-09-949-016-15005 Sequence 15005, A
1466 28.2 2.7 30780 4 US-09-902-540-1243 Sequence 1243, Ap
1467 28.2 2.7 41927 4 US-09-902-540-1268 Sequence 1268, Ap
1468 28.2 2.7 45337 4 US-09-949-016-13458 Sequence 13458, A
1469 28.2 2.7 48039 4 US-09-949-016-15990 Sequence 15990, A
1470 28.2 2.7 51807 4 US-09-949-016-15333 Sequence 15333, A
1471 28.2 2.7 63183 4 US-09-949-016-13047 Sequence 13047, A
1472 28.2 2.7 63183 4 US-09-949-016-13048 Sequence 13048, A
1473 28.2 2.7 67002 4 US-09-949-016-16803 Sequence 16803, A
1474 28.2 2.7 80161 3 US-09-036-987A-1 Sequence 1, Appl
1475 28.2 2.7 80161 3 US-09-370-700-1 Sequence 1, Appl
1476 28.2 2.7 80161 4 US-09-603-207-1 Sequence 1, Appl
1477 28.2 2.7 92139 4 US-09-918-686-1 Sequence 1, Appl
1478 28.2 2.7 97989 4 US-09-949-016-13208 Sequence 13208, A
1479 28.2 2.7 113186 4 US-09-949-016-17572 Sequence 17572, A
1480 28.2 2.7 134890 4 US-09-949-016-15602 Sequence 15602, A
1481 28.2 2.7 165651 4 US-09-949-016-13032 Sequence 13032, A
1482 28.2 2.7 314798 4 US-09-949-016-13539 Sequence 13539, A
1483 28.2 2.7 270 4 US-09-189-618A-3 Sequence 3, Appl
1484 28.2 2.7 270 4 US-09-189-618A-16 Sequence 16, Appl
1485 28.2 2.7 311 4 US-09-313-294A-4662 Sequence 4662, Ap
1486 28.2 2.7 316 4 US-09-313-294A-3850 Sequence 3850, Ap
1487 28.2 2.7 364 4 US-09-621-976-17202 Sequence 17202, A
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RESULT 1

US-09-700-397-2
; Patent No. 6664383

; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of

; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485

; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 1693

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Clone OCO01 derived from human brain

; NAME/KEY: CDS

; LOCATION: (130)..(1161)

; NAME/KEY: sig_peptide

; LOCATION: (130)..(213)

; NAME/KEY: mat_peptide

; LOCATION: (214)..()

US-09-700-397-2

Query Match 100.0%; Score 1035; DB 4; Length 1693;

Best Local Similarity 100.0%; Pred.No. 7.5e-307;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAATAATCATACTCTCTTGGGCAATCTTACGGGGGTG 60

Db 130 ATGAAACCATCCAGCCAAATAATCATACTCTCTTGGGCAATCTTACGGGGGTG 189

Qy 61 GCTCCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 120

Db 190 GCTCCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 249

Qy 121 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCACTATTGAC 180

Db 250 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCACTATTGAC 309

Qy 181 AACCGGTCACCCGGGTGGCTTGGCTAAACCGAGACCATCTCTATGCTGGGAATGAC 240

Db 310 AACCGGTCACCCGGGTGGCTTGGCTAAACCGAGACCATCTCTATGCTGGGAATGAC 369

Qy 241 AAGTGGTGCCTGGATCTCGCGTGGTCTTCTAGAGCAACCCAAACGACGTACGACATC 300

Db 370 AAGTGGTGCCTGGATCTCGCGTGGTCTTCTAGAGCAACCCAAACGACGTACGACATC 429

ALIGNMENTS

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Qy 301 GAGATCCAGAACGCTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC 360
Db 430 GAGATCCAGAACGCTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC 489
Qy 361 AACCACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTGTAG 420
Db 490 AACCACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTGTAG 549
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGATAGCAACT 480
Db 550 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGATAGCAACT 609
Qy 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 610 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 669
Qy 541 AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 600
Db 670 AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 729
Qy 601 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGGAGATGAAGGTCAACGTTGAC 660
Db 730 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGGAGATGAAGGTCAACGTTGAC 789
Qy 661 TATCCACCATACATTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Db 790 TATCCACCATACATTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 849
Qy 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGAAGGATGACAAA 780
Db 850 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGAAGGATGACAAA 909
Qy 781 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 840
Db 910 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 969
Qy 841 ATCTTCTCAATGTCTTGAACATGACTATGGGAATACACTTGGTGGCCCTCCAAACAG 900
Db 970 ATCTTCTCAATGTCTTGAACATGACTATGGGAATACACTTGGTGGCCCTCCAAACAG 1029
Qy 901 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCCGTCAGCGAGGTGAGC 960
Db 1030 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCCGTCAGCGAGGTGAGC 1089
Qy 961 AACGCGAGTCGAGAGGGGAGGCTGGCTTGGCTGGCTGGCTCTTCTGGCTTTCACCTG 1020
Db 1090 AACGCGAGTCGAGAGGGGAGGCTGGCTTGGCTGGCTGGCTCTTCTGGCTTTCACCTG 1149
Qy 1021 CTCTCAAAATTTGA 1035
Db 1150 CTCTCAAAATTTGA 1164

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RESULT 2

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US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-700-397-1
Query Match 99.7%; Score 1032; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 4.7e-306;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAAAAACCATCCAGCCAAATAATGCACAAATCTATCTCTTTGGGCAATCTTCACGGGGCTG 60
Db 1 ATGAAAAACCATCCAGCCAAATAATGCACAAATCTATCTCTTTGGGCAATCTTCACGGGGCTG 60
Qy 61 GCTGCTCTGTGTCTCTTTCCAAAGGAGTCCCGTGGCGAGCGAGATGCACTTCCCCAAA 120
Db 61 GCTGCTCTGTGTCTCTTTCCAAAGGAGTCCCGTGGCGAGCGAGATGCACTTCCCCAAA 120
Qy 121 GCTATGACAAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Db 121 GCTATGACAAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Qy 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
Db 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
Qy 241 AAGTGTGCTGTGATCTCTCGGTGGTCTCTTGTAGCAACACCCAAAACGAGTACAGCATC 300
Db 241 AAGTGTGCTGTGATCTCTCGGTGGTCTCTTGTAGCAACACCCAAAACGAGTACAGCATC 300
Qy 301 GAGATCCAGAACGTTGATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC 360
Db 301 GAGATCCAGAACGTTGATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC 360
Qy 361 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAG 420
Db 361 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAG 420
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACTGATAGCAACT 480
Db 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACTGATAGCAACT 480
Qy 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Qy 541 AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTACAGGGGACTACGAG 600
Db 541 AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTACAGGGGACTACGAG 600
Qy 601 TGCAGTGCCTCCAAATGACGTGGCGCGCCGTGGTACGAGAGTAAAGGTCAACGTTGAC 660
Db 601 TGCAGTGCCTCCAAATGACGTGGCGCGCCGTGGTACGAGAGTAAAGGTCAACGTTGAC 660
Qy 661 TATCCACCATACATTTCAGAGGCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Db 661 TATCCACCATACATTTCAGAGGCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Qy 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGAAGGATGACAAA 780
Db 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGAAGGATGACAAA 780
Qy 781 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 840
Db 781 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 840
Qy 841 ATCTTCTCAATGTCTTGAACATGACTATGGGAATACACTTCCGTGGCCCTCCAAACAG 900
Db 841 ATCTTCTCAATGTCTTGAACATGACTATGGGAATACACTTCCGTGGCCCTCCAAACAG 900
Qy 901 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCCGTCAGCGAGGTGAGC 960
Db 901 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCCGTCAGCGAGGTGAGC 960
Qy 961 AACGCGAGTCGAGAGGGGAGGCTGGCTTGGCTGGCTGGCTCTTCTGGCTTTCGACCTG 1020
Db 961 AACGCGAGTCGAGAGGGGAGGCTGGCTTGGCTGGCTGGCTCTTCTGGCTTTCGACCTG 1020

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QY 1021 CTTCTCAAAATTT 1032
Db 1021 CTTCTCAAAATTT 1032

RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-5

Query Match 90.7%; Score 939; DB 4; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.5e-277; Indels 0; Gaps 0;
Matches 939; Conservative 0; Mismatches 0;

QY 94 CGCAGCGAGATGCCACCTTCCCAAAGCTATGGACAAACGTCGCGTCCGGCAGGGGAG 153
Db 1 CGCAGCGAGATGCCACCTTCCCAAAGCTATGGACAAACGTCGCGTCCGGCAGGGGAG 60

QY 154 AGCGCCACCTCAGGTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGCTAAACCGC 213
Db 61 AGCGCCACCTCAGGTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGCTAAACCGC 120

QY 214 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCTCGGTGGTCTCTG 273
Db 121 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCTCGGTGGTCTCTG 180

QY 274 AGCAACACCCAAACCGCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACGAGGCG 333
Db 181 AGCAACACCCAAACCGCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACGAGGCG 240

QY 334 CTTTACACCTGCTCGGTGACAGACAGACAAACCCAAAGACCTCTAGGGTCACTCAAT 393
Db 241 CTTTACACCTGCTCGGTGACAGACAGACAAACCCAAAGACCTCTAGGGTCACTCAAT 300

QY 394 GTGCAAGTATCTCCAAATTTGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 453
Db 301 GTGCAAGTATCTCCAAATTTGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 360

QY 454 AATATTAGCCTCACCTGCATAGCACTGGTAGACAGACGCTTACGGTTACTTTGAGACAC 513
Db 361 AATATTAGCCTCACCTGCATAGCACTGGTAGACAGACGCTTACGGTTACTTTGAGACAC 420

QY 514 ATCTCTCCAAAGCGGTTGGCTTTGTGATGTAAGACGAATATTGGAAATTTCAAGGCAATC 573
Db 421 ATCTCTCCAAAGCGGTTGGCTTTGTGATGTAAGACGAATATTGGAAATTTCAAGGCAATC 480

QY 574 ACCCGGAGCAGTACAGGAGCTTACAGTGCAGTGCCTCCATGAGTGGCGCGCCGCTG 633
Db 481 ACCCGGAGCAGTACAGGAGCTTACAGTGCAGTGCCTCCATGAGTGGCGCGCCGCTG 540

QY 634 GTACGAGAGTAAAGGTCAACCGTGAATCTATCCACCATACATTTCAAGAGCCAAAGGTTACA 693
Db 541 GTACGAGAGTAAAGGTCAACCGTGAATCTATCCACCATACATTTCAAGAGCCAAAGGTTACA 600

QY 694 GGTGTCTCCCGTGGGACAAAGGGGACACTGTCAGTGTGAAAGCCTCAGCAGTCCCTCTCAGCA 753

Db 601 GGTGTCTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCA 660
QY 754 GAAATTCAGTGTACAAAGATGACAAAAGACTGATTGAAGGAAAAGAGGGGTGAAAGTG 813
Db 661 GAATTCAGTGTACAAAGATGACAAAAGACTGATTGAAGGAAAAGAGGGGTGAAAGTG 720

QY 814 GAAACACAGACCTTTCTCTCCTCAAAAATCATCTCTTCTCAATGTCTCTGAACATGACTATGG 873
Db 721 GAAACACAGACCTTTCTCTCCTCAAAAATCATCTCTTCTCAATGTCTCTGAACATGACTATGG 780

QY 874 AACTACACTTGGTGGCTCCAAAGCTGGGCGACACCAATGCCAGCATCATGCTATTT 933
Db 781 AACTACACTTGGTGGCTCCAAAGCTGGGCGACACCAATGCCAGCATCATGCTATTT 840

QY 934 GGTCCAGGCGCGTCCAGCGAGTGAAGCAACCGGCGCTGAGGAGGCGAGGCTGCTCTGG 993
Db 841 GGTCCAGGCGCGTCCAGCGAGTGAAGCAACCGGCGCTGAGGAGGCGAGGCTGCTCTGG 900

QY 994 CTGCTGCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 1032
Db 901 CTGCTGCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 939

RESULT 4
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:

US-08-414-657D-3

Query Match 33.0%; Score 342; DB 2; Length 1238;
Best Local Similarity 61.9%; Pred. No. 2.6e-94;
Matches 597; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

QY 72 TCTCTTCCAAAGAGTCCCGTCCGAGCGGAGATGCCACCTTCCCAAGCTATGGACAA 131
DB 121 TCTTCCACAGACTGCCCGTTCCGAGCGTGGAT-----TTTAAACCGAGCGACGACAA 174

QY 132 CGTGACGGTCCGCGAGCGGGGAGAGCGCCACCTCAGGTGSCACTATTGCAACCCGGGTGCAC 191
DB 175 CATCACCGTGAAGCGAGCGGACACGGCCATCTCAGGTGTGTGGTAGAAGCAAGAACTC 234

QY 192 CCGGTGCGCTGGCTAAACCGCAGACCATCTCTATGCTGGGAATGACAAAGTGGTGCCT 251
DB 235 GAAAGTGGCCCTGGTTGAACCGCTCTGGGCATCATCTTCGTCGACGCAAGTGGTCTCT 294

QY 252 GGATCCTCGCTGGTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 311
DB 295 GGACCTCGGTTGAGCTGGAGAAACGCCATGTCTTGGANATACAGCTTCCGAATCCAGAA 354

QY 312 CGTGATGTGATGACAGGGGCCCTTTACACTGCTCGGTGCAGACAGACAAACCCAAA 371
DB 355 GGTGATGTCTATGATGAAGGATCCTACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

QY 372 GACCTTAGGTCCACCTCATTTGCAAGTATCTCCCAAATTTGAGAGATTTCTTCAGA 431
DB 415 GACCTCTCAAGTTTACTTGATTTGTAACAAGTTCACCAAAAGATCTCCACATCTCTCCGA 474

QY 432 TATCTCCATTAATGAAGGGAACAATATTAGCTCTACCTGCATAGCAACTGGTAGACAGA 491
DB 475 TGTACTGTGAATGAGGCGAGCAATGTAAACCTGTCTGCAATGGCCATGGCGCCCTGA 534

QY 492 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTTGTGAGTGAAGACA 551
DB 535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAAGAAATTTGAAGGAGAAGA 594

QY 552 ATACTTGAATTCAGGCGNTACCCGGGAGCATCAGGGAGTACGAGTGCAGTGCCTC 611
DB 595 ATATCTGAGATCTTAGGCNTACACAGGGAACAGTCAGGCAAAATATGAGTGCAGAGGCTGC 654

QY 612 CAATGACGTGGCGCGCGGTGAGTACGAGAGTAAAGGTACCGTGAACCTATCCACATA 671
DB 655 CAACGAGTCTCTCCGCGGATGTCAACAAGTCAAGTCACTGTGAACCTATCCACCCAC 714

QY 672 CATTTCAAGAACGAGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGTGA 731
DB 715 CATCACAGTCTAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCCCTCAAAATGTGA 774

QY 732 AGCCTCAGCAGTCCCTCAGCAGATTCAGTGGTTACAGGATGACAAAGACTGATGA 791
DB 775 AGCCTCAGCGGTGCTGCACCTGACTTTGAGTGGTACCGGATGACACG---GATAAA 831

QY 792 AGGAAGAAAGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACCTCATCTTCTTCAA 851
DB 832 CAGTGCAAAACGCGCTTGAGATTAGAGCACTGAGGGCCAGTCTCCCTGACGGTGAACCA 891

QY 852 TGTCTCTGAACATGACTATGGAACTACACTTGGGTGGCCCTTCCAAACAGTGGGCGCAC 911
DB 892 CGTCACTGAGGAACACTACCGCAACTATACCTGTGTGGCTGCGCAACAGCTCGGCGTCAC 951

QY 912 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGACGACGCGCATC 971
DB 952 CAATGCCAGCCTAGTCTCTTTTTCAGACCCCGGCTCGGTGAG---AGGAATCAACGGATTCAT 1008

QY 972 GAGGAGGCGAGCTCGCTGCTGCTCTCTTCTGCTGCTTGTGACCTGCTTCTCAAAAT 1031
DB 1009 CAGTCTGCGGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCTTCTCAGCAATG 1068

QY 1032 TTGA 1035
DB 1069 TTAA 1072

RESULT 5

US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827

GENERAL INFORMATION:

APPLICANT: Levitt, Pat R.
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/135,080

FILING DATE: 17-AUG-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/414,657

FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1238 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 56...1069

OTHER INFORMATION:

US-09-135-080-3

Query Match 33.0%; Score 342; DB 3; Length 1238;

Best Local Similarity 61.9%; Pred. No. 2.6e-94;

Matches 597; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

QY 72 TCTCTTCCAAAGAGTCCCGTCCGAGCGGAGATGCCACCTTCCCAAGCTATGGACAA 131
DB 121 TCTTCCACAGACTGCCCGTTCCGAGCGTGGAT-----TTTAAACCGAGCGACGACAA 174

QY 132 CGTGACGGTCCGCGAGCGGGGAGAGCGCCACCTCAGGTGCACTATTGCAACCCGGGTGCAC 191
DB 175 CATCACCGTGAAGCGAGCGGAGACAGCCATCTCAGGTGTGTGGTAGAAGCAAGAACTC 234

QY 192 CCGGTGCGCTGGCTAAACCGCAGACCATCTCTATGCTGGGAATGACAAAGTGGTGCCT 251
DB 235 GAAAGTGGCCCTGGTTGAACCGCTCTGGGCATCATCTTCGTCGACGCAAGTGGTCTCT 294

QY 252 GGATCCTCGGTGGTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 311
DB 295 GGACCTCGGTTGAGCTGGAGAAACGCCATGTCTTGGANATACAGCTTCCGAATCCAGAA 354


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QY 312 CQTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACACACCCAAA 371
Db 355 GGTGATGTCTATGATGAGGATCTTACACATGCTCAGTTACAGACACGATGAGCCAA 414
QY 372 GACCTCTAGGGTCCACCTCATTTGTCAGATCTCCCAAAATTTGATGAGATTTCTTCA 431
Db 415 GACCTCTCAAGTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGAT 474
QY 432 TATCTCCATTAATGAAGGAAACAATATTTAGCCCTCAGCTGATGATGATGATGATGAT 491
Db 475 TGTCACTGTGATGAGGAGCAATGATTAACCTGCTGATGATGATGATGATGATGATGAT 534
QY 492 GCTTACGTTTACTTGGAGACATCTCTCCAAAGGGTGTGCTTTGATGATGATGATGAT 551
Db 535 ACCTGTTTATCCTGAGACACCTTTACACCACTTGAAGAGAAATTTGAAGGAGAAAGA 594
QY 552 ATACTTGAATTTAGGGGATCACCGGAGCAGTACAGGGGACTACGAGTGCAGTGCCTC 611
Db 595 ATATCTGGAGATCTTAGGATCACAGGGAACAGTCAGGCAAAATATGATGATGATGATGAT 654
QY 612 CAATGACGTGGCGCGCGCTGTACGGAGATGAAGGTCAAGGTGAATATCCACCATATA 671
Db 655 CAACGAGTCTCTCGCGGATGTCAACAAGTCAAGTCACTGTGAATATCCACCCAC 714
QY 672 CATTTACAGAGCAAGGTGACAGGTGTCCTCCGAGGACAAAGGGGACATGCACTGTGA 731
Db 715 CATCACAGAGTCTAAGAGCAATGAAGGACCAACACAGGACGACAAAGCTTCCCTCAATGTGA 774
QY 732 AGCCTCAGAGTCCCTCAGCAGATTCAGGTGATCAAGGTGATCAAGGATGACAAAGTGA 791
Db 775 AGCCTCAGCGGTCTGACCTGACCTTTGAGTGGTACCGGATGACACAG---GATAAA 831
QY 792 AGGAAGAAAGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 851
Db 832 CAGTGCMAACGGCTTGAGATTAAGGACATGAGGCGGAGTCTCCTCGAGGTGACCAA 891
QY 852 TGTCTCTGAACATGATGAGGAACTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db 892 COTCACTGAGGAACACTACGGCAACTATACCTGTGTGGTGGTGGTGGTGGTGGTGGTGGT 951
QY 912 CAATGCCAGCATCATGCTATTTGTCAGGCGGCTGAGGAGTGAAGGAGTGAAGGAGTGA 971
Db 952 CAATGCCAGCTTGTCTTTTTCAGACCCGCGGTGCTGAG---AGGAATCAAGGATTCAT 1008
QY 972 GAGGAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
Db 1009 CAGTCTGGCGGTACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
QY 1032 TTGA 1035
Db 1069 TTAA 1072

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RESULT 6

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US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..924
; OTHER INFORMATION:
US-08-414-657D-7

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Query Match 32.9%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 5.9e-94;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;
QY 72 TCTCTTCAAGAGTGGCCGTCGCGAGCGGAGATGCCACCTTCCCAAGCTATGACAA 131
Db 45 TCTTCCACAGAGTGCCTGTTCGAGCGTGGAT-----TTTAAACCGAGGACGACAA 98
QY 132 CGTACGCTCGCGAGCGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGCTCAC 191
Db 99 CATCACCTGAGGAGCGGAGACACGCCATCTCAGGTGCGTTCTAGAGACAGAACTC 158
QY 192 CCGGTGCTGCTGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGTGCT 251
Db 159 AAAGTGGCTGTTGAACCGTTCTGGCATCATTTTCTGTCATGACATGACAAAGTGTCT 218
QY 252 GATCTCTGCTGCTGCTTCTTGAGCAACACCCAAAGCAGTACAGCATGAGATCCAGAA 311
Db 219 GGACCCACGGGTGAGCTGGAGAAACGCCATTTCTTGGAAATACAGCTCCGAATCCAGAA 278
QY 312 CGTGTATGTATGACGAGGCGCTTACACCTGCTCGGTGACAGACAGACACCCCAAA 371
Db 279 GGTGATGTCTATGATGAGGTTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 338
QY 372 GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCA 431
Db 339 GACCTCCCAAGTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 398
QY 432 TATCTCCATTAATGAAGGAAACAATATTTAGGCTTACCTGCTGATGATGATGATGATGAT 491
Db 399 TGTCACTGTGAATGAGGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
QY 492 GCCTACGGTACTTGGAGACATCTCTCCAAAGCGGTTCGCTTTGTGATGATGATGATGAT 551
Db 459 ACCTGTTATACCTGGAGACACCTTACACCACTGGAAGGGAATTTGAAGGAGAAAGA 518
QY 552 ATACTTGAATTTAGGGGATCACCGGAGCAGTACAGGGGACTACAGTGTGAGTGCCTC 611
Db 519 ATATCTGGAGATCTTGGCATCACAGGAGCAGTACAGGCAAAATATGATGCAAGTGC 578
QY 612 CAATGACGTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671

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Db 579 CAACGAGTCTCTCCGCGGATGTCAAAACAGTCAAGGTCACTGTGAACATATCTCCAC 638
 Qy 672 CATTTGAGAACCAAGGTACAGGTGTCCCGTGGGACAAAGGGACACTGCAAGTGTGA 731
 Db 639 TATCACAGATCCAAAGAGCAATGAAGCACCACACAGGACGACAAGCTTCACTCAAAATGTGA 698
 Qy 732 AGCCTCAGCAGTCCCTCCAGCAGAAATCCAGTGGTACAAAGGATGACAAAGACTGATTGA 791
 Db 699 GGCCTCGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGATGACACTAG---GATAAA 755
 Qy 792 AGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCAATCTTTCAA 851
 Db 756 TAGTGCCAAATGSCCTTGAGATTAAAGACACGGAGGCGCAGTCTTCCCTGACGGTGACCAA 815
 Qy 852 TGTCTGAAACATGACTATGGGAACACTACATTTGGTGGCCTCCAAAGCTGGGCCACAC 911
 Db 816 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAAGCTGGGGGTGAC 875
 Qy 912 CAATGCCAGCATCATGCTATTATTGGTCCAGGGCGCGTCAAGCG 952
 Db 876 CAATGCCAGCCTAGTCTCTTTTCAGACCTGGGTGCGTGAGAG 916

RESULT 7

US-08-414-657D-1

; Sequence 1, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Lambic System-Aesociated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 977 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 2...976
 ; OTHER INFORMATION:
 ; US-08-414-657D-1

Query Match 32.9%; Score 340.6; DB 2; Length 977;
 Best Local Similarity 63.3%; Pred. No. 6.1e-94;
 Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;
 Qy 72 TCTCTTCCAAAGGAGTGCCTCGTGGCAGCGAGATGCCACCTTCCCAAAGACTATGGACAA 131
 Db 46 TCTTCCACAGGACTGCTGTTCGACGGTGGAT-----TTTAAACCGAGGACGACAA 99
 Qy 132 CGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTTCACACACCGGGTGCAC 191
 Db 100 CATCACCGTGGAGGAGGGGACACAGCCATCTCAGGTGGCTTCTAGAAGACAAAGAACTC 159
 Qy 192 CCGGTGCGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGGTGCCT 251
 Db 160 AAGGTGGCTGGTTGAACCGTCTTGGCATCATTTTGTGGACATGACAAAGTGGTCTCT 219
 Qy 252 GGATCTCTCGGTGGTCTCTTCTGAGCAACACCCAAACGACGTACAGCATCGAGATCCAGAA 311
 Db 220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGNAATCCAGAA 279
 Qy 312 CGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGGACAGACACACACCCAAA 371
 Db 280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGTCTCAGTTTCAGACACAGCATGAGCCCA 339
 Qy 372 GACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGA 431
 Db 340 GACCTCCCAAGTTTACTTTGATCGTAAAGTCCCAACCAAGATCTCCAAATATCTCTCGGA 399
 Qy 432 TATCTCCATTAATGAAGGGGAAACAATATTAGCTCTCACCTGCATAGCAACTGGTAGACAGA 491
 Db 400 TGTCACTGTGAATGAGGGGACGACGTAAGTCTGTGCTGTCATGSCCAATGSCCGTCTCTGA 459
 Qy 492 GCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGCGGTGGCTTTGTGAGTAGAGACGA 551
 Db 460 ACCTGTTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519
 Qy 552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTTACAGGTGCAAGTGCCTC 611
 Db 520 ATATCTGGAGATCTTGGCATCACAGGAGCAGTCAAGGCAAGTCACTGTGAACTATCTCCAC 579
 Qy 612 CAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACCGTGAACCTATCCACCAATA 671
 Db 580 CAACGAGTCTCTCTCGCGGATGTCAAAACAAGTCAAGTCACTGTGAACTATCTCCAC 639
 Qy 672 CATTTGAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGTGA 731
 Db 640 TATCACAGAAATCCAAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCACTCAAAATGTA 699
 Qy 732 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAAGACTGATTGA 791
 Db 700 GGCCTCGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGAGACACTAG---GATAAA 756
 Qy 792 AGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCAATCTTTCAA 851
 Db 757 TAGTGCCAAATGGCTTCAGATTTAAGACACAGGAGGCGCAGTCTTCCCTGACGGTGACCAA 816
 Qy 852 TGTCTCTGAACATGACTATGGGAACACTACATTTGGTGGCCTCCAAAGCTGGGCCACAC 911
 Db 817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAAGCTGGGGGTGAC 876
 Qy 912 CAATGCCAGCATCATGCTATTATTGGTCCAGGGCGCGTCAAGCG 952
 Db 877 CAATGCCAGCCTAGTCTCTTTTCAGACCTGGGTGCGTGAGAG 917

RESULT 8

US-09-135-080-1
 ; Sequence 1, Application US/09135080
 ; Patent No. 6423827
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat R.
 ; APPLICANT: Pimenta, Aurea

Db	400	TGTCACTGTGAATGAGGGCAGCAACGTA	CTCTGCTGTGCAATGGCCGCTCTGA	459
Qy	492	GCCTACGGTTACTTTGGAGACACATCT	CTCTCCCAAAGCGGTGTGGCTTTGTG	551
Db	460	ACCTGTTATCACTTGGAGACACCTTAC	CACTCACTGGAAGGGAATTTGAAGGA	519
Qy	552	ATACTTGGAAATTCAGGGCATCACCC	CGGGAGCAGTCAGGGGACTACGAGT	611
Db	520	ATATCTGGAGATCTTGGCATCAC	CAGGGAGCAGTCAGGCAAAATATGAG	579
Qy	612	CAATGACGTGGCCGGCCGGTGGTAC	GGGAGAGTAAGGTCAACCTGAACTAT	671
Db	580	CAACGAGGTCTCTCTCGCGGATGT	CAAACTCAAGGTCACTGTGAACTAT	639
Qy	672	CATTTCAGAAAGCAAGGTAACAGGT	GTCCCGTGGGACAAAGGGGACACT	731
Db	640	TATCACAGATCTCAAGAGCAATGA	AGCCACACAGGACGACNAGCTTCT	699
Qy	732	AGCCTCAGCAGTCCCTCAGCAGAA	TTCAGTGTGTACAAAGGACTGATGA	791
Db	700	GGCCTCGCAGTGCCTGCACCTGAC	TTTGAGTGGTACCGGATGACACTAG	756
Qy	792	AGNAAGAAAGGGGTGAAGTGGAA	ACAGACACTTCTCTCAAACTCATCT	851
Db	757	TAGTGCCTCAATGGCCTTGAGAT	TAAAGACGCGAGGGCCAGTCTTCC	816
Qy	852	TGCTCTCGAAATGACTATGGA	AACTACACTTGGTGGCTTCCAAAG	911
Db	817	CGTCACATGAGGACACTACGG	CACTACCTGTGTGTGCTGCAAA	876
Qy	912	CAATGCCAGCATCATGCTATT	TGGTCAGGCGCCGTACAGCG	952
Db	877	CAATGCCAGCTAGTCTCTTT	CAGACCTGGGTGCGTGAGAG	917

RESULT 9

US-08-414-657D-5

; Sequence 5, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

; APPLICANT: Levitt, Pat

; APPLICANT: Pimenta, Aurea

; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane

; TITLE OF INVENTION: Protein and DNA

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/414,657D

; FILING DATE: 31-MAR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bloom, Allen

; REGISTRATION NUMBER: 29,135

; REFERENCE/DOCKET NUMBER: 31/7743-102

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-520-3214

```

; TELFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
US-08-414-657D-5

```

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Query Match 32.9%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 6.2e-94;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 72 TCTCTTCCAAAGGAGTCCCGTCCGAGGAGATGCCACCTTCCCAAGCTATGGCAA 131
Db 66 TCTTCCCAAGAGTCCCGTCCGAGGAGATGCCACCTTCCCAAGCTATGGCAA 119

Qy 132 CGTGACGGTCCGAGGAGGAGCGCCACCTTCAGGTGCACTATTGCAACCGGGTCA 191
Db 120 CATCACGGTCCGAGGAGGAGCGCCACCTTCAGGTGCACTATTGCAACCGGGTCA 179

Qy 192 CCGGTGCGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGCAAGTGGTCT 251
Db 180 GAAAGTGGCTGGTGAACCGCTTCGGCATCATCTTCGCTGGACACGCAAGTGGTCT 239

Qy 252 GGATCTCGCTGGTCTTCTTGAGCAACACCAACGAGTACAGCATCGAGATCCGAA 311
Db 240 GGACCTCGGTGAGCTGGAGAAACGCCATGCTTGAATACAGCTCCGAATCCGAA 299

Qy 312 CGTGATGTGATGACGAGGCGCTTACACCTGCTCGGTGAGAGACAGCAACCCCAA 371
Db 300 GGTGATGTCTATGATGAAGGATCTACACATGCTCAGTTCAGACACAGCATGAGCC 359

Qy 372 GACCTTAGGTCCACCTCATTTGCAAGTATCTCCCAAAATTTGAGATTTCTTCA 431
Db 360 GACCTCTCAAGTTACTTGTGTTGTAACAGTTCCCAAAAGATCTCCCAACATCTCT 419

Qy 432 TATCTCCATTAAGGAGAAATATTAGCTTACCTGCTACCTGATAGCACTGTAGAC 491
Db 420 TGTACTGTGATGAGGCGAGCAATGTAACCTGCTGATGCGCAATGGCGCCCTGA 479

Qy 492 GCCTACGGTTACTTGGAGACATCTCTCCAAAGCGGTTCGCTTTGTGAGTGAAGCA 551
Db 480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAGAGAAATTTGAAGGAGA 539

Qy 552 ATACTTGAATTCAGGCGCATCACCGGAGGAGTACAGGAGTACAGTGCAGTGCCT 611
Db 540 ATATCTGAGATCTTAGGATCATCACAGGAAACAGTCAGGCAAAATATGATGCA 599

Qy 612 CAATGACGTGCGCGCGGTGATGAGAGAGTAAAGTTCACCGTGAATATTCACCA 671
Db 600 CAACGAGTCTCTCCGCGGATGTCAACAAAGTCAAGTCACTGTGAACTATCCACC 659

Qy 672 CATTTCAAGAACCAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCA 731
Db 660 CATCACAGTCTAAGAGCAATGAAGCAACACAGGAGGACAAAGCTTCCCTCAAA 719

Qy 732 AGCCTCAGCTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAAGACTGAT 791
Db 720 AGCCTCAGCGGTCTGCACTGATCTTGAAGTGTACCGGATGACACAG---GATA 776

Qy 792 AGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAATCATCTTCTTCA 851
Db 777 CAGTCAAAAGCGCTTGAGATTGAAGCACTGAGGCGGAGTCTCCCTGACGGTGAC 836

Qy 852 TGTCTCTGAACATGATAGGAACTACATTTGCTGGCTTCAACAAAGCTGGGCA 911
Db 837 GGTCACTGAGGAACACTACGGCAACTATACCTGTGTGCTGCTGCCAACAAAGCT 896

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RESULT 10
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
US-09-135-080-7

```

```

Query Match 32.9%; Score 340.6; DB 3; Length 1014;
Best Local Similarity 61.9%; Pred. No. 6.2e-94;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 72 TCTCTTCCAAAGGAGTCCCGTCCGAGGAGATGCCACCTTCCCAAGCTATGGCAA 131
Db 66 TCTTCCCAAGAGTCCCGTCCGAGGAGATGCCACCTTCCCAAGCTATGGCAA 119

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QY 132 CGTGGCTCCGCGAGGGGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGAC 191
Db 120 CATACCGGTGAGCGGGGACACGGCCATCTCTGAGTGTGGTAGAAGACAAGAACTC 179
QY 192 CCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGTGCT 251
Db 180 GAAAGTGGCTGGTGAACCGCTCTGGCATCATCTCTGCTGACACGACAGTGTCT 239
QY 252 GGATCCTCGCGGTCTTCTGAGCAACACCCAAACGCAAGTACAGCATCGAGATCCAGAA 311
Db 240 GGACCTCGGTGAGCTGGAGAAACCGCATCTCTGGAATACAGCTCCGAATCCAGAA 299
QY 312 CGTGATGTATGACGAGGGCCCTTACACCTGCTGGTGACAGACAGCAACCCAAA 371
Db 300 GGTGATGTATGATGAAGGATCTTACACATGCTCAGTTTCAGACACAGCATGAGCCAA 359
QY 372 GACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCA 431
Db 360 GACCTCTAGGTTACTTGTATGATGAGTTCACAAAGATCTTCAAGATCTCTCTCGA 419
QY 432 TATCTCCATTAAAGAGGAAACAATATTAGCTCTACCTGATAGCAACTGGTGAACCA 491
Db 420 TGTCACTGTGATGAGGCGCAATGTAACCTGCTGATGGCCCAATGGCGCCCTGA 479
QY 492 GCCTAGGTTACTTGGAGACATCTCTCCAAAGGGTGTGGCTTTGTGAGTGAAGACA 551
Db 480 ACCTGTATACCTCGGAGACCTTACACCACTTGGAAAGAAATTTGAAGGAGAAAGA 539
QY 552 ATACTTGAATTTAGGCGCATCACCGGAGCAGTCAGGGACTACGAGTGCAGTGCCT 611
Db 540 ATATCTGAGATCTTAGGATCACAGGGAAACGTGAGCAAAATATGATGAGTGCAG 599
QY 612 CAATGACGTGGCGCGCTGGTACGGAGTAAAGGTCAACGCTGAACTATCCACCATA 671
Db 600 CAACGAGTCTCTCCGCGGATGTCAAAACAGTCAAGGTCACTGTGAATCCACCCAC 659
QY 672 CATTTGAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTA 731
Db 660 CATCACAGTCTAAGAGCAATGAAGCAACCAACAGGACGACAAAGCTTCCCTCAAA 719
QY 732 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGACAGGATGACAAAGACTGATTGA 791
Db 720 AGCCTCAGCGTCTGACCTGACCTTTGAGTGGTACCGGGATGACACAG---GATAAA 776
QY 792 AGGAAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCTCTCAAAACTCATCTTCTCAA 851
Db 777 CAGTGCAAAACGCGCTTGAGATTAAGAGCAGTGAAGGCGCAGTCTCTCCGACGGTGAC 836
QY 852 TGTCTTGAAACATGACTATGGGAACATACATTTGCGTGGCTTCAACAAAGTGGGCAAC 911
Db 837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGTGCCAAACAAAGCTCGCGTCA 896
QY 912 CAATGCCAGCATCATGCTATTGTCAGGCGCGCTGACGAGGTGACAAACGGCACGTC 971
Db 897 CAATGCCAGCTAGTCTTTTTCAGACCCGGGTGGTGAG---AGGAATCAACGGATCCAT 953
QY 972 GAGGAGGCGAGCTCGCTGCTGCTCTCTGCTTGTGCTTGTGACCTGCTTCTCAAAAT 1031
Db 954 CAGTCTGGCGGTACCACTGTGGCTCTGGCAGCGTCCCTGTTCTGCTTCTCAGCAATG 1013
QY 1032 T 1032
Db 1014 T 1014

RESULT 11
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

Query Match 32.9%; Score 340.6; DB 4; Length 1195;
Best Local Similarity 63.3%; Fred. No. 6.9e-94;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 72 TCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGACAA 131
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QY 132 CGTGACGTCCGCGCAGGCGGAGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGAC 191
Db 120 CATCACCGTGGCAGGCGGAGGACACAGCCATCTCAGGTGCGTTCTAGAAGACAAGAACTC 179
QY 192 CCGGTGCGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGTGCT 251
Db 180 AAGGTGCGCTGGTTGAACCGCTTCTGGCATCATTTTGTGTCGACATGACAAAGTGTCT 239
QY 252 GGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAAGTACAGCATCGAGATCCAGAA 311
Db 240 GGACCCAGGCTGAGCTGGAGAAACGCCATCTCTGGAATACAGCTCCGAATCCAGAA 299
QY 312 CGTGATGTGATGACGAGGGCCCTTACCTGCTCGGTGCGACAGACAAACCCAAA 371
Db 300 GGTGATGTCTATGATGAGGGTTCCTACACTTGTCTCAGTTTCAGACACAGCATGAGCCAA 359
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Db 360 GACCTCCCAAGTTACTTTGATCGTAAAGTCCCAAGATCTCCAATATCTCTCTCGA 419
QY 432 TATCTCCATTAAAGGGAAACAATATTAGCTCTACCTGCAATAGCAACTGGTAGACCA 491
Db 420 TGTCACTGTGATGAGGCGACGACGTCGTCTGCTGCAATGGCCAATGGCGCTCTGA 479
QY 492 GCCTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTGAGTGAAGACA 551
Db 480 ACCTGTTATCACCTGGAGACCTTTACACCAACTGGAAGGGAATTTGAAGGAGAAAGA 539
QY 552 ATACTTGAATTTAGGCGCATCACCGGAGCAGTCAAGGAGTAAAGGTCAACGCTGAACTATCCACCATA 611
Db 540 ATATCTGAGATGCTTGGCATCACCGGAGGAGTCAAGGCAATATGATGAGTGAAGAGTGC 599
QY 612 CAATGACGTGGCGCGCTGGTACGGAGTAAAGGTCAACGCTGAACTATCCACCATA 671
Db 600 CAACGAGTCTCTCGCGGATGTCAAAACAGTCAAGGTCACTGTGAATCTCTCCAC 659
QY 672 CATTTGAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTA 731
Db 660 TATCACGAATCCAAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCACTCAATGTGA 719
QY 732 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGACAGGATGACAAAGACTGATTGA 791
Db 720 GGCCTCGCAGTGCCTGCACTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 776
QY 792 AGGAAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCTCTCAAAACTCATCTTCTCAA 851
Db 777 TAGTGCCCAATGGCTTGAATTAAGAGCAGGAGGCGCAGTCTTCCCTGACGGTGACCA 836
QY 852 TGTCTTGAAACATGACTATGGGAACATACATTTGCGTGGCTTCAACAAAGTGGGCAAC 911
Db 837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGTGCCAAACAAAGCTCGCGTCA 896
QY 912 CAATGCCAGCATCATGCTATTGTCAGGCGCGCTGACGAGGTGACAAACGGCACGTC 971
Db 897 CAATGCCAGCTAGTCTTTTTCAGACCCGGGTGGTGAG---AGGAATCAACGGATCCAT 953
QY 972 GAGGAGGCGAGCTCGCTGCTGCTCTCTGCTTGTGCTTGTGACCTGCTTCTCAAAAT 1031
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RESULT 12

US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
US-08-414-657D-9

Query Match 32.7%; Score 338.6; DB 2; Length 861;
Best Local Similarity 63.7%; Pred. No. 2.3e-93;
Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
Qy 120 AGCTATGACAACTGAGCGTCCGCGAGGGGAGCGCCCTCAGGTGCATTTGA 179
Db 24 AGGCAGGACAACTACCGTGAGCGAGGGGACACAGCATCTCTCAGGTGCTTGA 83
Qy 180 CAACCGGTACCCGGGTGGCTAAACCGAGCACCCTCTATGCTGGGAATGA 239
Db 84 AGACAAGAACTCAAGGTGGCTGGTTGAACCGTTCTGGCATCATTTTCTGGACATGA 143
Qy 240 CAAGTGGTGCCTGGATCTCGCGTGGTCTTTCTGAGCAACCAACCAACGAGTACAGCAT 299

Db 144 CAAGTGTCTCTGACCCACCGGTTGAGTGGAGAAACGCCATTCTCTGTAATACAGCCT 203
Qy 300 CGAGATCCAGAACGTGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGA 359
Db 204 CCGAATCCAGAAAGGTGATGTCTATGATGAGGGTTCCTACACTTTGCTCAGTTCAAGACA 263
Qy 360 CAACCAACCCAAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGA 419
Db 264 GCATGAGCCCAAGACCTCCCAAGTTTACTGATCGTACAGTCCCAACAAAGATCTCCAA 323
Qy 420 GATTTCTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCCTCACTGCATAGCAAC 479
Db 324 TATCTCTCGATGTCTACTGTGAATGAGGCGAGCAACGTGACTCTGTGCTGTCATGGCCAA 383
Qy 480 TGGTAGACGAGCCTAGGTTACTTGGAGACACATCTCTCCCAAGGGTGGCTTTGT 539
Db 384 TGGCCGTCCTGAACCTGTTATCACTGGAGACACCTTACACCAACTGGAAGGGAATTGA 443
Qy 540 GAGTGAAGACGAATACTTTGGAATTTCAAGGGCATCACCGGGAGCAGTCAGGGGACTACGA 599
Db 444 AGGAGAAGAGATATCTGGAGATCTTGGCATCACCAAGGAGCAGTCAGGCAATATGA 503
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Qy 780 AAGACTGATTGAAGGAAGAAAGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACT 839
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Qy 900 GCTGGGCGCACACCAATGCCAGCATCATGCTATTTTGGTCCAGGCGCGCTCAGCG 952
Db 801 GCTGGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGTGGTGGAG 853

RESULT 13

US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D

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; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...912
; OTHER INFORMATION:
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; US-08-414-657D-6
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; Query Match 32.7%; Score 338.6; DB 2; Length 912;
; Best Local Similarity 63.7%; Pred. No. 2.4e-93;
; Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
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; QY 120 AGCTATGACAACTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGTGCACATTTGA 179
; DB 24 AGGCACGGACAACTACCGTGGAGCGGGGACACAGCCATCTCCAGTGGCTTGA 83
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; QY 180 CAACCGGGTCAACCGGGTGGCTGCTAAACCGAGCACCACCTCTATGCTGGGAATGA 239
; DB 84 AGACAGAACTCAAGGTGGCTGGTGAACCGTCTGGCATCATTTTGGTGGACATGA 143
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; QY 240 CAAGTGGTCTGAGTCTCGGGTGGTCTTCTGAGCAACCCCAACCGCAGTACAGCAT 299
; DB 144 CAAGTGGTCTGAGCACCACCGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203
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; QY 300 CGAGATCCAGAACGTTGATGATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 359
; DB 204 CCGAATCAGAAAGTGGATGTCTATGATGAGGGTTCTTACACCTGCTCAGTTCAGACACA 263
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; QY 360 CAACCAACCAAGACCTCTAGGGTCCACTCATTGTGCAAGTATCTCCAAAATTTGTAGA 419
; DB 264 GCATGAGCCCAAGACCTCCAGTTTACTTGATGTACAGTCCACCAAAAGATCTCAA 323
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; QY 420 GATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCCTCCTCTGCATAGCAAC 479
; DB 324 TATCTCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383
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; QY 480 TGGTAGACAGAGCTAGCTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTGT 539
; DB 384 TGGCGGCTCTGAACCTGTATCACTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443
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; QY 540 GAGTGAACAAATACTTGGAAATTCAGGGCATCACCGGAGCAGTCCAGGGGACTACGA 599
; DB 444 AGGAGAGAGAGATATCTGGAGATCTTGGCATCACAGGGAGCGATCAGGCAATATGA 503
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; QY 600 GTGAGTGCCTCCAAATGACGTGGCGCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAA 659
; DB 504 GTGCAAAAGCTCCCAACAGAGGTCTCTCGCGGATGTCAAAACAAGTCAAGGTCACTGTGAA 563
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; QY 660 CTATCCACCATACATTTCAAGAGCCAGGATACAGGTGTCCCGTGGGACAAAAGGGAC 719
; DB 564 CTATCCTCCCACTATCAAGAAATCCAGAGAAATGAAGCCACCAAGCAGACGACAGCTTC 623
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; QY 720 ACTGAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATTCAGTGTGACAGGATGACAA 779
; DB 624 ACTCAATGTGAGGCTTCGGCAGTGCCTGCACCTTGTGAGTGTACCGGGATGACAC 683
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; QY 780 AAGACTGATCAAGAAAGAAAGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAACT 839
; DB 684 TAG--GATAAATAGTGCCTTGAAGTAAAGAGCACGGAGGCGCAGTCTTCCCT 740
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; QY 840 CATCTTCTCAATGCTCTGAACATGACTATGGGAACCTACACTTGCCTGGCTCCCAACA 899
; DB 741 GACGCTGACCAACGCTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACA 800
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; QY 900 GCTGGGCCACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGCTCAGCG 952
; DB 801 GCTGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGTCTGGTGAGAG 853
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; RESULT 14
; US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...945
; OTHER INFORMATION:
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; US-08-414-657D-8
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; Query Match 32.6%; Score 337.4; DB 2; Length 945;
; Best Local Similarity 63.1%; Pred. No. 5.8e-93;
; Matches 556; Conservative 0; Mismatches 316; Indels 9; Gaps 2;
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; QY 72 TCTCTTCAAGAGTGGCGCGCAGCGGAGATGCCACCTTCCCAAGCTATGACAA 131
; DB 66 TCTTCCACAGGACTGCCGTTCCAGGTGGAT-----TTTAAACCGAGCAGGACAA 119
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; QY 132 CGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACCGGGTCAAC 191
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Db 120 CATCACCTGAGGAGGGGACACGGCCATCTCAGGTGTGTGTAGAGACAAAGACTC 179
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Db 240 GGAACCTCGGGTTGAGCTGGGAAACGCCATGTCTTGGAATACAGCCCTCCGAAATCCAGAA 299
Qy 312 CGTGGATGTATACACAGGCGCCCTTACACCTGTCTGGTGACAGACAGACACCCAA 371
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Db 360 GACCTCTCAAGTTTACTTGTATGTACAAAGTTCCACCAAGATCTCCAAACATCTCTCGGA 419
Qy 432 TATCTCCATTAATGAGGACAAATATTAGCCTCACCTGCATAGCAACTGTTAGACAGCA 491
Db 420 TGTCACTGTGAATGAGGACAAATGTAAACCTGTCTGCAATGGCCCAATGGGCGCCCTGA 479
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Db 480 ACCTGTTATACCTGGAGACACCTTACACACTTTGGAGAGAAATTTGAAGAGAGAGA 539
Qy 552 ATACTTGAANAATCAGGCGATCACCCGGGAGCAGTCAAGGGAGCTACGAGTGCAGTGCTC 611
Db 540 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCAAGGCAAAATATGAGTCAAGGCTGC 599
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Qy 672 CATTTCAAGACCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGTGA 731
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Qy 792 AGGAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAAACTCATCTTTCTCAA 851
Db 777 CAGTGCAACCGCTTGAGATTAAGACACTGAGGCGCAGTCTCTCCCTGACGGTGAACCA 836
Qy 852 TGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTTCCAAACAGCTGGGCCACAC 911
Db 837 CGTCACTGAGGAACACTACGGCACTATACCTGTGTGGCTGCCAACCAAGCTCGGGTCAC 896
Qy 912 CAATGCCAGCATCATGTATTTGGTTCAGGCGCGCTGACGG 952
Db 897 CAATGCCAGCTAGTCTCTTTTCAGACCGCGGTGCGTGAGAG 937
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RESULT 15

US-08-414-657D-10

; Sequence 10, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

; APPLICANT: Levitt, Pat

; APPLICANT: Pimenta, Aurea

; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane

; TITLE OF INVENTION: Protein and DNA

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

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; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
; US-08-414-657D-10
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Query Match 32.3%; Score 333.8; DB 2; Length 861;

Best Local Similarity 63.4%; Pred. No. 6.9e-92;

Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

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Qy 180 CAAACCGGCTCACCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGA 239
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Perfect score: 1035

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Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 309930249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
51	1035	100.0	1679	14	US-10-066-269-103	Sequence 103, App
63	1035	100.0	1679	15	US-10-167-749-522	Sequence 522, App
225	1035	100.0	1679	14	US-10-223-085-55	Sequence 55, Appl
231	1035	100.0	1679	15	US-10-219-065-125	Sequence 125, App
261	1035	100.0	1679	15	US-10-223-084-55	Sequence 55, Appl
262	1035	100.0	1679	15	US-10-223-088-55	Sequence 55, Appl
263	1035	100.0	1679	15	US-10-223-090-55	Sequence 55, Appl
268	1035	100.0	1679	15	US-10-223-087-55	Sequence 55, Appl

270	1035	100.0	1679	15	US-10-223-083-55	Sequence 55, Appl
273	1035	100.0	1679	15	US-10-223-089-55	Sequence 55, Appl
448	1035	100.0	1679	16	US-10-223-081-55	Sequence 55, Appl
486	1035	100.0	1679	16	US-10-223-082-55	Sequence 55, Appl
555	1035	100.0	1679	17	US-10-170-481A-522	Sequence 522, App
557	1035	100.0	1679	17	US-10-210-028-522	Sequence 522, App
617	1035	100.0	1679	17	US-10-162-521A-522	Sequence 522, App
625	1035	100.0	1679	17	US-10-305-654-55	Sequence 55, Appl
640	1035	100.0	1679	18	US-10-081-056-55	Sequence 52, App
659	1035	100.0	1679	21	US-10-918-851-522	Sequence 522, App
660	1035	100.0	1679	21	US-10-931-886-375	Sequence 375, App
661	1035	100.0	1679	21	US-10-905-667-522	Sequence 522, App
662	1035	100.0	1679	21	US-10-897-359-522	Sequence 522, App
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676	955	92.3	1061	14	US-10-161-572-19	Sequence 19, Appl
677	955	92.3	1678	13	US-10-098-841-72	Sequence 72, Appl
678	953.4	92.1	1839	14	US-10-161-572-16	Sequence 16, Appl
679	953.4	92.1	1839	17	US-10-295-027-455	Sequence 455, App
680	933.4	92.1	3987	20	US-10-723-860-5804	Sequence 5804, App
681	933.4	92.1	3987	20	US-10-723-860-7421	Sequence 7421, App
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683	912	88.1	1094	14	US-10-161-572-17	Sequence 17, Appl
684	910.4	88.0	2129	15	US-10-306-133-2	Sequence 2, Appli
685	872.8	84.3	1130	14	US-10-161-572-18	Sequence 18, Appl
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687	537.2	51.9	3092	21	US-10-696-639-8	Sequence 8, Appli
688	537.2	51.9	3110	14	US-10-161-572-32	Sequence 32, Appl
689	535.6	51.7	1071	14	US-10-161-572-34	Sequence 34, Appl
690	535.6	51.7	1080	14	US-10-161-572-33	Sequence 33, Appl
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762	492	47.5	503	17	US-10-210-028-524	Sequence 524, App
767	492	47.5	503	17	US-10-162-521A-524	Sequence 524, App
779	492	47.5	503	21	US-10-918-851-524	Sequence 524, App
780	492	47.5	503	21	US-10-805-667-524	Sequence 524, App
781	492	47.5	503	21	US-10-897-359-524	Sequence 524, App
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783	492	47.5	503	21	US-10-897-360-524	Sequence 524, App
784	449.4	43.4	617	17	US-10-187-975-107	Sequence 107, App
785	404	39.0	437	10	US-09-918-995-2450	Sequence 2450, App
786	362.2	35.0	537	17	US-10-378-029-21	Sequence 21, Appl
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792	337.4	32.6	1757	21	US-10-485-231-37	Sequence 37, Appl
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796	313.8	30.3	898	14	US-10-161-572-31	Sequence 31, Appl
797	279	27.0	1809	14	US-10-161-572-27	Sequence 27, Appl
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799	272.6	26.3	1196	17	US-10-038-854-23	Sequence 23, Appl
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855	272.6	26.3	4834	15	US-10-219-065-1	Sequence 1, Appli
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988	269.4	26.0	2840	17	US-10-210-028-611	Sequence 611, App

993	269.4	26.0	2840	17	US-10-162-521A-611	Sequence 611, App	1077	39.4	3.8	2650	21	US-10-887-553A-246	Sequence 246, App
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1006	289.4	26.0	2840	21	US-10-805-667-611	Sequence 611, App	1079	39.4	3.8	2650	21	US-10-369-493-42950	Sequence 42950, A
1007	269.4	26.0	2840	21	US-10-897-359-611	Sequence 611, App	1080	38.8	3.7	2952	17	US-10-369-493-40511	Sequence 40511, A
1008	269.4	26.0	2840	21	US-10-893-802-611	Sequence 611, App	1081	38.8	3.7	5913	19	US-10-367-094-161	Sequence 161, Appl
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1021	211.4	20.4	754	19	US-10-480-172-9	Sequence 9, Appl	1094	38.4	3.7	2375	17	US-10-104-047-1229	Sequence 1229, Ap
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1026	156	15.1	619	17	US-10-027-632-12436	Sequence 12436, A	1099	37.8	3.7	885	17	US-10-350-923B-31	Sequence 31, Appl
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1030	73	7.1	293	14	US-09-764-853-347	Sequence 347, App	1103	37.8	3.7	2803	14	US-10-102-806-84	Sequence 84, Appl
1031	73	7.1	293	9	US-10-091-438-112	Sequence 112, App	1104	37.6	3.6	387	16	US-10-117-109-2	Sequence 2, Appl
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1057	41.2	4.0	2522	21	US-10-481-041-20	Sequence 20, Appl	1130	37.6	3.6	510	16	US-10-407-078-70	Sequence 70, Appl
1058	41.2	4.0	2633	15	US-10-207-655-179	Sequence 179, App	1131	37.6	3.6	510	16	US-10-407-078-72	Sequence 72, Appl
1059	41.2	4.0	2633	18	US-10-641-643-950	Sequence 950, App	1132	37.6	3.6	572	10	US-09-919-039-1	Sequence 1, Appl
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1066	41.2	4.0	4978	13	US-10-044-090-89	Sequence 89, Appl	1139	37.6	3.6	831	16	US-10-407-078-65	Sequence 65, Appl
1067	41.2	4.0	8513	17	US-10-182-329-9	Sequence 9, Appl	1140	37.6	3.6	843	16	US-10-117-109-15	Sequence 15, Appl
1068	40.8	3.9	1316	21	US-10-956-157-151	Sequence 151, App	1141	37.6	3.6	843	16	US-10-407-078-15	Sequence 15, Appl
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1072	40.2	3.9	5297	20	US-10-723-860-1338	Sequence 1338, Ap	1145	37.6	3.6	855	16	US-10-407-078-16	Sequence 16, Appl
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1158	36.4	3.5	1299	14	US-10-161-572-14
1159	36.4	3.5	1376	14	US-10-161-572-13
1160	36.4	3.5	1515	17	US-10-282-122A-25918
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1162	36.4	3.5	1542	14	US-10-004-860-123
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1376	36.4	3.5	1685	15	US-10-223-088-43
1377	36.4	3.5	1685	15	US-10-223-090-43
1378	36.4	3.5	1685	15	US-10-223-087-43
1380	36.4	3.5	1685	15	US-10-223-083-43
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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	878.2	84.9	1808	3	AK045973 Mus muscu
2	878.2	84.9	1808	3	AK046377 Mus muscu
3	852	82.3	874	9	AY406347 Homo sapi
4	743.2	71.8	773	9	AY406348 Pan trogl
5	709.6	68.6	876	9	AY406349 Mus muscu
6	664.8	64.2	856	5	BUI55617 AGENCOURT
7	640	61.8	748	7	CN3622339
8	635.2	61.4	1039	2	BE798585
9	619.6	59.9	765	6	CD354474 UI-M-GMO-
10	564.8	54.6	1450	7	CO635648 Contig266
11	544	52.6	600	7	CF737474 UI-M-HDO-
12	542.4	52.4	759	7	CF737474
13	541	52.3	865	4	BI666583
14	531.4	51.3	545	2	BE263639
15	521	50.3	732	4	BI551784
16	510	49.3	1027	1	AL533026
17	508.4	49.1	2512	3	CR602526 full-len
18	507	49.0	636	7	CR340711
19	495.4	47.9	784	4	BI549918
20	494.8	47.8	580	4	BI548566
21	494.2	47.7	680	7	CR751151
22	470.8	45.5	737	7	CN533076
23	466.8	45.1	601	6	CN582386
24	465	44.9	661	4	BM009450

c	98	273.8	26.5	394	5	B0184395	UI-E-EJ1-
c	99	273.8	26.5	394	5	B0184512	UI-E-EJ1-
c	100	273.8	26.5	394	7	CK300895	UI-E-EJ1-
c	101	273.8	26.5	403	4	BM684212	UI-E-EJ1-
c	102	273.8	26.4	815	5	B0230452	603320607
c	103	272	26.3	390	4	BM719375	UI-E-EJ1-
c	104	272	26.3	390	4	BM719757	UI-E-EJ1-
c	105	272	26.3	390	5	BM931279	UI-E-EJ1-
c	106	272	26.3	608	5	BQ188988	UI-E-EJ1-
c	107	272	26.3	734	6	BQ187606	UI-E-EJ1-
c	108	271.8	26.3	827	6	CK306798	UI-E-F71-
c	109	271.8	26.3	2096	3	AK035218	Mus muscu
c	110	271	26.2	700	5	B0189788	UI-E-EJ1-
c	111	270.2	26.1	1953	3	AK030503	Mus muscu
c	112	267.6	25.9	888	6	CD325821	AGENCOURT
c	113	267.2	25.8	284	7	CR543721	DKFzp459H
c	114	264.8	25.6	695	7	CN228731	RJB060E12
c	115	264	25.5	456	1	A1369684	Qy71G03.x
c	116	263.6	25.5	2534	3	AK039193	Mus muscu
c	117	263	25.4	2330	3	EC080168	Xenopus l
c	118	255.8	24.7	754	7	C0043662	UI-M-ER0-
c	119	255.2	24.7	587	7	CN088583	EC2BBA30B
c	120	252.4	24.4	478	5	BY245406	BY245406
c	121	247	23.9	796	7	C0399311	AGENCOURT
c	122	246.4	23.8	849	6	CA472810	AGENCOURT
c	123	243.8	23.6	652	7	CN078144	EC2BBA14C
c	124	240.8	23.3	621	5	BK312928	BK312928
c	125	240.6	23.2	496	5	BP201259	BP201259
c	126	240.6	23.2	926	6	CD325412	AGENCOURT
c	127	240.2	23.2	456	6	CD0803885	UI-M-GV0-
c	128	239	23.1	511	5	BK493152	DKFzp781G
c	129	238.8	23.1	611	7	CN075612	EC2BBA10C
c	130	238	23.0	282	7	R753931	MB0556R MO
c	131	235.8	22.8	445	5	BY269882	BY269882
c	132	235.6	22.8	788	4	B767217	603057906
c	133	235.4	22.7	492	2	AW967001	EST379075
c	134	235	22.7	674	6	CD767791	AGENCOURT
c	135	234	22.6	934	7	CN015939	AGENCOURT
c	136	233.2	22.5	599	7	CN229507	RJB072D02
c	137	231.8	22.4	277	4	B1011319	QV2-EN009
c	138	230.8	22.3	481	5	BY256150	BY256150
c	139	230.2	22.2	457	5	BY249728	BY249728
c	140	226.4	21.9	772	7	CK776016	967158 MA
c	141	225.8	21.8	564	7	C0602836	DG8-24911
c	142	225.8	21.8	639	7	CN030684	9878 Full
c	143	225	21.7	660	7	CK543517	DKFzp459N
c	144	225	21.7	795	7	C0395735	AGENCOURT
c	145	224	21.6	673	7	CR736885	CR736885
c	146	220	21.3	444	1	AA682970	ae89a04.s
c	147	214.6	20.7	697	5	B0021243	UI-H-DH1-
c	148	213.8	20.7	640	7	CK545244	DKFzp459F
c	149	213	20.6	229	1	AA450172	2x42d09.r
c	150	212.4	20.5	867	6	CD300857	AGENCOURT
c	151	212.2	20.5	672	6	CA444805	UI-H-DH1-
c	152	211	20.4	664	7	CN362538	170006001
c	153	210.6	20.3	656	7	CK619540	mk25d06.y
c	154	209	20.2	257	2	AW327110	20640 MAR
c	155	208.4	20.1	678	5	B0624639	UI-H-FG1-
c	156	208.4	20.1	1148	4	BM466102	AGENCOURT
c	157	204.2	19.7	726	5	BY912600	BY912600
c	158	204	19.7	357	5	BY303236	BY303236
c	159	203.4	19.7	625	2	B8643056	BB643056
c	160	203.4	19.7	771	7	CN528825	UI-M-HQ0-
c	161	203.2	19.6	636	7	CK843444	UI-R-BU2-
c	162	202.8	19.6	656	6	CA307492	UI-H-F71-
c	163	202.6	19.6	1084	6	CD255729	AGENCOURT
c	164	200.2	19.3	719	7	CK465166	936244 MA
c	165	200	19.3	786	7	C0811192	AGENCOURT
c	166	200	19.3	858	7	C0914076	AGENCOURT
c	167	198.6	19.2	663	2	B8633037	B8633037
c	168	198	19.1	519	7	CN038761	4136000 B
c	169	195.6	18.9	347	7	CN094278	EC2BBA9CA
c	170	194.4	18.8	670	7	CN083622	EC2BBA22D

c	171	194.4	18.8	708	7	CN083621	EC2BBA22D
c	172	192.8	18.6	825	5	BP166655	BP166655
c	173	191.4	18.5	294	7	W15256	zcl6h07.81
c	174	191.2	18.5	659	2	AW149545	xf39c10.x
c	175	189.4	18.3	764	6	CA350929	621861 NC
c	176	188	18.2	611	6	CA355517	627428 NC
c	177	186.8	18.0	565	2	BE663866	147903 MA
c	178	186.8	18.0	593	7	CK845949	968393 MA
c	179	186.8	18.0	880	6	CD303536	AGENCOURT
c	180	186.2	18.0	572	6	CB265380	1004285 H
c	181	186	18.0	640	7	CO351229	DR_AOV_FL
c	182	186	18.0	753	1	A1589824	tm74g09.x
c	183	185.2	17.9	906	5	BU186468	AGENCOURT
c	184	184.4	17.8	392	2	BE651010	UI-M-BH3-
c	185	183	17.7	410	5	BY276506	BY276506
c	186	183	17.7	835	5	EX881962	EX881962
c	187	181	17.5	755	5	EX913106	EX913106
c	188	180.6	17.4	647	7	CV030870	10123 Full
c	189	179.8	17.4	220	7	H16176	ym21g09.r1
c	190	178.2	17.2	578	2	BE121132	UI-R-CA0-
c	191	178	17.2	178	6	CB118055	K-EST0164
c	192	178	17.2	909	5	BU132565	603120307
c	193	175.6	17.0	2296	3	CR592222	full-1eng
c	194	175.2	16.9	795	1	AU080106	AU080106
c	195	175	16.9	666	5	BM951674	UI-M-EGO-
c	196	174.6	16.9	867	7	CO543917	LYEST116
c	197	173.4	16.8	572	2	BP407747	UI-R-BU2-
c	198	171.8	16.6	415	5	BY263876	BY263876
c	199	171.4	16.6	862	7	CK397022	AGENCOURT
c	200	170.6	16.5	768	5	EX868437	EX868437
c	201	169.8	16.4	584	5	BP257486	BP257486
c	202	169.6	16.4	637	6	CB528708	UI-H-F72-
c	203	169	16.3	378	2	BP601149	266043 MA
c	204	169	16.3	470	5	EX954423	DKFzp781K
c	205	167.8	16.2	791	7	CK308721	SB02047A2
c	206	167.4	16.2	923	1	AL583491	AL583491
c	207	167	16.1	617	6	BY730405	BY730405
c	208	166.6	16.1	458	7	CO667956	DG33-31f8
c	209	166.2	16.1	568	7	CF977262	2-84-B04
c	210	165.8	16.0	541	5	BU735309	UI-E-DW0-
c	211	165.6	16.0	535	9	AY409767	Homo sapi
c	212	165.4	16.0	580	7	CN089827	EC2BBA32B
c	213	165	15.9	488	5	BK477962	DKFzp686N
c	214	164.6	15.9	544	6	CA439326	UI-H-DT1-
c	215	164.4	15.9	651	6	BY726997	BY726997
c	216	164.2	15.9	450	5	BY263302	BY263302
c	217	164	15.8	773	4	BG208674	RST28306
c	218	163.6	15.8	527	5	BY243052	BY243052
c	219	163.2	15.8	894	6	CB199088	AGENCOURT
c	220	162.4	15.7	535	9	AY409769	Mus muscu
c	221	161.8	15.6	936	5	BQ227365	AGENCOURT
c	222	160.8	15.5	892	5	BP462753	BP462753
c	223	160.6	15.5	268	1	AA296886	EST112650
c	224	158.8	15.3	481	5	BY247646	BY247646
c	225	158.8	15.3	494	1	AA548396	nj14e04.s
c	226	157.2	15.2	858	2	BF676478	602086277
c	227	156.4	15.1	739	7	CK679857	CK679857
c	228	156.4	15.1	884	5	BU323269	BU323269
c	229	155.8	15.1	815	1	AU079716	AU079716
c	230	155.2	15.0	431	5	BY276402	BY276402
c	231	154.6	14.9	733	7	CO619752	DG9-1d13
c	232	151	14.6	411	5	BY288341	BY288341
c	233	150.2	14.5	456	5	BY249027	BY249027
c	234	149.2	14.4	497	7	CV036959	4134532 B
c	235	148.4	14.3	465	1	A1934791	wp89e04.x
c	236	147.4	14.2	429	5	BY272572	BY272572
c	237	146.4	14.1	600	6	CA526928	8023-83 M
c	238	146.2	14.1	862	5	BP462754	BP462754
c	239	145.4	14.0	385	6	CB806970	AMGNNUC.N
c	240	144.8	14.0	703	7	CF530869	UI-M-GH0-
c	241	144.6	14.0	703	5	BU117309	BU117309
c	242	144	13.9	511	1	A1415689	mc70a03.x
c	243	144	13.9	953	5	BU116264	603139651

c	243	144	13.9	953	5	BU116264	603139651
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c 244	143.8	13.9	519	1	AA826266	od03e04.s	317	105.2	10.2	364	1	AI940007	AI940007 QV0-CT001
245	143.4	13.9	878	5	BP165624	BP165624	318	104.6	10.1	651	6	CB557691	CB557691 AMGNNUC:N
246	142.2	13.7	535	9	AY409768	Pan trogl	319	104.2	10.1	473	5	BY261511	BY261511 BY261511
247	141.2	13.6	853	5	BP164129	BP164129	320	103.8	10.0	761	6	CD755145	CD755145 AGENCOURT
c 248	141	13.6	470	1	AI580850	ta33e06.x	c 321	102.4	9.9	770	2	AW117456	AW117456 xg92a06.x
249	140.4	13.6	478	6	CA885050	BO115E08-	c 322	102	9.9	684	5	BU625289	BU625289 UI-H-FGI-
c 250	140.4	13.6	585	7	CO628980	DG9-3m14	c 323	101.2	9.8	412	5	BY274659	BY274659 BY274659
251	139.4	13.5	801	5	BU357013	BU357013 603475462	c 324	100.4	9.7	604	2	AW025115	AW025115 wu71n04.x
252	139.4	13.5	809	2	BF304194	601887043	c 325	100.2	9.7	359	2	BE156390	BE156390 QV0-HT036
253	138.4	13.4	402	5	BY289266	BY289266	c 326	99.2	9.6	489	6	CB726015	CB726015 AMGNNUC:N
254	138.2	13.4	914	5	BX843874	BX843874	c 327	99	9.6	402	2	AW522667	AW522667 UI-R-BOO-
255	138	13.3	775	4	BI119955	602761121	c 328	98.6	9.5	594	7	CK699353	CK699353 ZF101-P00
256	137.8	13.3	718	6	CB460692	CB460692 720592 MA	c 329	98.4	9.5	392	5	BY267956	BY267956 BY267956
257	136.4	13.2	661	6	CA452139	CA452139 UI-N-F20-	c 330	97.2	9.4	421	5	BY275639	BY275639 BY275639
258	136	13.1	496	7	CK693129	CK693129 ZF101-P00	c 331	97.2	9.4	656	2	BB617916	BB617916 BB617916
259	135.4	13.1	372	6	BY768835	BY768835	c 332	95.8	9.3	763	1	AI427225	AI427225 mc70a03.y
260	134.6	13.0	386	5	BY263646	BY263646	c 333	95.6	9.2	385	1	BY275013	BY275013 BY275013
261	134.4	13.0	594	5	BU400899	BU400899 603481850	c 334	95	9.2	602	5	BU741589	BU741589 UI-E-E01-
262	134.2	13.0	778	7	CK315507	CK315507 SB02028A1	c 335	94.4	9.1	646	4	BI393264	BI393264 P9p1n.pk0
263	134	12.9	855	5	BP158085	BP158085	c 336	94.2	9.1	354	2	BB826697	BB826697 QV1-EN004
264	130.6	12.6	700	7	CM458398	CM458398 UI-N-HN0-	c 337	93.6	9.0	401	5	BY266910	BY266910 BY266910
265	129.8	12.5	801	7	CK303983	CK303983 SB02022A1	c 338	93.4	9.0	683	2	BB318882	BB318882 BB318882
266	129	12.5	487	7	CR536826	CR536826 DKF2p459J	c 339	92.8	9.0	377	2	BF358688	BF358688 QV1-ET000
267	128.6	12.4	803	5	BP168056	BP168056	c 340	92	8.9	640	9	CC573801	CC573801 CH240_450
268	128.4	12.4	348	7	R55964	Y898e11.r1	c 341	91.4	8.8	374	5	BY294857	BY294857 BY294857
269	126.2	12.2	641	2	AW379374	AW379374 CM2-HT024	c 342	91.4	8.8	452	1	AI262821	AI262821 QK35h10.x
270	126	12.2	825	5	BP464677	BP464677	c 343	91.4	8.8	653	7	CF180026	CF180026 815076 MA
271	125	12.1	646	7	CA334396	CA334396 NISC 1A08	c 344	91	8.7	656	2	BB645027	BB645027 BB645027
272	124.4	12.0	377	7	CF977263	CF977263 2-98-A10	c 345	90	8.7	194	4	BI337742	BI337742 361363 MA
273	124.2	12.0	868	5	BO672092	BO672092 AGENCOURT	c 346	88.6	8.6	700	2	BB652926	BB652926 BB652926
274	124	12.0	870	4	BI913885	BI913885 603183295	c 347	88.4	8.5	733	9	BI190380	BI190380 Danio rer
275	123.8	12.0	617	4	BU622933	BU622933	c 348	88.2	8.5	374	2	BB826640	BB826640 QV1-EN004
276	123.4	11.9	562	5	BU381982	BU381982 603582664	c 349	85.8	8.3	285	7	CN209637	CN209637 4115576 B
277	121.4	11.7	711	7	CO669353	CO669353 DG33-50b1	c 350	85.6	8.3	332	2	BB826737	BB826737 QV1-EN004
278	120	11.6	504	5	BX281785	BX281785	c 351	84.8	8.2	625	6	BY729404	BY729404 BY729404
279	120	11.6	729	2	BB585976	BB585976	c 352	84	8.1	657	2	BB618284	BB618284 BB618284
280	119.4	11.5	613	7	CF892168	CF892168 AO106B07-	c 353	84	8.1	723	9	AG035406	AG035406 Pan trogl
281	119.4	11.5	863	6	CA475514	CA475514 AGENCOURT	c 354	83.8	8.1	2594	3	AK047122	AK047122 Mus muscu
282	119	11.5	801	5	BX852740	BX852740	c 355	83.4	8.1	479	2	AW524531	AW524531 UI-R-BOO-
283	117	11.3	552	4	BI337752	BI337752 361275 MA	c 356	83.4	8.1	550	2	BE012499	BE012499 121990 MA
c 284	115.8	11.2	422	1	AI288864	AI288864 qm24f12.x	c 357	83	8.0	563	5	BO637244	BO637244 he07e09.y
c 285	115.8	11.2	737	4	BM679797	BM679797 UI-E-EJ0-	c 358	82.4	8.0	728	7	CN530285	CN530285 UI-N-HQ0-
c 286	115.6	11.2	461	2	BP463934	BP463934 UI-N-CG0P	c 359	82	7.9	272	2	BB596160	BB596160 BB596160
287	115.6	11.2	790	5	BP141505	BP141505	c 360	81.8	7.9	392	2	AW291014	AW291014 UI-H-BI2-
c 288	115.4	11.1	336	5	BY134531	BY134531	c 361	81.6	7.9	586	4	BM696801	BM696801 UI-E-DW0-
c 289	115	11.1	368	2	BF350775	BF350775 QV0-HT036	c 362	80.6	7.8	1463	8	CC288776	CC288776 CH261-170
c 290	113.8	11.0	579	7	CN089828	CN089828 CB28BA32B	c 363	80.4	7.8	529	6	CD284927	CD284927 G39161.77
c 291	113.6	11.0	514	1	AI285235	AI285235 QK59h04.x	c 364	79.4	7.7	583	6	CA353359	CA353359 624860 NC
c 292	112.8	10.9	665	9	EX243020	EX243020 Danio rer	c 365	79.2	7.7	562	5	EX952176	EX952176 DKF2p781K
c 293	112.4	10.9	582	7	CO626674	CO626674 DG9-278a2	c 366	78.6	7.6	375	5	BY292584	BY292584 BY292584
c 294	112	10.8	316	1	AI1884993	AI1884993 w186c02.x	c 367	78.6	7.6	442	7	CN081576	CN081576 EC2BBA19C
c 295	111.2	10.7	446	7	CO352257	CO352257 DR AOV SU	c 368	78.6	7.6	916	5	BO672140	BO672140 AGENCOURT
c 296	110.8	10.7	994	6	CD325921	CD325921 AGENCOURT	c 369	78.2	7.6	335	4	BI198531	BI198531 RST18822
c 297	110.6	10.7	528	2	AW490008	AW490008 UI-N-BH3-	c 370	78	7.5	547	6	BY727136	BY727136 BY727136
c 298	110.4	10.7	382	9	AY400235	AY400235 Mus muscu	c 371	78	7.5	660	5	BB337636	BB337636 Mus muscu
c 299	110.4	10.7	417	6	CA884109	CA884109 BO107H12-	c 372	78	7.5	854	3	AK020998	AK020998 Bw337636
c 300	110.4	10.7	782	8	AZ731274	AZ731274 RPTC-24-1	c 373	76.8	7.4	467	4	BI134406	BI134406 UI-N-BH3-
c 301	110.2	10.6	451	1	AA933871	AA933871 ol91d04.s	c 374	76.8	7.4	581	8	BH269028	BH269028 CH230-66P
c 302	109.4	10.6	525	1	AL919221	AL919221	c 375	76.8	7.4	779	8	BH292378	BH292378 CH230-44D
303	109	10.5	711	5	BU363662	BU363662 603790080	c 376	76.6	7.4	1127	9	GGA200118	GGA200118 Gallus ga
304	107.8	10.4	422	4	BI390270	BI390270 P9p1c.pk0	c 377	76.6	7.4	411	5	BY276562	BY276562 BY276562
305	107.2	10.4	514	4	BG814603	BG814603 dat69d01.x	c 378	76.6	7.4	418	5	BY278505	BY278505 BY278505
306	106.8	10.3	434	1	AI279142	AI279142 qm18e02.x	c 379	76.6	7.4	483	8	AZ457316	AZ457316 IM0260A07
c 307	106.8	10.3	442	5	BF112198	BF112198 BX112198	c 380	76.2	7.4	492	4	BI359722	BI359722 384371 MA
308	106.8	10.3	468	2	BF110673	BF110673 7n55h10.x	c 381	76.2	7.4	960	5	BQ933325	BQ933325 AGENCOURT
309	106.8	10.3	502	1	AL1796834	AL1796834 we2zh06.x	c 382	75.8	7.3	368	7	CN086072	CN086072 EC2BBA26C
310	106.8	10.3	523	2	BB550993	BB550993 7B67a03.x	c 383	75.6	7.3	433	1	AL921475	AL921475 AL921475
311	106	10.2	705	7	CN108877	CN108877 EC2CAA32D	c 384	75.2	7.3	652	8	BH269030	BH269030 CH230-66P
c 312	105.8	10.2	598	1	AI1815935	AI1815935 au43g02.x	c 385	74.2	7.2	526	7	CO634943	CO634943 DG9-96n24
c 313	105.6	10.2	394	9	AY400233	AY400233 Homo sapi	c 386	74	7.1	457	7	W39242	W39242 zc16h07.r1
314	105.6	10.2	394	9	AY400234	AY400234 Pan trogl	c 387	72.8	7.0	687	5	BP461989	BP461989 BP461989
315	105.6	10.2	525	6	CB720159	CB720159 AMGNNUC:N	c 388	72.8	7.0	893	3	CN502MXY	AL204631 Tetraodon
c 316	105.2	10.2	314	7	CN075611	CN075611 EC2BBA10C	c 389	72.6	7.0	339	2	BB826667	BB826667 QV1-EN004

C 390	72.6	7.0	816	5	BU385923	603858616	463	49	4.7	983	9	CNS0489V	AL279004	Tetraodon
C 391	72.4	7.0	378	8	AZ089779	RPCT-23-2	464	48.8	4.7	256	2	BB595530	BB595530	BB595530
C 392	71.2	6.9	334	1	AI422503	tlfile04.x	465	48.6	4.7	899	5	BU134624	BU134624	603119839
C 393	70.8	6.8	474	2	BB682022	BB682022	466	48.4	4.7	706	2	BB351922	BB351922	BB351922
C 394	69.6	6.7	742	7	CO395507	AGENCOURT	467	48.4	4.7	3641	3	AK047548	AK047548	Mus muscu
C 395	68.2	6.6	313	2	AW430704	70599 MAR	468	48.2	4.7	866	5	BQ680977	BQ680977	AGENCOURT
C 396	67.2	6.5	821	5	BU389844	603511165	469	48	4.6	970	5	BU375142	BU375142	603812777
C 397	66	6.4	433	4	BG515406	dae04h10.	470	47.6	4.6	652	7	CK689464	CK689464	2F101-P00
C 398	65.8	6.4	726	5	BU395513	603404749	471	47.4	4.6	405	5	BY441604	BY441604	BY441604
C 399	65	6.3	259	2	BB607028	BB607028	C 472	47.4	4.6	496	4	BP995884	BP995884	QV1-GN020
C 400	64.8	6.3	702	9	CNS02PTU	Tetraodon	C 473	47.4	4.6	972	9	CNS041CJ	AL270028	Tetraodon
C 401	64.4	6.2	558	7	CK875240	SGP136467	C 474	47	4.5	572	8	AO680346	AO680346	HS 2275 B
C 402	63.4	6.1	527	1	AA741334	ob30f08.8	C 475	47	4.5	575	8	AO803771	AO803771	HS 3145 A
C 403	62.6	6.0	226	1	AA776056	ae79a07.s	C 476	47	4.5	834	8	AO899706	AO899706	HS 3145 A
C 404	62.6	6.0	539	1	AL918370	AL918370	477	46.6	4.5	216	8	BB054739	BB054739	BB054739
C 405	61.8	6.0	550	7	CR544600	DKF2p459F	478	46.4	4.5	603	8	BZ111682	BZ111682	CH230-208
C 406	60.8	5.9	247	7	CR474371	CR474371	479	46.4	4.5	781	6	CD348686	CD348686	UI-M-FY0-
C 407	60.8	5.9	255	2	BB577810	BB577810	480	46.2	4.5	1261	3	CR724321	CR724321	Tetraodon
C 408	60.4	5.8	484	5	EX099260	EX099260	481	46	4.4	382	6	CB809130	CB809130	AMGNNUC:C
C 409	60.2	5.8	1008	9	CL093894	ISBL-24C2	C 482	46	4.4	517	8	AO772307	AO772307	HS 5493 B
C 410	60	5.8	702	4	BG695650	NISC 1v20	C 483	45.6	4.4	299	2	BE943615	BE943615	UI-M-BR3-
C 411	59.6	5.8	420	6	CB798880	AMGNNUC:N	C 484	45.6	4.4	585	6	CB513897	CB513897	esalrpb54
C 412	59.6	5.8	845	4	BM042630	603615963	485	45	4.3	551	5	BU440266	BU440266	604147091
C 413	59.4	5.7	226	2	AW374585	MR1-CT005	486	45	4.3	695	9	AG164478	AG164478	Pan trogl
C 414	58.6	5.7	426	7	CK776772	CK776772	487	44.6	4.3	1233	3	CR724192	CR724192	Tetraodon
C 415	58.6	5.7	736	8	AZ989621	AZ989621	488	44	4.3	290	2	BF362977	BF362977	CM4-NN008
C 416	58.2	5.6	303	1	AI422504	tlfile05.x	489	44	4.3	600	5	BU922970	BU922970	7042-78 M
C 417	57.6	5.6	276	2	BB268580	BB268580	490	44	4.3	614	6	CD351134	CD351134	UI-M-FY0-
C 418	57.4	5.5	565	7	CO590783	DG2-41K22	491	44	4.3	740	7	CNS31505	CNS31505	UI-M-HQO-
C 419	56.8	5.5	569	5	BP377634	BP377634	492	44	4.3	760	7	CNS31514	CNS31514	UI-M-HQO-
C 420	56.8	5.5	582	5	BP208357	BP208357	493	44	4.3	3037	3	AK052440	AK052440	Mus muscu
C 421	56.6	5.5	964	9	CNS050CXJ	Tetraodon	494	43.8	4.2	491	4	BI067139	BI067139	pgfin.pk0
C 422	55.8	5.4	929	9	CNS050XX	Tetraodon	495	43.8	4.2	615	4	BI067145	BI067145	pgfin.pk0
C 423	55.6	5.4	502	7	CO691339	DG11-30F1	496	43.6	4.2	1010	1	AL546361	AL546361	AL546361
C 424	55.4	5.4	311	4	BG193769	BG193769	497	43.4	4.2	613	7	CF918937	CF918937	Bf1or531.
C 425	55.4	5.4	626	8	AZ385580	1M0144G07	498	43.4	4.2	651	7	CF919117	CF919117	Bf1or531.
C 426	54.6	5.3	390	1	AA490022	ab02b04.8	499	43.4	4.2	701	7	CF919027	CF919027	Bf1or531.
C 427	54.2	5.2	573	7	CF977921	FAR17G1.R	500	43.4	4.2	717	5	BU321343	BU321343	603854520
C 428	54.2	5.2	806	4	BI762516	603048638	501	43.4	4.2	841	6	CB999583	CB999583	AGENCOURT
C 429	53.8	5.2	244	2	BF362751	BF362751	502	43.4	4.2	883	8	BZ222298	BZ222298	CH230-324
C 430	53.8	5.2	569	8	AQ394216	CITBI-E1-	503	43.4	4.2	892	5	BU135652	BU135652	603124302
C 431	53.8	5.2	582	4	BG219746	BG219746	504	43.2	4.2	623	5	EX924232	EX924232	EX924232
C 432	53.4	5.2	254	7	CR774354	RST39511	505	43.2	4.2	3976	3	CR749215	CR749215	Homo sapi
C 433	52.8	5.1	234	1	AV3249585	AV3249585	506	43	4.2	675	7	CN060015	CN060015	Salamande
C 434	52.8	5.1	302	2	BF362739	BF362739	507	43	4.2	783	7	CN055172	CN055172	Salamande
C 435	52.6	5.1	271	2	BB432888	BB432888	508	42.6	4.1	392	5	BY094706	BY094706	BY094706
C 436	52.4	5.1	648	8	AZ379719	1M0135K02	509	42.4	4.1	418	4	BG142186	BG142186	1a51b01.y
C 437	52.4	5.1	826	4	BM041903	603615963	C 510	42.4	4.1	1039	5	BU951424	BU951424	in59d04.x
C 438	52.2	5.0	387	8	AZ878524	RPCT-23-1	C 511	42.4	4.1	1334	3	CR730479	CR730479	FGAS02605
C 439	52.2	5.0	584	4	BU519721	BU519721	512	42.4	4.1	1344	3	CR694719	CR694719	Tetraodon
C 440	52.2	5.0	712	4	BU532300	BU532300	513	42.4	4.1	1400	3	CR734232	CR734232	Tetraodon
C 441	52	5.0	590	9	BM240864	Danio rer	514	42.4	4.1	5626	3	CR749495	CR749495	Homo sapi
C 442	51.8	5.0	557	9	CE135710	tigr-gaes-	515	42.4	4.1	388	6	BY655441	BY655441	BY655441
C 443	51.6	5.0	780	9	CNS0414Z	AL291788	516	41.8	4.0	593	7	CF919555	CF919555	Bf1or531.
C 444	51.2	4.9	538	1	AL925790	AL925790	517	41.8	4.0	356	5	BY426574	BY426574	BY426574
C 445	51.2	4.9	657	5	BQ078813	fy81c06.y	518	41.6	4.0	356	5	BY426574	BY426574	BY426574
C 446	51	4.9	350	8	BB283073	BB283073	519	41.6	4.0	383	5	BY442078	BY442078	BY442078
C 447	51	4.9	386	1	AA401292	zvg63g05.r	520	41.4	4.0	522	5	EX528198	EX528198	EX528198
C 448	50.8	4.9	996	1	CNS04XL6	AL311811	C 521	41.4	4.0	549	2	BF465792	BF465792	UI-M-FBO-
C 449	50.6	4.9	337	5	B0780082	BQ780082	522	41.4	4.0	641	5	BQ571956	BQ571956	UI-M-FBO-
C 450	50.6	4.9	638	4	BG218217	BG218217	523	41.4	4.0	653	2	BB641148	BB641148	BB641148
C 451	50.6	4.9	826	9	CL043364	CL043364	524	41.4	4.0	693	5	BU707564	BU707564	UI-M-FRO-
C 452	50.6	4.9	1165	9	CL067381	CL067381	525	41.4	4.0	963	9	CNS005FY	AL059956	Drosophil
C 453	50.6	4.9	1165	9	CL051682	CH216-74F	526	41.4	4.0	1480	3	AK043555	AK043555	Mus muscu
C 454	50.4	4.9	141	7	CK467264	938548 MA	527	41.4	4.0	1845	3	BC053486	BC053486	BC053486
C 455	50.4	4.9	559	5	BY476545	BY476545	528	41.4	4.0	1996	1	AL697315	AL697315	AL697315
C 456	50.4	4.9	762	7	CK397238	CK397238	529	41.2	4.0	360	6	BY659253	BY659253	BY659253
C 457	50	4.8	646	5	BM346790	BM346790	530	41.2	4.0	394	5	BY442525	BY442525	BY442525
C 458	50	4.8	765	5	BU247998	BU247998	531	41.2	4.0	456	5	EX114096	EX114096	EX114096
C 459	49.8	4.8	544	8	AQ728858	HS 5464 B	532	41.2	4.0	516	4	BM264275	BM264275	1933c01.y
C 460	49.6	4.8	540	5	BU303720	603740472	533	41.2	4.0	523	2	BF063348	BF063348	7h8he07.x
C 461	49.4	4.8	1027	5	BU280790	BU280790	534	41.2	4.0	581	5	BP217876	BP217876	BP217876
C 462	49	4.7	873	8	BZ182814	CH230-377	535	41.2	4.0	678	6	CD000661	CD000661	AGENCOURT

536	41.2	4.0	925	4	BG419088	602446318	C 609	39.8	3.8	779	9	CL446432	CL446432
537	41.2	4.0	962	5	EX432004	EX432004	610	39.8	3.8	968	5	CNS030Y6	AL256551 Tetraodon
538	41.2	4.0	1080	5	BM916998	AGENCOURT	611	39.6	3.8	372	5	BP112250	BP112250
539	41.2	4.0	1267	3	HS4802162	AL137451 Homo sapi	612	39.6	3.8	849	6	CD103751	AGENCOURT
540	41.2	4.0	1291	3	BC019687	Homo sapi	613	39.4	3.8	458	2	BB744766	BB744766
541	41.2	4.0	1871	3	BC029119	BC029119 Homo sapi	614	39.4	3.8	472	2	BS405848	BE405848 WHE0425 A
542	41.2	4.0	1914	3	BC032460	BC032460 Homo sapi	615	39.4	3.8	582	2	BM232196	BM232196 K0319G07
543	41.2	4.0	2190	9	AY418857	AY418857 Homo sapi	616	39.4	3.8	661	7	CV333279	CV333279 IL3-MT046
544	41	4.0	384	1	AY967999	AY967999 uh06903.r	617	39.4	3.8	734	7	CF735216	CF735216 UI-M-HB0-
545	41	4.0	400	5	BY430494	BY430494	618	39.4	3.8	782	2	BE548025	BE548025 601072053
546	41	4.0	426	4	BB679934	BB679934	619	39.2	3.8	323	2	BF428743	BF428743 WHE1412 G
547	41	4.0	426	4	BG082901	BG082901	620	39.2	3.8	416	7	CN010218	CN010218 WHE3868 B
548	41	4.0	427	2	BE200430	BE200430 u951f03.x	621	39.2	3.8	424	4	BM352364	BM352364 i98509.y
549	41	4.0	427	6	CB571416	CB571416 AGENCOURT	622	39.2	3.8	427	5	BQ271919	BQ271919 iK16602.y
550	41	4.0	428	4	AG060667	AG060667 L0906D05-	623	39.2	3.8	430	4	BM352585	BM352585 1968f04.x
551	41	4.0	436	2	BB690772	BB690772	624	39.2	3.8	433	6	CA866435	CA866435 i163b10.y
552	41	4.0	449	4	AG070044	AG070044 B3082B03-	625	39.2	3.8	439	1	A1034354	A1034354 ox20608.x
553	41	4.0	462	2	AW987067	AW987067 u1f3e02.x	626	39.2	3.8	439	4	BJ282278	BJ282278
554	41	4.0	484	4	BG060519	BG060519 L0904B04-	627	39.2	3.8	439	5	BQ286383	BQ286383 iK29406.y
555	41	4.0	487	1	A1551138	A1551138 vx41b04.x	628	39.2	3.8	448	6	CA774485	CA774485 iP22f06.x
556	41	4.0	488	1	A1429407	A1429407 mm98b02.x	629	39.2	3.8	457	6	CA774738	CA774738 iPl1e06.x
557	41	4.0	525	1	AU021475	AU021475	630	39.2	3.8	463	2	BF473831	BF473831 WHE0837 H
558	41	4.0	588	1	AW985812	AW985812 uf86c06.x	631	39.2	3.8	464	6	CA775983	CA775983 iO97b06.y
559	41	4.0	588	1	AW985812	AW985812	632	39.2	3.8	471	7	CN008668	CN008668 WHE2643 G
560	41	4.0	610	5	BM939848	BM939848 UI-M-CS0p	633	39.2	3.8	476	6	CA772586	CA772586 iO82c09.y
561	41	4.0	618	4	B1257435	B1257435 602967780	634	39.2	3.8	483	6	CA773899	CA773899 iM58g03.y
562	41	4.0	637	2	BB667278	BB667278	635	39.2	3.8	488	2	BF428626	BF428626 WHE1411 D
563	41	4.0	661	2	BB053589	BB053589	636	39.2	3.8	493	4	BG909869	BG909869 TaLr1110B
564	41	4.0	722	2	AW146368	AW146368 um56d04.x	637	39.2	3.8	495	6	CA731880	CA731880 wlp1c.pk0
565	41	4.0	762	3	BC038902	BC038902 Mus muscu	638	39.2	3.8	495	6	CD861413	CD861413 AZ01.002B
566	41	4.0	768	7	CK022378	CK022378 AGENCOURT	639	39.2	3.8	505	6	CD881005	CD881005 Fl.100K06
567	41	4.0	807	1	A1747300	A1747300 ull4g02.x	640	39.2	3.8	507	4	BG656094	BG656094 iB36h11.y
568	41	4.0	846	1	A1746549	A1746549 ul08d10.x	641	39.2	3.8	519	1	AJ610908	AJ610908
569	41	4.0	1017	5	BQ918508	BQ918508 AGENCOURT	642	39.2	3.8	523	5	BQ0805985	BQ0805985 WHE3573 D
570	41	4.0	1216	3	CR725879	CR725879 Tetraodon	643	39.2	3.8	534	1	AJ611394	AJ611394
571	41	4.0	1216	3	AK078556	AK078556 Mus muscu	644	39.2	3.8	534	4	BI4677039	BI4677039 iC19e10.y
572	40.8	3.9	339	4	BJ287376	BJ287376	645	39.2	3.8	546	9	FR0026920	FR0026920
573	40.8	3.9	417	1	A1041669	A1041669 oy33e02.x	646	39.2	3.8	565	6	CD102156	CD102156 AGENCOURT
574	40.8	3.9	490	7	CF919116	CF919116 Bflor531.	647	39.2	3.8	569	5	BU949310	BU949310 iN65d03.y
575	40.8	3.9	520	1	AA890428	AA890428 ak10g03.s	648	39.2	3.8	571	5	BU786551	BU786551 iN56f10.y
576	40.8	3.9	550	6	CA684216	CA684216 wlm96.pk0	649	39.2	3.8	573	6	CA867255	CA867255 iR59f08.x
577	40.8	3.9	565	4	BI713451	BI713451 iE03a03.x	650	39.2	3.8	576	6	CB067498	CB067498 iQ37f08.x
578	40.8	3.9	589	5	BU072469	BU072469 iM47e01.x	651	39.2	3.8	577	6	CB068936	CB068936 iB35f02.x
579	40.8	3.9	589	6	CA776810	CA776810 iM03a07.x	652	39.2	3.8	582	5	BU785471	BU785471 iN46a08.x
580	40.8	3.9	589	5	BQ631321	BQ631321 i119f04.x	653	39.2	3.8	586	4	BM3110606	BM3110606 iG50c04.x
581	40.8	3.9	590	5	BQ951928	BQ951928 iN74g09.x	654	39.2	3.8	588	4	BM311552	BM311552 iG66h07.x
582	40.8	3.9	1377	3	CR725714	CR725714 Tetraodon	655	39.2	3.8	588	6	CB069338	CB069338 iB16h05.x
583	40.8	3.9	1740	3	CR723886	CR723886	656	39.2	3.8	589	4	BI713519	BI713519 iE04a02.x
584	40.6	3.9	403	5	BY423102	BY423102	657	39.2	3.8	590	4	BM352104	BM352104 i986e12.x
585	40.6	3.9	671	7	BU344752	BU344752 603407056	658	39.2	3.8	601	5	BU077943	BU077943 iM63e04.x
586	40.6	3.9	701	7	CO422929	CO422929 GGEZHT102	659	39.2	3.8	617	4	BM264266	BM264266 i933b03.y
587	40.6	3.9	1116	1	AL556150	AL556150	660	39.2	3.8	620	6	CD104694	CD104694 AGENCOURT
588	40.4	3.9	435	1	A1672771	A1672771 we58f05.x	661	39.2	3.8	621	6	CD103792	CD103792 AGENCOURT
589	40.4	3.9	506	8	AQ394051	AQ394051 CITEI-E1-	662	39.2	3.8	625	6	CD103713	CD103713 AGENCOURT
590	40.4	3.9	562	1	AV614571	AV614571	663	39.2	3.8	627	6	CD512424	CD512424 AGENCOURT
591	40.4	3.9	802	7	CK777862	CK777862 965008 MA	664	39.2	3.8	647	4	BG704056	BG704056 602687196
592	40.4	3.9	2821	3	BC033247	BC033247 Homo sapi	665	39.2	3.8	648	4	BG700455	BG700455 602680444
593	40.2	3.9	564	4	BI342191	BI342191 369892 MA	666	39.2	3.8	648	4	BG713927	BG713927 602674304
594	40.2	3.9	568	2	BI191702	BI191702 239364 MA	667	39.2	3.8	650	4	BG701218	BG701218 602680672
595	40.2	3.9	699	7	CF366889	CF366889 841594 MA	668	39.2	3.8	656	6	CD104701	CD104701 AGENCOURT
596	40.2	3.9	714	6	CB527370	CB527370 UI-M-FY0-	669	39.2	3.8	664	6	CD102292	CD102292 AGENCOURT
597	40.2	3.9	745	6	CD0802869	CD0802869 UI-M-GV0-	670	39.2	3.8	680	1	AV652098	AV652098 AV652098
598	40	3.9	393	5	BY440000	BY440000	671	39.2	3.8	693	7	CK781175	CK781175 UI-M-GV0-
599	40	3.9	403	6	BY657380	BY657380	672	39.2	3.8	738	6	CD103461	CD103461 AGENCOURT
600	40	3.9	410	5	BY437397	BY437397	673	39.2	3.8	749	6	CD104003	CD104003 AGENCOURT
601	39.8	3.8	208	1	AU281844	AU281844	674	39.2	3.8	763	6	CD102386	CD102386 AGENCOURT
602	39.8	3.8	279	2	BB598990	BB598990	675	39.2	3.8	763	6	CD104349	CD104349 AGENCOURT
603	39.8	3.8	447	8	AZ622055	AZ622055 iM045FP05	676	39.2	3.8	781	6	CD000264	CD000264 AGENCOURT
604	39.8	3.8	467	1	AV610373	AV610373	677	39.2	3.8	782	6	CD512365	CD512365 AGENCOURT
605	39.8	3.8	568	4	BM313055	BM313055 i982g08.x	678	39.2	3.8	791	6	CD104786	CD104786 AGENCOURT
606	39.8	3.8	670	4	BM171749	BM171749 iMaegeqc.5	679	39.2	3.8	792	6	CD102761	CD102761 AGENCOURT
607	39.8	3.8	710	7	CD225540	CD225540 WLA073F11	680	39.2	3.8	795	6	CD512411	CD512411 AGENCOURT
608	39.8	3.8	735	6	CD921512	CD921512 G608.1200	681	39.2	3.8	799	6	CD102757	CD102757 AGENCOURT

682	39.2	3.8	800	6	CD103030	CD103030	AGENCOURT	755	38	3.7	667	2	BB659444
683	39.2	3.8	804	6	CD512491	CD512491	AGENCOURT	756	38	3.7	686	6	CD103837
684	39.2	3.8	811	6	CD000531	CD000531	AGENCOURT	757	38	3.7	773	6	CB999985
685	39.2	3.8	813	6	CB999989	CB999989	AGENCOURT	758	38	3.7	779	6	CD000450
686	39.2	3.8	814	6	CD103471	CD103471	AGENCOURT	759	38	3.7	816	1	AU117395
687	39.2	3.8	838	6	CD001024	CD001024	AGENCOURT	760	38	3.7	832	6	CB999251
688	39.2	3.8	842	6	CD104017	CD104017	AGENCOURT	761	38	3.7	851	6	CD000325
689	39.2	3.8	845	6	CB998993	CB998993	AGENCOURT	762	38	3.7	878	6	CB999408
690	39.2	3.8	878	6	CD512192	CD512192	AGENCOURT	763	38	3.7	893	5	BU523040
691	39.2	3.8	904	5	BU144883	BU144883	603229661	764	38	3.7	1098	6	CB999002
692	39	3.8	401	2	BB004414	BB004414	BB004414	765	38	3.7	1863	9	CL960212
693	39.2	3.8	427	5	BY421952	BY421952	BY421952	766	38	3.7	3651	3	AK084752
694	39	3.8	427	7	CO436236	CO436236	ddPCR2.17	767	38	3.7	3869	3	AK031112
695	39	3.8	445	1	AA698719	AA698719	BL05552.5	768	38	3.7	3924	3	AK083538
696	39	3.8	460	2	BB761314	BB761314	BB761314	769	37.8	3.7	437	7	CN391010
697	39	3.8	545	4	BM440456	BM440456	Pgrin.pk0	770	37.8	3.7	479	1	AA688911
698	39	3.8	548	1	AA567371	AA567371	HL01080.5	771	37.8	3.7	493	6	CA943388
699	39	3.8	582	5	BP354326	BP354326	BP354326	772	37.8	3.7	499	7	CV336344
700	39	3.8	600	4	BM147637	BM147637	TCRAP1013	773	37.8	3.7	500	4	BM146494
701	39	3.8	719	4	BG775252	BG775252	602650266	774	37.8	3.7	546	7	CN391011
702	39	3.8	782	4	BG490422	BG490422	602519448	775	37.8	3.7	551	4	BM147912
703	39	3.8	832	4	BM048129	BM048129	603620480	776	37.8	3.7	558	2	CN391008
704	39	3.8	879	5	BU050483	BU050483	AGENCOURT	777	37.8	3.7	565	2	BE264631
705	39	3.8	951	5	BQ944019	BQ944019	AGENCOURT	778	37.8	3.7	569	4	BM759253
706	39	3.8	1005	5	BQ944936	BQ944936	AGENCOURT	779	37.8	3.7	581	5	BP356172
707	39	3.8	1011	4	BM554297	BM554297	AGENCOURT	780	37.8	3.7	582	5	BP286742
708	39	3.8	1044	5	BM925155	BM925155	AGENCOURT	781	37.8	3.7	582	7	CN483145
709	38.8	3.7	269	1	AA365469	AA365469	EST762250	782	37.8	3.7	583	5	BP284410
710	38.8	3.7	655	5	BX422176	BX422176	BX422176	783	37.8	3.7	584	5	BP336907
711	38.8	3.7	673	4	BM791148	BM791148	K-BST0071	784	37.8	3.7	584	7	CN391006
712	38.8	3.7	862	6	CD357832	CD357832	AGENCOURT	785	37.8	3.7	587	2	BE894869
713	38.8	3.7	931	6	CB999539	CB999539	AGENCOURT	786	37.8	3.7	595	2	BE276689
714	38.8	3.7	1104	6	CB999061	CB999061	AGENCOURT	787	37.8	3.7	595	7	CN391009
715	38.8	3.7	1198	5	BQ955992	BQ955992	AGENCOURT	788	37.8	3.7	597	5	BP366089
716	38.6	3.7	505	4	BM253186	BM253186	512568 MA	789	37.8	3.7	603	5	BP277914
717	38.6	3.7	527	8	AQ457532	AQ457532	HS 5087 A	790	37.8	3.7	605	2	AW236141
718	38.6	3.7	565	5	BQ239435	BQ239435	TaE05031A	791	37.8	3.7	608	1	AL527352
719	38.6	3.7	596	7	CO288202	CO288202	EK067954	792	37.8	3.7	609	7	CF132379
720	38.6	3.7	940	5	BX369835	BX369835	BX369835	793	37.8	3.7	622	7	CN485198
721	38.6	3.7	4919	3	BC040674	BC040674	Homo sapi	794	37.8	3.7	633	7	CV026154
722	38.4	3.7	402	1	AA776183	AA776183	ae80d06.s	795	37.8	3.7	634	1	AV649762
723	38.4	3.7	532	4	BM152584	BM152584	TCRAP1E93	796	37.8	3.7	638	2	BF219760
724	38.4	3.7	592	6	CA384192	CA384192	644641 NC	797	37.8	3.7	661	4	BI826255
725	38.4	3.7	609	6	CD103749	CD103749	AGENCOURT	798	37.8	3.7	670	4	BI829519
726	38.4	3.7	619	9	CR842092	CR842092	GR0AA76C	799	37.8	3.7	672	2	BE894852
727	38.4	3.7	620	7	CV088415	CV088415	CS_gil_42	800	37.8	3.7	672	7	CN391003
728	38.4	3.7	832	7	CN047600	CN047600	V2_p13_P8	801	37.8	3.7	675	4	BG490460
729	38.4	3.7	910	9	CNS0060N	AL065629	Drosophila	802	37.8	3.7	677	4	BI090613
730	38.4	3.7	1064	5	BU174116	BU174116	AGENCOURT	803	37.8	3.7	695	4	BM046512
731	38.4	3.7	1066	4	BM808284	BM808284	AGENCOURT	804	37.8	3.7	697	2	BE280160
732	38.4	3.7	1178	8	B2553247	B2553247	pacel1-50	805	37.8	3.7	706	2	BE409866
733	38.4	3.7	1201	4	BM423379	BM423379	AGENCOURT	806	37.8	3.7	711	2	BE410468
734	38.2	3.7	274	1	AA364433	AA364433	EST75052	807	37.8	3.7	712	2	BE262862
735	38.2	3.7	319	1	AA364219	AA364219	EST74757	808	37.8	3.7	721	4	BI823887
736	38.2	3.7	336	1	AA364221	AA364221	EST74759	809	37.8	3.7	737	4	BG822539
737	38.2	3.7	349	6	CA652911	CA652911	wrein.pk1	810	37.8	3.7	748	4	BI912207
738	38.2	3.7	435	7	TC02899	TC02899	yb87e10.t1	811	37.8	3.7	750	4	BM720899
739	38.2	3.7	447	6	CD102287	CD102287	AGENCOURT	812	37.8	3.7	753	4	BG718997
740	38.2	3.7	467	4	BG322727	EM1_13_E0	EM1_13_E0	813	37.8	3.7	756	4	BG771599
741	38.2	3.7	504	8	A2699074	RPCT-23-2	RPCT-23-2	814	37.8	3.7	771	4	BI829464
742	38.2	3.7	520	2	B466906	B466906	hz28f07.x	815	37.8	3.7	776	5	BQ226952
743	38.2	3.7	531	4	BG654779	BG654779	lb44d10.x	816	37.8	3.7	782	4	BI518856
744	38.2	3.7	543	8	A2620467	A2620467	lm0453007	817	37.8	3.7	788	4	BI667679
745	38.2	3.7	572	5	BQ632353	BQ632353	1125h10.x	818	37.8	3.7	799	4	BM045780
746	38.2	3.7	579	6	CB086001	CB086001	ip39b08.x	819	37.8	3.7	808	4	BG740654
747	38.2	3.7	622	6	CA080065	CA080065	SCQ5AM210	820	37.8	3.7	810	4	BG252525
748	38.2	3.7	799	6	B2397301	B2397301	601288632	821	37.8	3.7	815	4	BG743989
749	38.2	3.7	796	5	CD512408	CD512408	AGENCOURT	822	37.8	3.7	819	4	BI836599
750	38.2	3.7	947	5	BX361563	BX361563	BX361563	823	37.8	3.7	825	4	BI862467
751	38.2	3.7	999	6	CD000244	CD000244	AGENCOURT	824	37.8	3.7	832	4	BI461274
752	38	3.7	471	4	BM690353	UI-B-C10-	UI-B-C10-	825	37.8	3.7	844	4	BG327069
753	38	3.7	529	7	CK822554	ig92b01.x	ig92b01.x	826	37.8	3.7	846	4	BI520512
754	38	3.7	624	6	CD000819	AGENCOURT	AGENCOURT	827	37.8	3.7	847	5	BQ218137

828	37.8	3.7	848	5	BU543660	AGENCOURT	BU543660	AGENCOURT	C 901	37.6	3.6	391	6	CA847779	icq42809.x
829	37.8	3.7	851	5	BU556865	AGENCOURT	BU556865	AGENCOURT	902	37.6	3.6	396	6	CA941077	icq42809.x
830	37.8	3.7	855	2	BE871126	601447382	BE871126	601447382	903	37.6	3.6	396	6	CA952703	icq42809.x
831	37.8	3.7	856	1	AL546240	AL546240	AL546240	AL546240	904	37.6	3.6	397	6	BM312530	icq42809.x
832	37.8	3.7	863	4	BI828042	603073787	BI828042	603073787	905	37.6	3.6	397	6	CA950923	icq42809.x
833	37.8	3.7	868	6	CA488022	AGENCOURT	CA488022	AGENCOURT	906	37.6	3.6	398	6	CA950923	icq42809.x
834	37.8	3.7	871	5	BU542727	AGENCOURT	BU542727	AGENCOURT	907	37.6	3.6	398	6	CA971267	icq42809.x
835	37.8	3.7	889	5	BQ954437	AGENCOURT	BQ954437	AGENCOURT	908	37.6	3.6	399	6	CA948194	icq42809.x
836	37.8	3.7	889	7	CF272496	AGENCOURT	CF272496	AGENCOURT	909	37.6	3.6	399	6	CA948194	icq42809.x
837	37.8	3.7	890	4	BG287979	602387754	BG287979	602387754	910	37.6	3.6	400	5	BM313334	icq42809.x
838	37.8	3.7	893	4	BG747004	602704582	BG747004	602704582	911	37.6	3.6	400	5	BQ631989	icq42809.x
839	37.8	3.7	895	5	BQ941900	AGENCOURT	BQ941900	AGENCOURT	912	37.6	3.6	400	6	CA943302	icq42809.x
840	37.8	3.7	896	5	BQ216489	AGENCOURT	BQ216489	AGENCOURT	913	37.6	3.6	400	6	CA943302	icq42809.x
841	37.8	3.7	900	5	BU957145	AGENCOURT	BU957145	AGENCOURT	914	37.6	3.6	402	6	CB067746	icq42809.x
842	37.8	3.7	900	5	BQ934527	AGENCOURT	BQ934527	AGENCOURT	915	37.6	3.6	403	5	BM663400	icq42809.x
843	37.8	3.7	900	5	BQ958970	AGENCOURT	BQ958970	AGENCOURT	916	37.6	3.6	403	5	BQ272140	icq42809.x
844	37.8	3.7	902	2	BE619521	601473077	BE619521	601473077	917	37.6	3.6	403	5	BM663400	icq42809.x
845	37.8	3.7	906	5	BU944646	AGENCOURT	BU944646	AGENCOURT	918	37.6	3.6	404	6	CF534956	icq42809.x
846	37.8	3.7	914	5	BQ944028	AGENCOURT	BQ944028	AGENCOURT	919	37.6	3.6	404	6	CA847866	icq42809.x
847	37.8	3.7	915	5	BQ955025	AGENCOURT	BQ955025	AGENCOURT	920	37.6	3.6	408	5	BU072900	icq42809.x
848	37.8	3.7	918	5	BU175422	AGENCOURT	BU175422	AGENCOURT	921	37.6	3.6	408	5	CA848527	icq42809.x
849	37.8	3.7	926	6	CD243465	AGENCOURT	CD243465	AGENCOURT	922	37.6	3.6	411	4	BI711815	icq42809.x
850	37.8	3.7	929	5	BQ227659	AGENCOURT	BQ227659	AGENCOURT	923	37.6	3.6	411	5	BQ478091	icq42809.x
851	37.8	3.7	936	4	BG326662	602425515	BG326662	602425515	924	37.6	3.6	414	6	CA867768	icq42809.x
852	37.8	3.7	942	5	BU542368	AGENCOURT	BU542368	AGENCOURT	925	37.6	3.6	414	6	CD102656	icq42809.x
853	37.8	3.7	945	5	BQ934742	AGENCOURT	BQ934742	AGENCOURT	926	37.6	3.6	414	7	W67833	icq42809.x
854	37.8	3.7	947	4	BG331675	602432685	BG331675	602432685	927	37.6	3.6	415	4	BI711532	icq42809.x
855	37.8	3.7	949	5	BQ889036	AGENCOURT	BQ889036	AGENCOURT	928	37.6	3.6	416	6	CA841844	icq42809.x
856	37.8	3.7	949	5	BQ958647	AGENCOURT	BQ958647	AGENCOURT	929	37.6	3.6	417	6	CA843168	icq42809.x
857	37.8	3.7	954	4	BM424036	AGENCOURT	BM424036	AGENCOURT	930	37.6	3.6	419	5	BU949461	icq42809.x
858	37.8	3.7	954	5	BQ919599	AGENCOURT	BQ919599	AGENCOURT	931	37.6	3.6	419	5	CB067105	icq42809.x
859	37.8	3.7	971	5	BX400451	AGENCOURT	BX400451	AGENCOURT	932	37.6	3.6	420	6	CA774942	icq42809.x
860	37.8	3.7	972	5	BQ952738	AGENCOURT	BQ952738	AGENCOURT	933	37.6	3.6	422	6	CA775577	icq42809.x
861	37.8	3.7	978	5	BQ943836	AGENCOURT	BQ943836	AGENCOURT	934	37.6	3.6	422	6	CD104022	icq42809.x
862	37.8	3.7	986	5	BQ954806	AGENCOURT	BQ954806	AGENCOURT	935	37.6	3.6	423	6	BM663222	icq42809.x
863	37.8	3.7	992	2	BE736855	AGENCOURT	BE736855	AGENCOURT	936	37.6	3.6	423	6	CA773973	icq42809.x
864	37.8	3.7	1009	5	BM917953	AGENCOURT	BM917953	AGENCOURT	937	37.6	3.6	424	5	BU072096	icq42809.x
865	37.8	3.7	1011	1	AL539344	AGENCOURT	AL539344	AGENCOURT	938	37.6	3.6	424	5	BU074641	icq42809.x
866	37.8	3.7	1018	2	BE790356	601480536	BE790356	601480536	939	37.6	3.6	425	6	CA950242	icq42809.x
867	37.8	3.7	1018	2	BE902991	601676948	BE902991	601676948	940	37.6	3.6	425	6	CA950242	icq42809.x
868	37.8	3.7	1038	2	BE733347	601570567	BE733347	601570567	941	37.6	3.6	425	5	BM352914	icq42809.x
869	37.8	3.7	1041	4	BG3331618	602432618	BG3331618	602432618	942	37.6	3.6	425	5	BQ269014	icq42809.x
870	37.8	3.7	1041	5	BQ073173	AGENCOURT	BQ073173	AGENCOURT	943	37.6	3.6	426	6	CD102521	icq42809.x
871	37.8	3.7	1044	4	BG342082	602463078	BG342082	602463078	944	37.6	3.6	427	1	AV647145	icq42809.x
872	37.8	3.7	1055	2	BE778041	601463144	BE778041	601463144	945	37.6	3.6	427	6	BG656273	icq42809.x
873	37.8	3.7	1066	5	BQ052829	AGENCOURT	BQ052829	AGENCOURT	946	37.6	3.6	428	6	CA842802	icq42809.x
874	37.8	3.7	1124	4	BM810321	AGENCOURT	BM810321	AGENCOURT	947	37.6	3.6	428	6	CA868528	icq42809.x
875	37.8	3.7	1129	2	BE729283	AGENCOURT	BE729283	AGENCOURT	948	37.6	3.6	428	6	CD105140	icq42809.x
876	37.8	3.7	1130	4	BM462207	AGENCOURT	BM462207	AGENCOURT	949	37.6	3.6	429	5	BQ286494	icq42809.x
877	37.8	3.7	1172	9	CNS020MV	AGENCOURT	AL209488	Tetraodon	950	37.6	3.6	429	6	CA950242	icq42809.x
878	37.8	3.7	1178	3	CR624380	full1-leng	CR624380	full1-leng	951	37.6	3.6	429	6	CB070396	icq42809.x
879	37.8	3.7	2167	3	AA365847	EST76701	AA365847	EST76701	952	37.6	3.6	429	6	CB178556	icq42809.x
880	37.6	3.6	226	1	BU078232	im66601.y	BU078232	im66601.y	953	37.6	3.6	430	6	CD000232	icq42809.x
881	37.6	3.6	319	5	BU078232	im66601.y	BU078232	im66601.y	954	37.6	3.6	430	6	CA947190	icq42809.x
882	37.6	3.6	342	6	CA843160	icq42809.y	CA843160	icq42809.y	955	37.6	3.6	431	5	BQ287841	icq42809.x
883	37.6	3.6	342	6	CA941507	icq42809.y	CA941507	icq42809.y	956	37.6	3.6	432	6	CA774877	icq42809.x
884	37.6	3.6	342	6	CA947024	icq42809.y	CA947024	icq42809.y	957	37.6	3.6	432	6	CA848213	icq42809.x
885	37.6	3.6	342	6	CA947074	icq42809.y	CA947074	icq42809.y	958	37.6	3.6	434	6	CA941881	icq42809.x
886	37.6	3.6	342	6	CA948274	icq42809.y	CA948274	icq42809.y	959	37.6	3.6	435	4	BI712910	icq42809.x
887	37.6	3.6	360	6	CA950974	icq42809.y	CA950974	icq42809.y	960	37.6	3.6	436	1	AI635292	icq42809.x
888	37.6	3.6	367	6	CA946943	icq42809.y	CA946943	icq42809.y	961	37.6	3.6	436	6	BM314673	icq42809.x
889	37.6	3.6	369	6	BM312077	icq42809.y	BM312077	icq42809.y	962	37.6	3.6	438	6	CA774730	icq42809.x
890	37.6	3.6	369	6	CA841363	icq42809.y	CA841363	icq42809.y	963	37.6	3.6	439	5	BU071699	icq42809.x
891	37.6	3.6	369	6	CA942296	icq42809.y	CA942296	icq42809.y	964	37.6	3.6	440	6	CD104454	icq42809.x
892	37.6	3.6	369	6	CA948215	icq42809.y	CA948215	icq42809.y	965	37.6	3.6	441	4	BM353023	icq42809.x
893	37.6	3.6	369	6	CB067182	icq42809.y	CB067182	icq42809.y	966	37.6	3.6	441	5	BU078941	icq42809.x
894	37.6	3.6	370	6	CA946979	icq42809.y	CA946979	icq42809.y	967	37.6	3.6	442	6	CB069653	icq42809.x
895	37.6	3.6	370	6	CA9494022	icq42809.y	CA9494022	icq42809.y	968	37.6	3.6	442	6	CD000564	icq42809.x
896	37.6	3.6	379	6	CB178027	icq42809.x	CB178027	icq42809.x	969	37.6	3.6	443	4	BI438421	icq42809.x
897	37.6	3.6	381	6	CA867987	icq42809.x	CA867987	icq42809.x	970	37.6	3.6	443	5	BQ269877	icq42809.x
898	37.6	3.6	386	6	CA946938	icq42809.y	CA946938	icq42809.y	971	37.6	3.6	444	5	BU951035	icq42809.x
899	37.6	3.6	387	6	CA775628	icq42809.y	CA775628	icq42809.y	972	37.6	3.6	444	6	CA775784	icq42809.x
900	37.6	3.6	389	5	BU072158	im55a05.y	BU072158	im55a05.y	973	37.6	3.6	444	6	CA867251	icq42809.x

974	37.6	3.6	444	6	CA867536	ir29f03.Y	1047	37.6	3.6	464	4	BM314769	ig54h05.Y
975	37.6	3.6	444	9	AY412722	Homo sapi	c1048	37.6	3.6	464	6	CA771893	io84f04.X
976	37.6	3.6	445	4	BM353367	ig46b04.Y	c1049	37.6	3.6	464	6	CA775574	io25a02.X
c 977	37.6	3.6	445	5	BQ271813	ik18h01.X	c1050	37.6	3.6	464	6	CA775314	io87g08.X
978	37.6	3.6	445	5	BQ777123	ig143f06.Y	1051	37.6	3.6	464	6	CA848746	ir24h09.Y
979	37.6	3.6	445	6	CA948857	iq28g04.Y	1052	37.6	3.6	464	6	CA865936	ir42g11.Y
980	37.6	3.6	445	6	CB070020	ig32e12.Y	1053	37.6	3.6	464	6	CA948344	iq21b05.Y
981	37.6	3.6	445	6	CD103969	AGENCOURT	1054	37.6	3.6	464	6	CD103677	AGENCOURT
982	37.6	3.6	446	5	BQ417393	ik37d05.Y	c1055	37.6	3.6	466	6	CA775761	io98a06.X
c 983	37.6	3.6	446	5	BQ778637	ig13g01.Y	1056	37.6	3.6	466	6	CA776515	ip06b07.Y
984	37.6	3.6	446	5	BQ069246	im59g11.X	1057	37.6	3.6	466	6	CA776666	ip09b05.Y
985	37.6	3.6	447	5	BQ286305	ig18d09.Y	1058	37.6	3.6	467	1	AA063095	zf67e02.X
c 986	37.6	3.6	447	6	CA841741	ip27d06.X	1059	37.6	3.6	467	4	BM312614	ig76h02.Y
987	37.6	3.6	448	4	BM313502	ig71b04.Y	1060	37.6	3.6	467	5	BU951791	in60h03.Y
988	37.6	3.6	448	7	N72965	ig48h10.X	1061	37.6	3.6	468	5	BQ271854	ik15d01.Y
c 989	37.6	3.6	449	1	A1640312	wa16g04.X	1062	37.6	3.6	468	5	BU072867	ig13g04.Y
990	37.6	3.6	449	4	BM311107	ig60h04.Y	1063	37.6	3.6	468	6	CA773262	im61g06.Y
991	37.6	3.6	449	6	CA388990	cs04e12.Y	1064	37.6	3.6	468	6	CA777288	ip05g02.Y
992	37.6	3.6	450	5	BU785777	in46a08.Y	1065	37.6	3.6	468	6	CA849181	ir70g10.Y
993	37.6	3.6	450	6	CA842422	ir26h08.Y	1066	37.6	3.6	468	6	CA867456	ir28e08.Y
994	37.6	3.6	451	6	CA866270	ir36e02.Y	1067	37.6	3.6	469	5	BU072655	im46a05.Y
995	37.6	3.6	451	6	CB177238	is18b03.Y	1068	37.6	3.6	469	6	CD102863	AGENCOURT
996	37.6	3.6	451	6	CB177488	is22a03.Y	1069	37.6	3.6	469	6	CD103553	AGENCOURT
997	37.6	3.6	452	5	BQ632610	ir125e05.Y	1070	37.6	3.6	470	5	BU072227	im55h04.Y
c 998	37.6	3.6	452	6	CA866104	ir38b10.X	1071	37.6	3.6	471	4	BM313157	ig80c04.Y
999	37.6	3.6	452	6	CD104127	AGENCOURT	1072	37.6	3.6	471	5	BU786011	in48h12.Y
1000	37.6	3.6	453	6	CA777093	ip03a07.Y	1073	37.6	3.6	472	6	CA772763	io84f04.Y
c 1001	37.6	3.6	453	6	CA843373	ir49h01.Y	1074	37.6	3.6	472	6	CD000428	AGENCOURT
c1002	37.6	3.6	454	1	A1052008	oe29d05.X	1075	37.6	3.6	472	7	CF535047	ui-M-G10-
1003	37.6	3.6	454	4	BI791818	ie05a03.Y	1076	37.6	3.6	473	6	CA778394	ip17h12.Y
1004	37.6	3.6	455	5	BQ632776	il27g09.Y	1077	37.6	3.6	473	6	BQ272115	ik18e05.Y
1005	37.6	3.6	455	6	CA843709	ir51b02.Y	1078	37.6	3.6	474	5	CA776652	ip08h12.Y
1006	37.6	3.6	455	6	CB067044	iq31d04.Y	1079	37.6	3.6	475	4	BM272354	ig39g07.Y
1007	37.6	3.6	456	4	BM352424	ig86e12.Y	1080	37.6	3.6	475	4	BM311219	ig62d08.Y
1008	37.6	3.6	456	5	BQ270038	ik33b10.Y	1081	37.6	3.6	475	4	BM312612	ig76g12.Y
1009	37.6	3.6	456	5	BQ777797	il37b04.Y	1082	37.6	3.6	475	5	BQ417176	ik42f10.Y
1010	37.6	3.6	456	5	BU072068	im53h03.Y	1083	37.6	3.6	475	5	BQ631425	il117b09.Y
1011	37.6	3.6	457	5	BU790328	in49f12.Y	1084	37.6	3.6	475	6	CA772615	io82f08.Y
c1012	37.6	3.6	457	6	CA771783	io82h02.X	1085	37.6	3.6	475	6	CA775613	io88a07.Y
c1013	37.6	3.6	457	6	CA774562	ip24g10.X	1086	37.6	3.6	475	6	CA777648	ip13d01.Y
1014	37.6	3.6	457	6	CA867802	ir81d08.Y	1087	37.6	3.6	475	6	CA777669	ip19f06.Y
1015	37.6	3.6	458	5	BQ631712	il21c03.Y	1088	37.6	3.6	475	6	CA777811	ip21f07.Y
1016	37.6	3.6	458	5	BU071978	im52g02.Y	1089	37.6	3.6	475	6	CD511934	AGENCOURT
c1017	37.6	3.6	458	6	CA771959	io93f05.X	1090	37.6	3.6	476	5	BU074727	im75g12.Y
c1018	37.6	3.6	458	6	CA775898	io99h12.X	1091	37.6	3.6	476	6	CA772593	io82d06.Y
c1019	37.6	3.6	458	6	CA777412	ip19f05.X	1092	37.6	3.6	476	6	CA775595	io87g08.Y
1020	37.6	3.6	458	6	CA842190	ip29e05.Y	1093	37.6	3.6	476	6	CB067672	iq36a07.Y
1021	37.6	3.6	458	6	CA948436	ig22e11.Y	1094	37.6	3.6	476	6	CD357989	AGENCOURT
1022	37.6	3.6	458	6	CA952240	ig16h10.Y	1095	37.6	3.6	477	6	CA777743	ip20g02.Y
1023	37.6	3.6	459	5	BU071927	im52a12.Y	1096	37.6	3.6	477	6	CA847912	iq40a06.Y
c1024	37.6	3.6	459	6	CA773911	im58h09.Y	1097	37.6	3.6	477	6	CA848722	ir24f02.Y
c1025	37.6	3.6	459	6	CA777479	ip20g02.X	1098	37.6	3.6	477	6	CD512586	AGENCOURT
c1026	37.6	3.6	459	6	CA777904	ip15a06.X	1099	37.6	3.6	478	4	BG656007	ib33h01.Y
c1027	37.6	3.6	460	6	CA777428	ip19h04.X	1100	37.6	3.6	478	6	CA566557	K0402G07-
1028	37.6	3.6	460	6	CA865926	ir43f04.Y	1101	37.6	3.6	478	6	CA776117	io99h12.Y
1029	37.6	3.6	460	6	CA866612	ir73h04.Y	1102	37.6	3.6	478	6	CA842032	ip27d06.Y
1030	37.6	3.6	460	6	CA951115	ir95b11.Y	1103	37.6	3.6	479	5	BQ417028	ik40g11.Y
1031	37.6	3.6	461	4	BG654513	ib41e01.Y	1104	37.6	3.6	479	5	BU785761	in45h03.Y
1032	37.6	3.6	461	4	BG656008	ib35h02.Y	1105	37.6	3.6	479	5	BU786499	in55f02.Y
c1033	37.6	3.6	461	6	CA771967	ig93g03.X	1106	37.6	3.6	479	5	BU952695	io73g07.Y
c1034	37.6	3.6	461	6	CA772105	io95g06.X	1107	37.6	3.6	479	6	CA773770	im56h06.Y
c1035	37.6	3.6	461	6	CA774621	ip25f07.X	1108	37.6	3.6	479	6	CA775657	io88e11.Y
c1036	37.6	3.6	461	6	CA775245	io86e08.X	1109	37.6	3.6	480	6	CA774975	ip11d02.Y
c1037	37.6	3.6	461	6	CA777341	ip18e03.X	1110	37.6	3.6	480	6	CA942266	ir60e06.Y
c1038	37.6	3.6	461	6	CA777456	ip20d06.X	c1111	37.6	3.6	481	1	AA937375	oj03b07.s
1039	37.6	3.6	461	6	CA941588	ir33c06.Y	1112	37.6	3.6	481	4	BM314734	ig54d04.Y
c1040	37.6	3.6	461	6	CB178807	is40f07.X	1113	37.6	3.6	481	5	BQ417079	ik41d07.Y
1041	37.6	3.6	462	4	BM313201	ig80g08.Y	1114	37.6	3.6	481	6	CA865813	ir42a06.Y
1042	37.6	3.6	462	5	BQ269741	ik23e08.X	1115	37.6	3.6	481	6	CA948409	iq22b01.Y
c1043	37.6	3.6	462	6	CA771733	io82b02.X	1116	37.6	3.6	481	6	CB178473	ib33c04.Y
1044	37.6	3.6	462	6	CA772248	io93g03.Y	c1117	37.6	3.6	481	6	CD608274	56098855H
1045	37.6	3.6	462	6	CB068299	is17g10.X	1118	37.6	3.6	481	6	CD608275	56098855J
1046	37.6	3.6	463	5	BQ632778	il27g11.Y	1119	37.6	3.6	482	4	BM314634	ig53b01.Y

1120	37.6	3.6	482	5	BU072878	BU072878	l135h05.y	1193	37.6	3.6	503	4	BM313560	BM313560	ig71g03.y
1121	37.6	3.6	482	5	BU078192	BU078192	im65e010.y	1194	37.6	3.6	504	4	BM504034	BM504034	ig99h07.y
1122	37.6	3.6	482	5	BU0786545	BU0786545	im65e02.y	1195	37.6	3.6	504	6	CA847987	CA847987	ig41b07.y
1123	37.6	3.6	482	6	CA848096	CA848096	ig42g04.y	1196	37.6	3.6	504	6	CD102368	CD102368	AGENCOURT
1124	37.6	3.6	482	6	CB177539	CB177539	ig23a06.y	1197	37.6	3.6	505	1	AA719715	AA719715	ig53c09.y
1125	37.6	3.6	483	5	BQ417092	BQ417092	ig41f07.y	1198	37.6	3.6	505	4	BM505147	BM505147	ig90h11.y
1126	37.6	3.6	483	6	CA848467	CA848467	ig35a08.y	1199	37.6	3.6	505	5	BQ417442	BQ417442	ig38a09.y
1127	37.6	3.6	484	6	BM314473	BM314473	ig51a05.y	1200	37.6	3.6	505	5	BQ951073	BQ951073	ig75e04.y
1128	37.6	3.6	484	6	CA777179	CA777179	ig04c02.y	1201	37.6	3.6	505	6	CA842373	CA842373	ig75e02.y
1129	37.6	3.6	484	6	CD102603	CD102603	AGENCOURT	1202	37.6	3.6	506	1	AA719616	AA719616	ig75e02.y
1130	37.6	3.6	484	6	CD512027	CD512027	AGENCOURT	1203	37.6	3.6	506	1	BG655893	BG655893	ig40d04.y
1131	37.6	3.6	485	5	BQ416997	BQ416997	ig40d10.y	1204	37.6	3.6	506	4	BG655893	BG655893	ig40d04.y
1132	37.6	3.6	485	6	CA777020	CA777020	ig02a09.y	1205	37.6	3.6	506	4	BG655893	BG655893	ig40d04.y
1133	37.6	3.6	485	6	CA777689	CA777689	ig19h04.y	1206	37.6	3.6	506	4	BM263570	BM263570	ig27g03.y
1134	37.6	3.6	485	6	CA952306	CA952306	ig18a04.y	1207	37.6	3.6	506	4	BM313577	BM313577	ig27g03.y
1135	37.6	3.6	486	4	BM313506	BM313506	ig18a04.y	1208	37.6	3.6	506	5	BU949483	BU949483	ig18a10.y
1136	37.6	3.6	486	6	CA943144	CA943144	ig39b08.y	1209	37.6	3.6	506	6	CA843196	CA843196	ig18a10.y
1137	37.6	3.6	486	6	CA946958	CA946958	ig09c11.y	1210	37.6	3.6	507	4	BM312299	BM312299	ig41f09.y
1138	37.6	3.6	487	6	CA776566	CA776566	ig09c06.y	1211	37.6	3.6	507	5	BQ477906	BQ477906	ig41f09.y
1139	37.6	3.6	487	6	CA865916	CA865916	ig43e03.y	1212	37.6	3.6	508	5	BU951671	BU951671	ig41f09.y
1140	37.6	3.6	487	6	CB067623	CB067623	ig35c12.y	1213	37.6	3.6	508	6	CA947221	CA947221	ig41f09.y
1141	37.6	3.6	488	5	BQ778075	BQ778075	ig14f08.y	1214	37.6	3.6	509	5	BQ776769	BQ776769	ig13a04.y
1142	37.6	3.6	488	5	BU948942	BU948942	ig17b02.y	1215	37.6	3.6	510	5	BU952185	BU952185	ig17a09.y
1143	37.6	3.6	488	5	BU952169	BU952169	ig17b02.y	1216	37.6	3.6	510	6	CA847891	CA847891	ig17a09.y
1144	37.6	3.6	488	6	CA842880	CA842880	ig45h05.y	1217	37.6	3.6	510	6	CB070342	CB070342	ig16e07.x
1145	37.6	3.6	488	6	CD109299	CD109299	AGENCOURT	1218	37.6	3.6	510	6	CD103048	CD103048	AGENCOURT
1146	37.6	3.6	489	4	BI438478	BI438478	ig23h12.y	1219	37.6	3.6	511	6	CA866243	CA866243	ig16a12.y
1147	37.6	3.6	489	4	BI467014	BI467014	ig18c07.y	1220	37.6	3.6	511	6	CA942950	CA942950	ig16b03.y
1148	37.6	3.6	489	6	CA941027	CA941027	ig37e05.y	1221	37.6	3.6	512	4	BM352814	BM352814	ig16b03.y
1149	37.6	3.6	489	6	CA948422	CA948422	ig22c11.y	1222	37.6	3.6	512	4	BM505043	BM505043	ig16b03.y
1150	37.6	3.6	489	6	CB066970	CB066970	ig34b08.x	1223	37.6	3.6	512	6	CA777321	CA777321	ig16b03.y
1151	37.6	3.6	490	4	BM263775	BM263775	ig30d05.y	1224	37.6	3.6	512	6	CA776636	CA776636	ig16b03.y
1152	37.6	3.6	491	6	CA843153	CA843153	ig18c05.y	1225	37.6	3.6	512	6	CA842213	CA842213	ig16b03.y
1153	37.6	3.6	491	6	CA868042	CA868042	ig17g11.y	1226	37.6	3.6	512	6	CA848014	CA848014	ig16b03.y
1154	37.6	3.6	491	6	CA868527	CA868527	ig18b05.x	1227	37.6	3.6	513	6	CA941539	CA941539	ig16b03.y
1155	37.6	3.6	491	6	CA948811	CA948811	ig28b06.y	1228	37.6	3.6	513	6	BI712659	BI712659	ig16b03.y
1156	37.6	3.6	491	6	CD109323	CD109323	AGENCOURT	1229	37.6	3.6	515	6	CA942222	CA942222	ig16b03.y
1157	37.6	3.6	492	6	CA866718	CA866718	ig17e02.y	1230	37.6	3.6	515	6	CB069531	CB069531	ig16b03.y
1158	37.6	3.6	493	4	BM263510	BM263510	ig27a02.y	1231	37.6	3.6	516	5	BP216474	BP216474	ig16b03.y
1159	37.6	3.6	493	4	BM312122	BM312122	ig16e09.y	1232	37.6	3.6	516	5	BP216509	BP216509	ig16b03.y
1160	37.6	3.6	493	5	BQ269913	BQ269913	ig26e05.y	1233	37.6	3.6	517	1	AA757582	AA757582	ig16b03.y
1161	37.6	3.6	493	5	BQ783912	BQ783912	ig11d10.x	1234	37.6	3.6	517	5	BP201090	BP201090	ig16b03.y
1162	37.6	3.6	493	6	CA772629	CA772629	ig08h02.y	1235	37.6	3.6	519	5	BU074680	BU074680	ig16b03.y
1163	37.6	3.6	493	6	CA772697	CA772697	ig08h12.y	1236	37.6	3.6	519	6	CA773126	CA773126	ig16b03.y
1164	37.6	3.6	493	6	CA772773	CA772773	ig08g06.y	1237	37.6	3.6	519	6	CB178713	CB178713	ig16b03.y
1165	37.6	3.6	493	6	CA777594	CA777594	ig18e03.y	1238	37.6	3.6	520	5	BU949872	BU949872	ig16b03.y
1166	37.6	3.6	493	6	CA842500	CA842500	ig43a11.y	1239	37.6	3.6	520	6	CB115409	CB115409	ig16b03.y
1167	37.6	3.6	494	5	BU784703	BU784703	ig15f02.x	1240	37.6	3.6	521	1	AA757575	AA757575	ig16b03.y
1168	37.6	3.6	494	6	CA775609	CA775609	ig08a02.y	1241	37.6	3.6	521	1	AI114753	AI114753	ig16b03.y
1169	37.6	3.6	494	6	CB999190	CB999190	AGENCOURT	1242	37.6	3.6	522	6	CA943549	CA943549	ig16b03.y
1170	37.6	3.6	495	5	BQ268058	BQ268058	ig19a05.y	1243	37.6	3.6	522	6	CA941182	CA941182	ig16b03.y
1171	37.6	3.6	495	6	CA774988	CA774988	ig11e06.y	1244	37.6	3.6	524	4	BM503363	BM503363	ig16b03.y
1172	37.6	3.6	496	4	BM663306	BM663306	ig11e06.y	1245	37.6	3.6	524	4	BM505091	BM505091	ig16b03.y
1173	37.6	3.6	497	4	CA842181	CA842181	ig29d04.y	1246	37.6	3.6	524	5	BQ631718	BQ631718	ig16b03.y
1174	37.6	3.6	498	1	AA707911	AA707911	ig29d03.x	1247	37.6	3.6	524	5	BQ776788	BQ776788	ig16b03.y
1175	37.6	3.6	498	5	BQ777929	BQ777929	ig13g12.y	1248	37.6	3.6	524	5	BU077981	BU077981	ig16b03.y
1176	37.6	3.6	498	6	CA772241	CA772241	ig03f05.y	1249	37.6	3.6	524	6	CA942423	CA942423	ig16b03.y
1177	37.6	3.6	498	6	CA848050	CA848050	ig42a09.y	1250	37.6	3.6	524	6	CB067481	CB067481	ig16b03.y
1178	37.6	3.6	499	4	BM312444	BM312444	ig18f06.x	1251	37.6	3.6	524	6	CD512175	CD512175	AGENCOURT
1179	37.6	3.6	499	6	CA774931	CA774931	ig10f05.y	1252	37.6	3.6	525	4	BM310883	BM310883	ig16b03.y
1180	37.6	3.6	499	6	CA867603	CA867603	ig13f02.y	1253	37.6	3.6	525	4	BM313073	BM313073	ig16b03.y
1181	37.6	3.6	500	4	BM510422	BM510422	ig14d04.y	1254	37.6	3.6	525	5	BU948757	BU948757	ig16b03.y
1182	37.6	3.6	500	6	CA777293	CA777293	ig05g08.y	1255	37.6	3.6	525	6	CA776402	CA776402	ig16b03.y
1183	37.6	3.6	500	6	CA865730	CA865730	ig14b01.y	1256	37.6	3.6	525	6	CA948579	CA948579	ig16b03.y
1184	37.6	3.6	500	6	CA866758	CA866758	ig17b01.x	1257	37.6	3.6	525	6	CA949665	CA949665	ig16b03.y
1185	37.6	3.6	500	6	CB153862	CB153862	ig17b01.x	1258	37.6	3.6	525	6	CD511976	CD511976	AGENCOURT
1186	37.6	3.6	501	4	BM522078	BM522078	ig03h1801	1259	37.6	3.6	526	4	BG656461	BG656461	ig16b03.y
1187	37.6	3.6	501	4	BM312144	BM312144	ig16g09.y	1260	37.6	3.6	527	4	BM509683	BM509683	ig16b03.y
1188	37.6	3.6	501	5	BU951702	BU951702	ig15e12.y	1261	37.6	3.6	527	7	CB821249	CB821249	ig16b03.y
1189	37.6	3.6	501	6	CA775505	CA775505	ig08e08.y	1262	37.6	3.6	528	5	BQ286058	BQ286058	ig16b03.y
1190	37.6	3.6	502	5	BQ286193	BQ286193	ig12b01.y	1263	37.6	3.6	528	6	CA947125	CA947125	ig16b03.y
1191	37.6	3.6	502	5	BU951052	BU951052	ig15c04.y	1264	37.6	3.6	529	4	BG656314	BG656314	ig16b03.y
1192	37.6	3.6	503	4	BM263800	BM263800	ig30f12.y	1265	37.6	3.6	530	4	BM310904	BM310904	ig16b03.y

c1266 37.6 3.6 530 5 BQ286698 ik33b10.x 1339 37.6 3.6 550 4 BM352286
c1267 37.6 3.6 531 4 BG56315 ib35h02.x 1340 37.6 3.6 550 9 CL723170
c1268 37.6 3.6 531 4 BM312674 ig77f06.y 1341 37.6 3.6 551 4 BM314579 ig55d09.y
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c1301 37.6 3.6 540 6 CD102288 AGENCOURT 1374 37.6 3.6 560 4 BM352936 ig96b11.y
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BU078104 im64a12.y
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CA941609 ir33f03.y
CA942163 ir47a09.y
CA942307 ir56b04.y
CA950002 ir85e04.y
CD104979 AGENCOURT
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BM685524 UI-E-C10-
BU785298 in43f10.y
CD104822 AGENCOURT
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BM685469 UI-E-C10-
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CA867809 ir81e05.y
BG654641 ib43c11.x
B1438951 ic24g02.y
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BQ635884 iq01e01.y
BM509718 ig93b07.y
CA866052 ir37e05.x
B1324987 ic20g07.x
B1467405 ic23h12.x
BM272504 ig24g04.y
BU077852 im64a12.x
BU950967 io74c05.y
CA773284 im62a10.y
CA841179 ip30f05.y
BM272397 ig40d04.y
BM352936 ig96b11.y
BU948658 in70f04.x
CA865484 ir40h01.x
B1438624 ic24g02.x
BM310826 ig49a11.y
BM505305 ig93b01.x
CD102390 AGENCOURT
BQ130238 ig82g07.y
BQ271234 ik11b10.y
CA943023 ig67c10.y
BM352931 ig69b04.y
BM690536 UI-E-C10-
BQ272133 ik18g05.y
BU947879 io54h08.y
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BQ417319 ik36e01.y
BU947260 io45f08.y
BU951722 in59g12.y
BM264215 ig32d06.y
BM315084 ig43c07.y
BM690602 UI-E-C10-
BQ777391 in44e05.y
BU785373 in44g09.y
BU950100 in64e07.y
BU949004 in72b10.y
B1713714 ie03a12.y
BM690371 UI-E-C10-
BQ417187 ik42g11.y
BU951519 in60h03.x
CA847718 iq41b07.x
B1713711 ie03a09.y
BM313590 ig72d03.y
BM352866 ig68c03.y
BM503450 ig74b05.y
BQ778563 il29d09.y

C1412	1412	37.6	3.6	568	5	BU074676	BU074676	im75b06.y	1485	37.6	3.6	581	5	BP294579	BP294579	BP294579	BP294579
C1413	1413	37.6	3.6	568	6	CA848239	CA848239	ip35h06.x	1486	37.6	3.6	581	5	BU949913	BU949913	BU949913	BU949913
C1414	1414	37.6	3.6	568	6	CA947131	CA947131	ip31f05.y	C1487	37.6	3.6	581	6	CA776761	CA776761	CA776761	CA776761
C1415	1415	37.6	3.6	568	6	CB067001	CB067001	iq34f08.x	C1488	37.6	3.6	581	6	CA842984	CA842984	CA842984	CA842984
C1416	1416	37.6	3.6	568	6	CD104431	CD104431	AGENCOURT	C1489	37.6	3.6	582	1	A1206584	A1206584	A1206584	A1206584
C1417	1417	37.6	3.6	569	1	A1093602	A1093602	ou82a12.e	C1490	37.6	3.6	582	4	BI438842	BI438842	BI438842	BI438842
C1418	1418	37.6	3.6	569	4	BG616643	BG616643	602814856	C1491	37.6	3.6	582	4	BI792382	BI792382	BI792382	BI792382
C1419	1419	37.6	3.6	569	4	BM352780	BM352780	ig67a08.y	C1492	37.6	3.6	582	4	BM311504	BM311504	BM311504	BM311504
C1420	1420	37.6	3.6	569	4	BM663138	BM663138	UI-E-C10-	C1493	37.6	3.6	582	4	BM352574	BM352574	BM352574	BM352574
C1421	1421	37.6	3.6	569	5	BQ777303	BQ777303	il34b12.y	C1494	37.6	3.6	582	5	BP200498	BP200498	BP200498	BP200498
C1422	1422	37.6	3.6	569	5	BQ777303	BQ777303	il46c06.y	C1495	37.6	3.6	582	5	BP214726	BP214726	BP214726	BP214726
C1423	1423	37.6	3.6	569	5	BQ777370	BQ777370	il47b11.y	C1496	37.6	3.6	582	5	BP294297	BP294297	BP294297	BP294297
C1424	1424	37.6	3.6	569	6	CA941296	CA941296	ir33c06.x	C1497	37.6	3.6	582	5	BQ269416	BQ269416	BQ269416	BQ269416
C1425	1425	37.6	3.6	569	6	CB999868	CB999868	AGENCOURT	C1498	37.6	3.6	582	5	BQ269662	BQ269662	BQ269662	BQ269662
C1426	1426	37.6	3.6	569	6	CD104370	CD104370	AGENCOURT	C1499	37.6	3.6	582	5	BU076472	BU076472	BU076472	BU076472
C1427	1427	37.6	3.6	570	5	BQ776911	BQ776911	il34g08.y	C1500	37.6	3.6	582	6	CA841884	CA841884	CA841884	CA841884
C1428	1428	37.6	3.6	570	6	CA950360	CA950360	ir91b02.x									
C1429	1429	37.6	3.6	571	4	BI712511	BI712511	ie08g11.x									
C1430	1430	37.6	3.6	571	5	BQ271012	BQ271012	ik12b10.x									
C1431	1431	37.6	3.6	571	5	BQ271137	BQ271137	ik13g08.x									
C1432	1432	37.6	3.6	571	5	BQ777991	BQ777991	il39f06.y									
C1433	1433	37.6	3.6	571	5	BU790334	BU790334	in49g07.y									
C1434	1434	37.6	3.6	571	7	CK822585	CK822585	ig93a01.x									
C1435	1435	37.6	3.6	572	4	BM310710	BM310710	ig47e06.y									
C1436	1436	37.6	3.6	572	4	BM503402	BM503402	ig73e06.y									
C1437	1437	37.6	3.6	572	5	BQ777101	BQ777101	ip36d07.y									
C1438	1438	37.6	3.6	572	6	CA848605	CA848605	ip36h09.y									
C1439	1439	37.6	3.6	573	4	BI467266	BI467266	ic22b07.x									
C1440	1440	37.6	3.6	573	4	BM310838	BM310838	ig49c04.y									
C1441	1441	37.6	3.6	573	5	BU071984	BU071984	im52g09.y									
C1442	1442	37.6	3.6	573	5	BU951435	BU951435	in59e11.x									
C1443	1443	37.6	3.6	573	6	CA773968	CA773968	im59g11.y									
C1444	1444	37.6	3.6	573	6	CA774693	CA774693	ip10f05.x									
C1445	1445	37.6	3.6	573	6	CA840923	CA840923	ip30f05.x									
C1446	1446	37.6	3.6	574	4	BI712946	BI712946	ig95b12.y									
C1447	1447	37.6	3.6	574	4	BM310813	BM310813	ig48h07.y									
C1448	1448	37.6	3.6	574	6	CB066780	CB066780	ig31d04.x									
C1449	1449	37.6	3.6	575	4	BM690511	BM690511	UI-E-C10-									
C1450	1450	37.6	3.6	575	6	CA842083	CA842083	ip28a09.y									
C1451	1451	37.6	3.6	575	6	BQ269252	BQ269252	ik23c03.y									
C1452	1452	37.6	3.6	576	5	BQ269539	BQ269539	ik26g12.y									
C1453	1453	37.6	3.6	576	5	BQ416722	BQ416722	ik40g11.x									
C1454	1454	37.6	3.6	576	5	BQ416869	BQ416869	ik42f10.x									
C1455	1455	37.6	3.6	576	5	BQ769523	BQ769523	il34h10.y									
C1456	1456	37.6	3.6	577	4	BI439204	BI439204	ic27g05.y									
C1457	1457	37.6	3.6	577	4	BM313496	BM313496	ig72h09.x									
C1458	1458	37.6	3.6	577	4	BM353029	BM353029	ig70f04.y									
C1459	1459	37.6	3.6	578	5	BQ271550	BQ271550	ik15d01.x									
C1460	1460	37.6	3.6	578	5	BU076667	BU076667	im50g12.y									
C1461	1461	37.6	3.6	578	6	CA952835	CA952835	ir45a06.x									
C1462	1462	37.6	3.6	578	6	CA952853	CA952853	ir45c09.x									
C1463	1463	37.6	3.6	579	4	BM313453	BM313453	ig72d03.x									
C1464	1464	37.6	3.6	579	4	BM353191	BM353191	ig76g12.x									
C1465	1465	37.6	3.6	579	5	BQ269841	BQ269841	ik30g04.x									
C1466	1466	37.6	3.6	579	5	BQ271806	BQ271806	ik18g05.x									
C1467	1467	37.6	3.6	579	5	BQ286366	BQ286366	ik29c01.y									
C1468	1468	37.6	3.6	579	6	BQ632319	BQ632319	il12e05.x									
C1469	1469	37.6	3.6	579	6	CA866691	CA866691	ir75e02.x									
C1470	1470	37.6	3.6	579	6	CA941935	CA941935	ir47h03.x									
C1471	1471	37.6	3.6	579	6	CA948140	CA948140	iq22b01.x									
C1472	1472	37.6	3.6	580	4	BI439214	BI439214	ic27h05.y									
C1473	1473	37.6	3.6	580	4	BI467404	BI467404	ic23h11.x									
C1474	1474	37.6	3.6	580	5	BU951102	BU951102	io75h05.y									
C1475	1475	37.6	3.6	580	6	CA841876	CA841876	ip29c06.x									
C1476	1476	37.6	3.6	580	6	CA848500	CA848500	ip35e06.y									
C1477	1477	37.6	3.6	580	6	CB069563	CB069563	is16h05.y									
C1478	1478	37.6	3.6	580	7	CK821354	CK821354	ig53b01.y									
C1479	1479	37.6	3.6	581	4	BG661244	BG661244	ia58d09.y									
C1480	1480	37.6	3.6	581	4	BI439121	BI439121	ic26g11.y									
C1481	1481	37.6	3.6	581	4	BM264169	BM264169	ig31g05.y									
C1482	1482	37.6	3.6	581	4	BM503241	BM503241	ig73e06.x									
C1483	1483	37.6	3.6	581	5	BP210223	BP210223	BP210223									
C1484	1484	37.6	3.6	581	5	BP217088	BP217088	BP217088									

ALIGNMENTS

RESULT 1	AK045973	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK045973	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
DEFINITION	AK045973	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
ACCESSION	AK045973	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
VERSION	AK045973.1	AK045973.1	GI:26337738	mRNA	linear	HTC 03-APR-2004
KEYWORDS	HTC; CAP trapper.	HTC; CAP trapper.	HTC; CAP trapper.	mRNA	linear	HTC 03-APR-2004
SOURCE	Mus musculus (house mouse)	Mus musculus (house mouse)	Mus musculus (house mouse)	mRNA	linear	HTC 03-APR-2004
ORGANISM	Mus musculus	Mus musculus	Mus musculus	mRNA	linear	HTC 03-APR-2004
REFERENCE	1	2	3	4	5	6
AUTHORS	Carninci, P. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253	99279253	99279253	99279253	99279253	99279253
PUBMED	10349636	10349636	10349636	10349636	10349636	10349636
REFERENCE	2	3	4	5	6	7
AUTHORS	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374	20499374	20499374	20499374	20499374	20499374
PUBMED	11042159	11042159	11042159	11042159	11042159	11042159
REFERENCE	3	4	5	6	7	8
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	Genome Res. 10 (11), 1757-1771 (2000)	Genome Res. 10 (11), 1757-1771 (2000)	Genome Res. 10 (11), 1757-1771 (2000)	Genome Res. 10 (11), 1757-1771 (2000)	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913	20530913	20530913	20530913	20530913	20530913
PUBMED	11076861	11076861	11076861	11076861	11076861	11076861
REFERENCE	4	5	6	7	8	9
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection	Functional annotation of a full-length mouse cDNA collection	Functional annotation of a full-length mouse cDNA collection	Functional annotation of a full-length mouse cDNA collection	Functional annotation of a full-length mouse cDNA collection	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)	Nature 409, 685-690 (2001)	Nature 409, 685-690 (2001)	Nature 409, 685-690 (2001)	Nature 409, 685-690 (2001)	Nature 409, 685-690 (2001)
REFERENCE	5	6	7	8	9	10
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)	Nature 420, 563-573 (2002)	Nature 420, 563-573 (2002)	Nature 420, 563-573 (2002)	Nature 420, 563-573 (2002)	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1808)	6 (bases 1 to 1808)	6 (bases 1 to 1808)	6 (bases 1 to 1808)	6 (bases 1 to 1808)	6 (bases 1 to 1808)

AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saico, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
	Direct Submission	
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]	
	JOURNAL	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 1808 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:B230328N06" /db_xref="taxon:10090" /clone="B230328N06" /sex="male" /tissue type="corpora quadrigemina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 204. 1238 /note="unnamed protein product; NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT 062718, evidence: PASTY, 99.4%ID, 92.1%length, match=951) putative" /codon_start=1 /protein_id="BAC32555.1" /db_xref="GI:26337739" /translation="MKTIQAKMHSISWAIFTGLAALCLFGVVPVRSDDATFPKAMDN VTVQGSATLRCTIDNRVFRVWLNRSITLYAGNDKWLDPVLLSNTQYSIEI QNVDYDEGPYTCVQTDNHPKTSRVHLIVQVSPKI VEISDSISINEGNISLFCIAI GRPEPTVWRHISPKAVGFVSEDEBYLEIQITREQSEYECSDNSNDVAAPVVRVKVT VNPPTYSKAGTGVPGVQKGLQCEASAVPSAEQFOWKDKRLVEKGGKGVKVENRPF LSKLTFNVSHDYGNYTCVASNKLGHNTASIMLFGPAVSEVNVNGTSRRAGCIWLLP LLVLLHLKPF"	
FEATURES	source	
	181 AACCGGTCCACCGGTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240 384 AACCGAGTACCCGGGTGGCTGGCTAAACCGCAGTACCATCTCTATGCTGGAAATGAC 443 241 AAGTGGTCCCTGGATCTCTCGCGTGGTCTTCTGTAGCAACACCCAAACGAGTACAGCATC 300 444 AAGTGGTCCCTAGATCTCTCGTGGTCTCTCTCTAGTAAACACCCAGAGCCAGTACAGCATT 503 301 GAGATCCAGAACGCTGGATGTATGACAGGGCCCTTACACCTGCTCGGTGCACAGACAG 360 504 GAGATCCAGAAATGTGGATGTGTACGATGAGGGCCCTTATACCTGCTCGGTGCACAGACAG 563 361 AACCACCAAGACCTCTAGGCTCCACTCATCTGTGCAAGTATCTCCCAAAATTTGTAGAG 420 564 AACCACCTTAGACCTTCAGGCTCCACTCATCTGTACAGTATCTCCCAAAATTTGTAGAG 623 421 ATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGTCATAGCAACT 480 624 ATTTCTTTCAGATATCTCCATTAATGAAGGGAACAACAATCAGCCTCACTTGCATAGCCACA 683 481 GGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540 684 GGTAGACCGGAGCTACAGTAACCTGGAGACATATTTCTCCAAAGGCGGTTGGCTTTGTG 743 541 AGTCAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600 744 AGTGAGATGATGACTTGGAGATCCAGGGCATCACTCGGNAACAGTCAGGCGAGTACGAG 803 601 TGCAGTGCCTTCAATAGCTGGCGCCCGTGTGTCGGAGAGTAAAGGTCACCGTGAAC 660 804 TGCAGCGCTTCAACGACGCTGGCGGCACCACTAGTGTGTAAGAGTGAAGGTCACCGTGAAC 863 661 TATCACCACATATTTTCAAGACCAAGGTACAGGTGTCCTCCGCTGGGACAAAGGGGACA 720 864 TATCACCACATATCTCAGAAGCTAAGGGGCAAGGTGTCCCGCTGGGGGACAAAGGGGACT 923 721 CTGCAGTGTGAAGCTCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGAGTGAACAA 780 924 CTGCAGTGTGAAGCTTTCGCGAGTCCCTTCAGCAGAAATTCAGTGTGTAAGAGTGAACAA 983 781 AGACTGATTTGAAGAAAGAAAGGGGTGAAAGTGAAGAAACAGACCTTCTCTCAAAACTC 840 984 AGACTGTCGAAGAAAGAAAGGGGAGTCAAAGTGGAAACAGACCTTCTCTCAAAACTC 1043 841 ATCTTCTTCAATGCTCTGACATGACTATGGGAACTACACTTCGCTGGCTCCCAACAG 900 1044 ACCTTTTTCACGCTCTGAAACATGACTATGGGAACTACACATGTGTGGCTCCCAACAG 1103 901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGCGCGCTCAGCGAGGTGAGC 960 1104 CTGGGTACACCAACGCGCAGCATCATGCTATTTGGTCCCGGTGCTGTCAGTGAGGTCAAC 1163 961 AACCGCAGCTCGAGAGGGCAGGTGCGTCTGGCTGTGCTCTCTCTCTTGTGACACCTG 1020 1164 AATGGGACATCAAGAGGCGGAGGCTGCATTTGGCTCTCTCTCTCTCTCTCTCTTACACCTG 1223 1021 CTCTCTCAAAATTTTGA 1035 1224 CTCCTCAAAATTTTGA 1238 	
ORIGIN	RESULT 2 AK046377 LOCUS DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230377K17 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence. AK046377 AK046377.1 GI:26338018 KEYWORDS HTC; CAP trapper. Mus musculus (house mouse) Mus musculus ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	1 ATGAAAACATCCAGGCAAAATGCACAAATCTATCTCTGGGCAATCTTCAACGGGGCTG 60 204 ATGAAAACATCCAGGCAAAATGCACAAATCTATCTCTGGGCAATCTTCAACGGGGCTG 263 61 GCTGCTGTGCTCTCTTCAAGAGGAGTGCCCGTGGCGACGAGATGCCACCTTCCCCAAA 120 264 GCGGCTCTGTGCTCTTCCAGAGGAGTGGCGTGGTACGAGATGCCACCTTCCCCAAA 323 121 GCTATGGACAAAGTGCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATTTTGAAC 180 324 GCTATGGACAAAGTGCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATTTTGAAC 383 	
Query Match	84.9%; Score 878.2; DB 3; Length 1808;	
	Best Local Similarity 90.5%; Pred. No. 5.4e-244;	
Matches	937; Conservative 0; Mismatches 98; Indels 0; Gaps 0;	

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Tanaka, T., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
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Nature 420, 563-573 (2002)
6 (bases 1 to 1808)

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Fukuda, J., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel. 81-45-503-9222,
Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

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/strain="C57BL/6J"

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ORIGIN

Query Match	84.9%	Score 878.2	DB 3	Length 1808
Best Local Similarity	90.5%	Pred. No. 5.4e-244		
Matches 937	Conservative 0	Mismatches 29	Indels 0	Gaps 0
Qy	1	ATGAAAACATCCAGCCAAATAATGCACAAATCTATCTCTGGGCAATCTTTCACGGGGCTG	60	
Db	204	ATGAAAACATCCAGCCAAATAATGCACAAATCTATCTCTGGGCAATCTTTCACGGGGCTG	263	
Qy	61	GCTGCTGTGTCTCTTCCAAAGAGTGCCCGTGGCGAGGAGATGCCACCTTCCCAA	120	
Db	264	GCGCTCTGTGCTCTTCCAAAGAGTGCCCGTGGCGAGGATGCCACCTTCCCAA	323	
Qy	121	GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC	180	
Db	324	GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC	383	
Qy	181	AACCGGGTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTATGTGGGAATGAC	240	
Db	384	AACCGAGTCACCCGGGTGGCTTAAACCGCAGTACATCTCTATGTGGGAATGAC	443	
Qy	241	AAGTGGTCCCTGGATCTCTCGGTGTCTCTTCTAGCAACACCCAAACAGTACAGCATC	300	
Db	444	AAGTGGTCCCTGGATCTCTCGGTGTCTCTTCTAGTAACACCCAGTACAGCATC	503	
Qy	301	GAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACTGCTCGGTGCAGACAGAC	360	
Db	504	GAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTATACCTGCTCGGTGCAGACAGAC	563	
Qy	361	AACCAACCAAGACCTCTAGGCTCCACCTCTATGTGCAAGTATCTCCCAAAATCTGAG	420	
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Qy	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAACATATATTAGCCTCACCTGCATAGCACT	480	
Db	624	ATTTCTTCAGATATCTCCATTAATGAAGGGAACATATATTAGCCTCACCTGCATAGCACT	683	
Qy	481	GGTAGACAGAGCCTTACCGTTTCTTGGAGACACATCTCTCCCAAAAGCGGTGGCTTTG	540	
Db	684	GGTAGACAGAGCCTTACAGTAACTCCGGAGACATATTTCTCCCAAGCGGTGGCTTTG	743	
Qy	541	AGTAGAGAGGATCTCTGGAAATTCAGGGCATCACCCGGAGCAGTACAGGGGACTACGAG	600	
Db	744	AGTAGAGGATGATCTCTGGAGATCCAGGGCATCTCCGGGAACAGTACAGGCGATGACGAG	803	
Qy	601	TGCAGTCCCAATGACGTGGCCCGCCCGCTGGTGTACGGAGAGTAAAGGTCCACCGTGAAC	660	
Db	804	TGCAGCGCTCCACGACGTGGCGCACCATGTTGGTACGAGAGTGAAGGTCCACCGTGAAC	863	
Qy	661	TATCCACCATCATTTTCAAGAGCCCAAGGGGTACAGGTGTCCCGTGGGACAAAGGGGACA	720	

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 773)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

1..773

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Best Local Similarity 98.4%; Pred. No. 8.8e-205;

Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

QY 168 GTGCACTATTGACAAACCGGGTCACCGGGTGCGCTGAGTGTATGACGAGGCGCTTACACCATCTCTTA 227

Db 1 GTGCACTATTGACAAACCGGGTCACCGGGTGCGCTGAGTGTATGACGAGGCGCTTACACCATCTCTTA 60

QY 228 TCGTGGGATGACAGTGTGCTGGATCTCGCTGGTGTCTTCTGAGCAACACCCCAAC 287

Db 61 TCGTGGGATGACAGTGTGCTGGATCTCGCTGGTGTCTTCTGAGCAACACCCCAAC 120

QY 288 CGAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTACACCATCTCTTA 347

Db 121 CGAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTACACCATCTCTTA 180

QY 348 GGTGAGACAGCAACACCCCAACCGGTCACCTTACGAGGCGCTTACACCATCTCTTA 407

Db 181 GGTGAGACAGCAACACCCCAACCGGTCACCTTACGAGGCGCTTACACCATCTCTTA 240

QY 408 CAAATTTGTAGAGATTTCTTCCAGATATCTCCATTAATGAGGGAACAATATTAGGCTCAC 467

Db 241 CAAATTTGTAGAGATTTCTTCCAGATATCTCCATTAATGAGGGAACAATATTAGGCTCAC 300

QY 468 CTGCATAGCACTGTGTAGACGAGGCTACGGTTACTTGGAGACACATCTCTCCAA--- 524

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QY 525 ---AGCGGTGGCTTTGTGAGTGAAGCGAATCTTGGAAATTCAGGGCATCACCCGGGA 581

Db 361 CGCAGCGGTGGCTTTGTGAGTGAAGCGAATCTTGGAAATTCAGGGCATCACCCGGGA 420

QY 582 GCAGTCAGGGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGCGCTGGTACGGAG 641

Db 421 GCAGTCAGGGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGCGCTGGTACGGAG 480

QY 642 AGTAAGGTACCGTGAACCTATCCACCATATTTTCAGAAAGCAAGGGTACAGGTGTCCC 701

Db 481 AGTAAGGTACCGTGAACCTATCCACCATATTTTCAGAAAGCAAGGGTACAGGTGTCCC 540

QY 702 CGTGGGACAAAGGGGACACTGACGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCGA 761

Db 541 CGTGGGACAAAGGGGACACTGACGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCGA 600

QY 762 GTGGTACAAAGGATGACAAAGACTGATTTGAAGGAAAGAGGGGTGAAGTGGAAGAACAG 821

Db 601 GTGGTACAAAGGATGACAAAGACTGATTGAAGAAAGAGGGGTGAAGAGTGAAGAACAG 660

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Db 721 TTGCGTGGCTTCAACAAAGCTGGGCGACACCAATGCCAGCATCATCTATTG 773

RESULT 5

AY406349

LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DEFINITION AY406349

ACCESSION AY406349.1 GI:39762323

VERSION AY406349.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 874)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 874)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

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/locus_tag="HCM2527"

ORIGIN

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Best Local Similarity 89.1%; Pred. No. 5.6e-195;

Matches 779; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 168 GTGCACTATTGACAAACCGGGTCACCGGGTGCGCTGAGTGTATGACGAGGCGCTTACACCATCTCTTA 227

Db 1 GTGCACTATTGACAAACCGGGTCACCGGGTGCGCTGAGTGTATGACGAGGCGCTTACACCATCTCTTA 60

QY 228 TCGTGGGATGACAGTGTGCTGGATCTCGCTGGTGTCTTCTGAGCAACACCCCAAC 287

Db 61 TCGTGGGATGACAGTGTGCTGGATCTCGCTGGTGTCTTCTGAGTGTATGAGGCGCTTATACCTCTCTC 120

QY 288 CGAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTACACCATCTCTTA 347

Db 121 CGAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTATACCTCTCTC 180

QY 348 GGTGAGACAGCAACACCCCAACCGGTCACCTTACGAGGCGCTTACACCATCTCTTA 407

Db 181 GGTGAGACAGCAACACCCCAACCGGTCACCTTACGAGGCGCTTACACCATCTCTTA 240

QY 408 CAAATTTGTAGAGATTTCTTCCAGATATCTCCATTAATGAGGGAACAATATTAGGCTCAC 467

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Qy 525 ---AGCGGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGGCATCACCCGGGA 581
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Qy 642 AGTAAAGTCAACGTAACATATCCACCATATTTTCAGAACCAAGGATACAGGTGTCCC 701
Db 481 AGTAAAGTCAACGTCAGTAACTATCCACCATATCTCAGAACTAAGGGCAAGGTGTCCC 540
Qy 702 GTGGGACAAAGGGGACACTGCACTGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCA 761
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Db 661 ACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAAATGATGACTATGGAACTACAC 720
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Db 781 TGCTGTGAGTGAAGTCAACATGAGCATCAAGGAGGCGAGGCTGCAATTTGGCTCCTCC 840
Qy 1002 TCTTCTGTCTTGCACCTGCTCTCAAAATTTGA 1035
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DEFINITION 5', mRNA sequence.
ACCESSION BU155617
VERSION BU155617.1 GI:22669149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
National Biotechnology Information
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLNL13527 row: m column: 16
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Location/Qualifiers
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FEATURES
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ORIGIN

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Best Local Similarity 97.6%; Pred. No. 6.3e-182;  
Matches 728; Conservative 0; Mismatches 12; Indels 6; Gaps 5;  
Qy 81 AGGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCAAAGCTATGGACAACGTGACGGT 140  
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RESULT 7

CN362539
LOCUS
DEFINITION

CN362539 748 bp mRNA linear EST 16-MAY-2004
LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN362539
VERSION CN362539.1 GI:47362473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 748)
JOURNAL Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
COMMENT Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 748 Std Error: 0.00.
FEATURES
Location/Qualifiers
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derived from H1, H7 and H9 cells"
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H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-174;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 81 AGGAGTCCCGCGGAGAGTCCACCTTCCCAAGAGTATGGACAAGTCAACGCT 140
DB 109 AGGAGTCCCGCGGAGAGTCCACCTTCCCAAGAGTATGGACAAGTCAACGCT 168
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QY 261 CTGGTCTCTTTCAGCAACACCAACCGAGTACAGTACGAGTCCAGAGCTGGATGT 320
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DB 409 GGTCACTCATGTGCAAGTATCTCCAAATTTGATAGATTTCTTGATATCTCCAT 468
QY 441 TAATGAGGGAACAATATTAGCTTCACTGATAGCACTGCTAGCAGAGCTTACCGT 500
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DEFINITION mRNA sequence.
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VERSION BE798585.1 GI:10219783
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1039)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCN779 row: d column: 04
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Location/Qualifiers
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 61.4%; Score 635.2; DB 2; Length 1039;
Best Local Similarity 97.6%; Pred. No. 2.8e-173;
Matches 656; Conservative 0; Mismatches 13; Indels 3; Gaps 1;
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DB 65 CAGGTGCACTATTGCAACACCGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 124
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DB 125 CTATGCTGGGAATGCAAGTGGTGGCTGGATCTCTCGCTGGTCTCTTCTGAGCAACACCA 184
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Db 721 TTC 723

RESULT 10
C0635648
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Contig2663 WL/RJ Phrased ESTs Gallus gallus cdna 5', mRNA sequence.
C0635648
C0635648.1 GI:50538871
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1450)
Fitzsimmons, C.J., Savolainen, P., Amini, B., Hjalms, G., Lundeberg, J.
and Anderson, L.
Detection of sequence polymorphisms in red junglefowl and White
Leghorn ESTs
Unpublished (2004)
Contact: Carolyn Fitzsimmons
Leif Andersson IMBIM/Dept. Animal Breeding and Genetics
Uppsala University/Swedish University of Agricultural Sciences
Box 597, SE-751 24 Uppsala, SWEDEN
Tel: 00 46 (0)18 471 4593
Fax: 00 46 (0)18 471 4833
Email: Carolyn.Fitzsimmons@bmc.uu.se
This EST is a consensus sequence obtained from a Phrap assembly of
4 cDNA libraries. The consensus sequence is submitted because SNP
data in the publication 'Detection of sequence polymorphisms in red
junglefowl and White Leghorn ESTs', is reported with reference to
positions in the Phrap consensus sequence.
Seq primer: (5'-end) M13 reverse.
FEATURES
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/organism="Gallus gallus"
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/strain="Red junglefowl/White Leghorn"
/db_xref="taxon:9031"
/sex="female/male"
/lab_host="ElectronMAX DH10B (Invitrogen)"
/clone_lib="WL/RJ Phrased ESTs"
/note="Organ: brain/testis; Vector: pSPORT-1; Site 1: Hind
III; Site 2: EcoRI; The cDNA libraries were created with
the SuperScript Plasmid System (Invitrogen)."

ORIGIN
Query Match 54.6%; Score 564.8; DB 7; Length 1450;
Best Local Similarity 75.6%; Pred. No. 9.8e-153;
Matches 726; Conservative 0; Mismatches 232; Indels 2; Gaps 2;
QY 78 CCAAGAGTCCCGTCGAGCGGAGATGCCACCTTCCCAAGCTATGGACAAGTGAC 137
DB 307 CCAAGAGTCCCGTCGAGCGGAGATGCCACCTTCCCAAGCTATGGACAAGTGAC 366
QY 138 GGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGTCACCGGCT 197
DB 367 TGTGCGGCAAGGGAGAGTGCACCGTCAAGTGTCTCGGTGGACACCGGTCACCGGCT 426
QY 198 GGCCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGGTGGATCC 257
DB 427 GGCCTGGCTTAAACCGCAGCAGCATCTCTATGCTGGGAATGACAAAGTGGTGGATCC 486
QY 258 TCGCGTGTCTTCTTAGACAAACCCCAACCGAGTACGATCGAGATCCAGAACGTGA 317
DB 487 GAGGCTGTGTCTTCTTAGACAAACCCCAACCGAGTACGATCCAGATCCAGAGTGA 546
QY 318 TGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGACACCCCAACGACCTC 377
DB 547 CGTGTACGATGAAGGGCCCTTACACCTGCTCGGTGAGACAGACATCCACCCCAACGACATC 606

QY 378 TAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATTCTTTCAGATATCTC 437
DB TCGCGTGCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATTCTTTCAGATATCTC 666
QY 438 CATTAAATGAAGGGAACAATATTTAGCTTCACCTGCATAGCAAACTGGTGTAGACAGAGCTAC 497
DB CATCAATGAGGTGCAAGCTCAGCTTACCTGCATAGCCAGCGGAGCGGAGAGAGAGAGAG 726
QY 498 GGTACTTTGGAGACACATCTCTCCCAAGCGGTGG-CTTTGTGAGTGAAGACGAATATCT 556
DB AATCACCTGGAGACACATCTCGCCCAAGCTGTGGGCTTTCATCAGCGAGGATGAGTACC 786
QY 557 TGGAAATTCAGGGGATCACCCGGGAGCAGTACGGGAGCTACAGTGCAGTGCCTCCAATG 616
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QY 617 AGCTGGCGCGCCCGTGTGAGCGAGTAAAGGTCAACCGTGAACCTATCCACCATACATTT 676
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DB CGGAGAGGAGTATGGCAACTACAGTGTGTGGCCACAAAGTTGGGCAACACCAATG 1146
QY 917 CCAGCATCATGCTAT-TTGGTCCAGCGCGCTCAGCGAGGTGAGCAACGGCAGCTCGAGG 975
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QY 976 AGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
DB GCAGCGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266

CR548212 600 bp mRNA linear EST 12-JUL-2004
DEFINITION
LOCUS
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CR548212 DKFZp459M1538_r1 459 (synonym: pcor1) Pongo pygmaeus cdna clone
CR548212 DKFZp459M1538 5', mRNA sequence.
CR548212.1 GI:50241868
EST.
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oanger, A.,
Fobbo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Koehler, K., Beyer, A., Mewes, H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clon from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKPZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by BMF (Biomedical
Research Center at the Heinrich-Heine-University,
Duesseldorf/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp459M1538) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:

clone@zpd.de Further information about the clone and the sequencing project is available at
http://mips.gsf.de/projects/cdna/.

FEATURES

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Best Local Similarity 99.1%; Pred. No. 8.7e-147;
Matches 547; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 395 TCGAAGTATCTCCCAAAATTGTAGAGATTCTTCAGATATCTCCATTAATGAAGGACACA 454
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QY 455 ATATTAGCTCACCTGCATAGCACTGTGTAGACAGAGCCTACGGTTACTTTGGAGACACA 514
Db 109 ATATCAGCTCACCTGCATAGCACTGTGTAGACAGCCTACGGTTACTTTGGAGACACA 168
QY 515 TCTTCCCAAAAGCGGTGGCTTTGTAGTGAAGACGAATACTTTGGAATTCAGGGCATCA 574
Db 169 TCTCCCCAAAGCGGTGGCTTTGTAGTGAAGACGAATACTTTGGAATTCAGGGCATCA 228
QY 575 CCGGGACAGTCAGGGGACTACGAGTCAGTGCGCTCCAAATGACGTGCGCCGCGCCGTGG 634
Db 229 CCGGGACAGTCAGGGGACTACGAGTCAGTGCGCTCCAAATGACGTGCGCCGCGCCGTGG 288
QY 635 TACGAGAGTAAAGGTACCGTGAACCTATCACCATACATTTTCAAGACCAAGGTTACAG 694
Db 289 TACGAGAGTAAAGGTACCGTGAACCTATCACCATACATTTTCAAGACCAAGGTTACAG 348
QY 695 GTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTTCAGCAGTCCCTCAGCAG 754
Db 349 GTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTTCAGCAGTCCCTCAGCAG 408
QY 755 AATTCAGTGTACAGGATACAAAACACTGATTTGAAGGAAGAAAGGGTGAAGTGG 814
Db 409 AATTCAGTGTGCAAGGATGACAAAAGACTGATTTGAAGGAAGAAAGGGTGAAGTGG 468
QY 815 AAAACAGACCTTTCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGA 874
Db 469 AAAACAGACCTTTCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGA 528
QY 875 ACTACATTTGGTGGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTGG 934
Db 529 ACTACATTTGGTGGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTGG 588
QY 935 GTCCAGGCGCCG 946
Db 589 GTCCAGGCGCCG 600
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RESULT 12

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LOCUS      CF737474
DEFINITION UI-M-HD0-cks-o-09-0-UI_r1 NIH_BMAP_HD0 Mus musculus cDNA clone
IMAGE:30614264 5', mRNA sequence.
ACCESSION CF737474
VERSION    CF737474.1 GI:37633810
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE

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1 (bases 1 to 759)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Dr. James Lin University of Iowa
    cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
    cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Distribution information can be found at
    http://genome.uiowa.edu/distribution/mousef1.html
    This clone was contributed by the Brain Molecular Anatomy Project
    (BMAP)
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Seq primer: PYX-5.

Location/Qualifiers

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  /lab_host="DH10B (T1 phage resistant)"
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  /note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
  Site_2: Not I; The library was constructed according
  Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
  1996. Denatured RNA was size fractionated on a 1% agarose
  gel. First strand cDNA synthesis was primed with oligo-dT
  primer containing a Not I site. Double strand cDNA was
  size selected according to mRNA size fraction, ligated
  with EcoR I adaptor, digested with NotI and then cloned
  directionally into pYX-Asc vector. The library tag
  sequence located between the Not I site and the polyA tail
  is TTATTGAGT. This library was created for the University
  Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the
  Developing Mouse Nervous System', supported by National
  Institute of Mental Health (NIMH)."
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ORIGIN

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Query Match      52.4%; Score 542.4; DB 7; Length 759;
Best Local Similarity 90.2%; Pred. No. 2.7e-146;
Matches 590; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 81 AGGAGTGCCTGTCGCGAGCGGAGATGCCACTTCCCAAGCTATGGACAACGTGACGGT 140
Db 101 AGGAGTGCCTGTCGCGAGCGGAGATGCCACTTCCCAAGCTATGGACAACGTGACGGT 160
QY 141 CCGGACGGGGAGAGCGCCACCTCAGTGCACATTTGACAAACCGGTCACCCGGGTGGC 200
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QY 201 CTGCTTAAACCCGACGACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG 260
Db 221 CTGCTTAAACCCGACGATCATCTCTATGCTGGGAATGACAAGTGGTGCCTAGATCTCTCG 280
QY 261 CGTGGTCTCTTGAGCAACACCCAAACGCACTGACAGATTCAGATTCAGAAACGTGGATGT 320
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QY 321 GTATGACGAGGGCCCTTACACCTGCTGGTCAGACAGACCAACCAACAGACCTCTAG 380
Db 341 GTACGATGAGGGCCCTTATACCTGCTGGTACAGACAGCAACCAACCTCTAGACCTCCAG 400
QY 381 GGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT 440
Db 401 GGTCCACCTCATTTGTACAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT 460
QY 441 TAATGAGGGGAACAATATTAGCCTTACCTGCATAGCAACTGCTGTAGACAGACGCTACCGGT 500
Db 461 TAATGAGGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGT 520
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ORIGIN

Query Match 52.3%; Score 541; DB 4; Length 865;
Best Local Similarity 99.8%; pred. No. 7.2e-146;
Matches 552; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGAAACCATCGCCAAAATGCACAAATCTATCTCTCTGGCAATCTTCACGGGGCTG 60
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Job time : 3837.97 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 16, 2005, 11:41:38 ; Search time 5167 Seconds
(without alignments)
3225.971 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTQPKMHSISWAIFGL.....RRAGCVMLLPLVLHLLKF 344

Scoring table: BLOSUMP62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MTN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ets.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	1032	6	AR439648 Sequence
2	1806	100.0	1679	6	CQ768055 Sequence
3	1806	100.0	1679	6	AR528639 Sequence
4	1806	100.0	1679	6	AX358872 Sequence

5	1806	100.0	1679	6	AX362365 Sequence
6	1806	100.0	1679	6	AX403748 Sequence
7	1806	100.0	1679	6	AX454470 Sequence
8	1806	100.0	1679	6	AX464242 Sequence
9	1806	100.0	1679	6	AX490948 Sequence
10	1806	100.0	1679	9	AY358331 Homo sapi
11	1806	100.0	1679	6	AR439649 Sequence
12	1665.5	92.2	1839	6	AX665342 Sequence
13	1665.5	92.2	1839	9	AF126426 Homo sapi
14	1650	91.4	1068	6	AX665344 Sequence
15	1647.5	91.2	1615	10	BC023307 Mus muscu
16	1644	91.0	1104	6	AX665346 Sequence
17	1642	90.9	939	6	AR439650 Sequence
18	1639.5	90.8	2040	10	RNU16845 Sequence
19	1638	90.7	1140	6	AX665348 Sequence
20	1616.5	89.5	1410	10	AF282980 Mus muscu
21	1517	84.0	868	6	CQ729109 Sequence
22	1500.5	83.1	1325	9	BC050716 Homo sapi
23	1477.5	81.8	1257	5	GSCERU1
24	1428	79.1	1058	5	AF292935 Gallus ga
25	1427.5	79.0	1035	5	AB011810 Gallus ga
26	1393	77.1	1638	12	AF271233 Synthetic
27	1357.5	75.2	1013	5	AF292936 Gallus ga
28	1307	72.4	6005	10	BC076581 Mus muscu
29	1306.5	72.3	3216	5	GSCERU5
30	1306	72.3	1533	5	FFNINH55A
31	1296.5	71.8	6380	9	HSMB05672
32	1286.5	71.2	3069	10	RATCALMA
33	1276.5	70.7	1370	5	BC074283
34	1275.5	70.6	1556	5	AF292934
35	1271.5	70.4	2935	12	AF271618
36	1270.5	70.3	1108	9	BC074773
37	1268	70.2	1111	9	BC074773
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39	1268	70.2	3110	6	AX665340
40	1267	70.2	2593	4	BTBOCAM
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43	993.5	55.0	2055	5	BC081685
44	951	52.7	756	12	AF271232
45	946	52.4	1107	5	GGLAMP9
46	938.5	52.0	1158	5	GGLAMP19
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48	932.5	51.6	1640	9	BC033803
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50	931.5	51.6	1195	6	AR447794
51	930.5	51.5	1194	5	GGLAMP11
52	926.5	51.3	1014	6	AR030577
53	926.5	51.3	1014	6	AR220260
54	926.5	51.3	1238	6	AR030575
55	926.5	51.3	1238	6	AR220258
56	926.5	51.3	1238	10	RNU31554
57	923.5	51.1	977	6	AR030574
58	923.5	51.1	977	6	AR220257
59	913	50.6	1276	10	AY362656
60	911	50.4	1410	5	BC074296
61	908	50.3	924	6	AR030579
62	907	50.2	945	6	AR030580
63	902	49.9	912	6	AR030578
64	893	49.4	1757	6	AX704805
65	886.5	49.1	861	6	AR030581
66	885.5	49.0	861	6	AR030582
67	868	48.1	1941	5	AF241638
68	859	47.6	503	6	CQ768057
69	842	46.6	1059	5	GGA132999
70	823	45.6	1196	6	AX662341
71	823	45.6	1327	6	AX704747
72	823	45.6	4834	6	AX358748
73	823	45.6	4834	6	AX362241
74	823	45.6	4834	6	AX403774
75	823	45.6	5582	9	HSMB06161
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77	820	45.4	2383	6	AX747470

78	820	45.4	2383	9	AK092307	AK092307 Homo sapi	151	297.5	16.5	84246	3	AC002512	AC002512 Drosophil
79	819	45.3	1165	6	AX662343	AX662343 Sequence	c 152	297.5	16.5	110000	3	AE001572_2	Continuation (3 of
80	815	45.1	1809	10	AB017139	AB017139 Rattus no	153	297.5	16.5	170801	3	AC095014	AC095014 Drosophil
81	815	45.1	2840	9	AX358132	AX358132 Homo sapi	154	297.5	16.5	298020	3	AE003674	AE003674 Drosophil
82	814	45.1	1179	10	MMU487032	AJ487032 Mus muscu	c 155	293	16.2	157263	2	EX597285	EX597285 Danio rer
83	796.5	44.1	756	6	AR030589	AR030589 Sequence	156	290.5	16.1	8546	6	AX828406	AX828406 Sequence
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86	761	42.1	1017	6	AX644995	AX644995 Sequence	159	290.5	16.1	18207	9	AF156100	AF156100 Homo sapi
87	761	42.1	1018	6	AX644993	AX644993 Sequence	160	288.5	16.0	4073	6	AX269342	AX269342 Sequence
88	757	41.9	1136	6	AX644997	AX644997 Sequence	161	287.5	15.9	4398	5	D85084	D85084 Cynops pyrr
89	755.5	41.8	2070	5	BC080221	BC080221 Danio rer	162	284.5	15.8	1710	6	CQ588165	CQ588165 Sequence
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91	742.5	41.1	1031	6	CQ728011	CQ728011 Sequence	164	282.5	15.6	2262	10	MMNCAMR1	X15049 Mouse commo
92	721	39.9	1169	6	AX644999	AX644999 Sequence	165	282.5	15.6	2544	10	BC011310	BC011310 Mus muscu
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c 94	670	37.1	197553	2	AC146103	AC146103 Pan trogl	167	279	15.4	237376	2	AC124949	AC124949 Rattus no
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96	652	36.1	5666	6	AX740565	AX740565 Sequence	169	278.5	15.4	1580	5	CR354352	CR354352 Gallus ga
97	632	35.0	537	6	AX593044	AX593044 Sequence	170	278.5	15.4	12699	5	D83390	D83390 Gallus gall
98	599	33.2	786	5	GGA132998	AJ132998 Gallus Ga	171	277.5	15.4	3170	10	RNNCAM14	X06564 Rat mRNa fo
99	578	32.0	452	6	AX079423	AX079423 Sequence	172	277.5	15.4	3720	5	XELNCAM	M25696 X.laevis ne
100	545	30.2	333	6	AX907426	AX907426 Sequence	173	277.5	15.4	4454	5	BC081181	BC081181 Xenopus l
101	545	30.2	333	6	BD042959	BD042959 Sequence	174	276.5	15.3	2256	5	BC057517	BC057517 Danio rer
102	509.5	28.2	531	6	CQ719449	CQ719449 Sequence	175	276	15.3	2256	9	H5NCAME	X16841 Human mRNa
103	490.5	27.2	585	6	AX079674	AX079674 Sequence	176	276	15.3	2960	6	AX658287	AX658287 Sequence
104	466.5	25.8	793	5	EX932289	EX932289 Gallus ga	177	276	15.3	2960	9	S71824	S71824 N-CAM-145 k
105	430	23.8	504	6	CQ715694	CQ715694 Sequence	178	276	15.3	3266	6	CQ728451	CQ728451 Sequence
106	429.5	23.8	20731	9	AP004721	AP004721 Homo sapi	179	276	15.3	3309	6	AX714869	AX714869 Sequence
107	429.5	23.8	43087	9	AP005155	AP005155 Homo sapi	180	276	15.3	3309	9	AK057509	AK057509 Homo sapi
108	424.5	23.5	168745	2	AC119552	AC119552 Rattus no	181	276	15.3	3309	6	AX207284	AX207284 Sequence
109	424.5	23.5	248329	2	AC109989	AC109989 Rattus no	182	275.5	15.3	3574	4	BTADVCV	X16451 Bovine mRNa
c 110	421	23.3	110000	2	AC102028_1	Continuation (2 of	183	275	15.2	2633	6	AR380405	AR380405 Sequence
c 111	400.5	22.2	408	6	AX684132	AX684132 Sequence	184	275	15.2	2633	9	HSU63041	U63041 Human neutra
112	391.5	21.7	540	6	AX665354	AX665354 Sequence	185	274	15.2	5807	6	AR447664	AR447664 Sequence
113	391.5	21.7	116069	2	AP000784	AP000784 Homo sapi	186	273.5	15.1	2118	6	AR506699	AR506699 Sequence
114	391.5	21.7	123320	9	AP000863	AP000863 Homo sapi	187	273.5	15.1	2118	6	AB008163	AB008163 Xenopus l
115	391.5	21.7	176676	2	AC012234	AC012234 Homo sapi	188	273.5	15.1	2178	5	AB008163	AB008163 Xenopus l
116	391.5	21.7	177102	2	AP002808	AP002808 Homo sapi	189	273	15.1	7097	6	AX921114	AX921114 Sequence
117	382	21.2	642	6	CQ732119	CQ732119 Sequence	c 190	273	15.1	191071	9	AP004248	AP004248 Homo sapi
c 118	382	21.2	184012	10	AC116523	AC116523 Mus muscu	191	272.5	15.1	2879	5	BC075300	BC075300 Xenopus t
c 119	382	21.2	242565	2	AC094728	AC094728 Rattus no	192	272.5	15.1	3971	5	CHKCONNE	D16541 Gallus gall
120	382	21.2	251570	2	AC094463	AC094463 Rattus no	193	272	15.1	131490	10	AC122207	AC122207 Mus muscu
121	378	20.9	371	6	CQ731074	CQ731074 Sequence	194	272	15.1	177251	10	AC124565	AC124565 Mus muscu
122	350.5	19.4	3847	3	BT010243	BT010243 Drosophil	195	271.5	15.0	4321	2	AX921112	AX921112 Sequence
123	349.5	19.4	3460	3	BT011190	BT011190 Drosophil	c 196	271.5	15.0	16582	2	AC102190	AC102190 Mus muscu
124	348	19.3	3590	3	BT003528	BT003528 Drosophil	197	271	15.0	4050	9	BC047244	BC047244 Homo sapi
125	344	19.0	352	6	AX886912	AX886912 Sequence	198	270.5	15.0	3814	5	XELNCAMA	M76710 Xenopus lae
126	344	19.0	352	6	BD026522	BD026522 Sequence	199	270	15.0	2190	6	CQ604731	CQ604731 Sequence
127	339	18.8	187203	2	AP000832	AP000832 Homo sapi	c 200	270	15.0	110000	2	AC102028_0	AC102028 Mus muscu
c 128	339	18.8	191204	9	AP000843	AP000843 Homo sapi	c 201	270	15.0	186110	2	AC102204	AC102204 Mus muscu
129	338.5	18.7	1242	6	CQ607488	CQ607488 Sequence	c 202	269.5	14.9	1912	3	SAREGALPT	X93601 S.americana
130	336.5	18.7	3106	3	AX060653	AX060653 Drosophil	c 203	269	14.9	142000	9	AC078813	AC078813 Homo sapi
131	336	18.6	292	6	CQ716587	CQ716587 Sequence	204	268.5	14.9	4491	6	CQ848038	CQ848038 Sequence
132	333	18.4	411	6	CQ731080	CQ731080 Sequence	205	268.5	14.9	4491	6	CQ848044	CQ848044 Sequence
133	333	18.4	948	6	CQ595959	CQ595959 Sequence	206	268.5	14.9	5510	6	AX409111	AX409111 Sequence
134	308.5	17.1	3927	3	DMU78177	U78177 Drosophila	207	268.5	14.9	5510	9	D86983	D86983 Human mRNa
135	306.5	17.0	2010	6	CQ586755	CQ586755 Sequence	208	268.5	14.9	6847	9	AF200348	AF200348 Homo sapi
136	306.5	17.0	4052	3	AX060363	AX060363 Drosophil	209	268.5	14.9	6939	6	AX780120	AX780120 Sequence
137	303.5	16.8	950	3	AX052162	AX052162 Drosophil	c 210	268.5	14.9	6939	6	AX780121	AX780121 Sequence
138	303.5	16.8	950	3	AX052163	AX052163 Drosophil	c 211	267	14.8	3060	6	CQ595958	CQ595958 Sequence
139	302.5	16.7	913	6	AR542162	AR542162 Sequence	212	267	14.8	64674	3	AC004247	AC004247 Drosophil
140	300.5	16.6	950	3	AX052156	AX052156 Drosophil	c 213	267	14.8	110526	2	AC019598	AC019598 Drosophil
141	300.5	16.6	950	3	AX052160	AX052160 Drosophil	c 214	267	14.8	174376	3	AC092230	AC092230 Drosophil
142	297.5	16.5	950	3	AX052157	AX052157 Drosophil	c 215	267	14.8	259718	3	AE003614	AE003614 Drosophil
143	297.5	16.5	950	3	AX052158	AX052158 Drosophil	216	266	14.7	268	4	AF271984	AF271984 Bos tauru
144	297.5	16.5	950	3	AX052159	AX052159 Drosophil	217	266	14.7	110000	2	AC110642_3	Continuation (4 of
145	297.5	16.5	950	3	AX052161	AX052161 Drosophil	218	265.5	14.7	6332	10	AK122223	AK122223 Mus muscu
146	297.5	16.5	1110	6	CQ575874	CQ575874 Sequence	219	265	14.7	8035	3	AF254867	AF254867 Drosophil
147	297.5	16.5	1563	3	AX051911	AX051911 Drosophil	c 220	264	14.6	110000	2	AC110642_2	Continuation (3 of
148	297.5	16.5	2135	3	DROAMA	M23561 D.melanogas	221	263.5	14.6	6814	6	AR220825	AR220825 Sequence
c 149	297.5	16.5	3426	6	CQ575873	CQ575873 Sequence	222	263	14.6	11850	4	AY136513	AY136513 Canis fam
c 150	297.5	16.5	6228	2	AC020270	AC020270 Drosophil	223	262	14.5	3738	5	AY029401	AY029401 Danio rer

224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
AC150028	Canis fam	AF538973	Homo sapi	Y14877	Gallus gall	Y00813	Chicken m8N	Y14852	Oryctolagus	BD935847	Gallus ga	BD985986	Method of	AF040989	Drosophil	AF525411	Rattus no	AF134113	Drosophil	AY047524	Drosophil	CQ585189	Sequence	BC014205	Homo sapi	CQ603804	Sequence	CQ730839	Sequence	HS01TINN2	Sequence	BD186121	Preventio	BD186121	Preventio	CQ730837	Sequence	CQ848088	Sequence	CQ715893	Sequence	AK125056	Homo sapi	AC123550	Mus muscu	AC079543	Mus muscu	BC045307	Danio rer	LI3255	Fruitfly la	CQ590793	Sequence	AY051829	Drosophil	AY051829	Drosophil	AC148913	Sus scrof	AC087123	Mus muscu	AF016619	Mus muscu	AF001287	Mus muscu	QF015482	Sequence	AF001286	Mus muscu	AC112456	Rattus no	AC114113	Rattus no	AC127766	Rattus no	AC106603	Rattus no	AC106602	Rattus no	CQ583539	Sequence	AF312580	Drosophil	BT015246	Drosophil	LI3256	Grasshopper	SCALACH	AY029403	Danio rer	AF029403	Danio rer	AP478693	Sequence	CQ870412	Sequence	AK124736	Homo sapi	Y68274	Homo sapien	AR453309	Sequence	AX305052	Sequence	HSTAG1A	Sequence	CQ870414	Sequence	AC134953	Pan trogl	QX732164	Sequence	CQ732164	Sequence	AX714170	Sequence	AK056336	Homo sapi	CQ605679	Sequence	CQ729908	Sequence	AL391239	Human DNA	AL356600	Human DNA	AC009694	Homo sapi	AC125214	Mus muscu	AL158079	Homo sapi	AC130272	Papio anu	BC036569	Homo sapi	AX556980	Sequence	U07819	Human conta	CQ727274	Sequence	AX556981	Sequence	U07820	Human conta	AC150028	Canis fam	AF538973	Homo sapi	Y14877	Gallus gall	Y00813	Chicken m8N	Y14852	Oryctolagus	BD935847	Gallus ga	BD985986	Method of	AF040989	Drosophil	AF525411	Rattus no	AF134113	Drosophil	AY047524	Drosophil	CQ585189	Sequence	BC014205	Homo sapi	CQ603804	Sequence	CQ730839	Sequence	HS01TINN2	Sequence	BD186121	Preventio	BD186121	Preventio	CQ730837	Sequence	CQ848088	Sequence	CQ715893	Sequence	AK125056	Homo sapi	AC123550	Mus muscu	AC079543	Mus muscu	BC045307	Danio rer	LI3255	Fruitfly la	CQ590793	Sequence	AY051829	Drosophil	AY051829	Drosophil	AC148913	Sus scrof	AC087123	Mus muscu	AF016619	Mus muscu	AF001287	Mus muscu	QF015482	Sequence	AF001286	Mus muscu	AC112456	Rattus no	AC114113	Rattus no	AC127766	Rattus no	AC106603	Rattus no	AC106602	Rattus no	CQ583539	Sequence	AF312580	Drosophil	BT015246	Drosophil	LI3256	Grasshopper	SCALACH	AY029403	Danio rer	AF029403	Danio rer	AP478693	Sequence	CQ870412	Sequence	AK124736	Homo sapi	Y68274	Homo sapien	AR453309	Sequence	AX305052	Sequence	HSTAG1A	Sequence	CQ870414	Sequence	AC134953	Pan trogl	QX732164	Sequence	CQ732164	Sequence	AX714170	Sequence	AK056336	Homo sapi	CQ605679	Sequence	CQ729908	Sequence	AL391239	Human DNA	AL356600	Human DNA	AC009694	Homo sapi	AC125214	Mus muscu	AL158079	Homo sapi	AC130272	Papio anu	BC036569	Homo sapi	AX556980	Sequence	U07819	Human conta	CQ727274	Sequence	AX556981	Sequence	U07820	Human conta	AR001474	Sequence	Q776853	Sequence	174665	Sequence	193559	Sequence	AX331543	Sequence	AX331937	Sequence	AX556979	Sequence	Z21488	H.sapiens c	AY495696	Rattus no	AY495695	Rattus no	AK123606	Homo sapi	CQ726266	Sequence	AC123606	Homo sapi	AC1018349	Homo sapi	AC130786	Papio anu	BC072368	Xenopus l	AC063977	Homo sapi	AX933439	Gallus ga	AX933439	Gallus ga	AX296535	Zebrafish	CR536619	Danio rer	AY358125	Homo sapi	D38492	Rat mRNA fo	AY371925	Mus muscu	BC052946	Homo sapi	AY369208	Homo sapi	X63101	G.domesticu	AY371924	Rattus no	BC066864	Mus muscu	D32135	Bovine mRNA	Q777685	Sequence	XL14943	Mouse mRNA	AX714318	Sequence	AK056557	Homo sapi	U75330	Human neu	AC137057	Rattus no	AC134313	Rattus no	AC094567	Rattus no	AC127219	Rattus no	M77174	Mouse perle	BC078550	Xenopus l	CR386716	Gallus ga	AX114541	Sequence	AX114540	Sequence	AX114542	Sequence	AX114543	Sequence	AX114539	Sequence	AX114544	Sequence	AK173030	Mus muscu	AR030583	Sequence	AR030584	Sequence	U92814	Hirudo medi	CQ850834	Sequence	AK128020	Homo sapi	AF461120	Danio rer	CQ850958	Sequence	AK128160	Homo sapi	AX309935	Gallus ga	AX273815	Homo sapi	AX935151	Gallus ga	AF103899	Manduca s	M31725	Rat axonal	AF103900	Manduca s	AC084594	Caenorhab	AX746808	Sequence	AK091149	Homo sapi	AX454490	Sequence	AX490968	Sequence	AB013803	Homo sapi	CQ875308	Sequence	AB013802	Homo sapi	CQ603803	Sequence	AC014298	Drosophil	AE003458	Drosophil																																																																																																																																																																																																																																																																																																																																															

370	233	12.9	3413	10	D87248	D87248 Rattus norv	443	224.5	12.4	7642	9	AF002246	AF002246 Homo sapi
371	233	12.9	4956	5	BC044084	BC044084 Xenopus l	444	224.5	12.4	7647	6	AR454602	AR454602 Sequence
372	232.5	12.9	1073	5	DRU63292	U63292 Danio rerio	445	224	12.4	2436	6	AL833710	AL833710 Homo sapi
373	232.5	12.9	2611	10	AF115400	AF115400 Mus muscu	446	224	12.4	2500	6	CQ783752	CQ783752 Sequence
c 374	232.5	12.9	36859	3	U80022	U80022 Caenorhabdi	447	224	12.4	2500	6	BD127814	BD127814 Primer fo
375	232.5	12.9	126899	3	AV130758	AV130758 Caenorhab	448	224	12.4	2500	9	AK074921	AK074921 Homo sapi
376	232	12.8	7876	6	AX592082	AX592082 Sequence	449	224	12.4	3662	6	BD172466	BD172466 Secreted
377	232	12.8	8270	6	AX592092	AX592092 Sequence	450	224	12.4	3662	6	BD172785	BD172785 Secreted
378	232	12.8	152686	2	AC018913	AC018913 Homo sapi	451	224	12.4	3662	6	BD173104	BD173104 Secreted
379	231.5	12.8	3218	5	D86505	D86505 Xenopus lae	452	224	12.4	3662	6	BD173423	BD173423 Secreted
380	231.5	12.8	3821	10	MUSLRAM	L02844 Mus musculu	453	224	12.4	3662	6	BD175457	BD175457 Secretory
381	231.5	12.8	173270	9	AC024886	AC024886 Homo sapi	454	224	12.4	3662	6	AR410836	AR410836 Sequence
382	231	12.8	3087	10	AB032602	AB032602 Mus muscu	455	224	12.4	3662	6	AR439200	AR439200 Sequence
383	231	12.8	3346	6	CQ728965	CQ728965 Sequence	456	224	12.4	3662	6	AR473220	AR473220 Sequence
384	231	12.8	3442	6	BD190857	BD190857 Secreted	457	224	12.4	3662	6	AR566239	AR566239 Sequence
385	231	12.8	3530	9	AB003592	AB003592 Homo sapi	458	224	12.4	3662	6	AX098383	AX098383 Sequence
386	231	12.8	4189	10	AF317839	AF317839 Mus muscu	459	224	12.4	3662	6	AX697698	AX697698 Sequence
387	230.5	12.8	1766	6	CQ731700	CQ731700 Sequence	460	224	12.4	3662	6	BD075606	BD075606 Secretory
388	230.5	12.8	2855	10	RNU34985	U34985 Rattus norv	461	224	12.4	3662	6	AX358295	AX358295 Homo sapi
389	230.5	12.8	2869	6	A72401	A72401 Sequence 2	462	224	12.4	3662	9	AF531873	AF531873 Mus muscu
390	230.5	12.8	2869	6	AR043363	AR043363 Sequence	463	224	12.4	3810	10	AF505340	AF505340 Homo sapi
391	230.5	12.8	2869	6	I60497	I60497 Sequence 2	464	224	12.4	4053	6	BD172468	BD172468 Secreted
392	230.5	12.8	2869	6	AR217165	AR217165 Sequence	465	224	12.4	4053	6	BD172787	BD172787 Secreted
393	230.5	12.8	4988	5	BC066766	BC066766 Danio rer	466	224	12.4	4053	6	BD173106	BD173106 Secreted
394	230.5	12.8	5868	10	BC066106	BC066106 Mus muscu	467	224	12.4	4053	6	BD173425	BD173425 Secreted
395	230.5	12.8	8455	6	CQ870409	CQ870409 Sequence	468	224	12.4	4053	6	BD175459	BD175459 Secretory
396	230.5	12.8	19376	6	CQ869763	CQ869763 Sequence	469	224	12.4	4053	6	AR410838	AR410838 Sequence
397	230	12.7	2610	6	AR043379	AR043379 Sequence	470	224	12.4	4053	6	AR439202	AR439202 Sequence
398	230	12.7	2610	6	CQ847968	CQ847968 Sequence	471	224	12.4	4053	6	AR473222	AR473222 Sequence
399	230	12.7	2610	6	I60505	I60505 Sequence 17	472	224	12.4	4053	6	AR527208	AR527208 Sequence
400	230	12.7	2610	6	AR217181	AR217181 Sequence	473	224	12.4	4053	6	AR528627	AR528627 Sequence
401	230	12.7	2659	10	AK129481	AK129481 Mus muscu	474	224	12.4	4053	6	AR566241	AR566241 Sequence
402	230	12.7	2666	9	AF006464	AF006464 Homo sapi	475	224	12.4	4053	6	AX058647	AX058647 Sequence
403	230	12.7	2692	9	AX358128	AX358128 Homo sapi	476	224	12.4	4053	6	AX098387	AX098387 Sequence
404	230	12.7	13793	9	HGBMHSF	X62515 H. sapiens m	477	224	12.4	4053	6	AX464218	AX464218 Sequence
405	229.5	12.7	2004	6	AX834890	AX834890 Sequence	478	224	12.4	4053	6	AX697702	AX697702 Sequence
406	229.5	12.7	2004	9	AK097578	AK097578 Homo sapi	479	224	12.4	4053	6	BD075608	BD075608 Secretory
407	229	12.7	5396	5	AF388036	AF388036 Xenopus l	480	224	12.4	4053	9	AX358288	AX358288 Homo sapi
408	228.5	12.7	3707	10	BC065142	BC065142 Mus muscu	481	224	12.4	4053	9	BC076578	BC076578 Mus muscu
409	228.5	12.7	3893	10	AY505341	AY505341 Mus muscu	482	224	12.4	4256	10	AB183401	AB183401 Mus muscu
410	228.5	12.7	3980	5	AF064799	AF064799 Danio rer	483	223	12.3	1254	10	AY351388	AY351388 Mus muscu
411	228	12.6	3613	10	BC076594	BC076594 Mus muscu	484	223	12.3	1254	10	BC047021	BC047021 Homo sapi
412	227.5	12.6	1954	10	AB114443	AB114443 Rattus no	485	223	12.3	1674	9	AC018368	AC018368 Homo sapi
413	227.5	12.6	3341	10	D87212	D87212 Rattus norv	486	223	12.3	184716	2	AC125960	AC125960 Rattus no
414	227.5	12.6	3788	5	CHKXGG	M63437 Chicken KLG	c 487	223	12.3	213331	2	AL16928	AL16928 Mus musculu
c 415	227.5	12.6	211829	10	AL645854	AL645854 Mouse DNA	488	222.5	12.3	3795	10	MUSC222A	AL359510 Human DNA
416	227	12.6	4009	6	AX405987	AX405987 Sequence	489	222.5	12.3	95745	9	AL359510	AL359510 Novel rpoA.
417	227	12.6	4036	9	AB037776	AB037776 Homo sapi	490	222	12.3	4783	6	E34511	E34511 Novel rata.
418	227	12.6	4230	10	BC040281	BC040281 Mus muscu	491	222	12.3	4783	6	E34511	E34511 Novel utili
419	227	12.6	4542	6	CQ718773	CQ718773 Sequence	492	222	12.3	4783	6	E34515	E34515 Human LIG-1
420	227	12.6	13149	6	CQ728817	CQ728817 Sequence	c 493	222	12.3	4783	6	E34515	CQ604730 Sequence
421	227	12.6	186110	2	AC102204	AC102204 Mus muscu	c 494	222	12.3	7171	6	CQ604730	AC020372 Drosophil
422	226.5	12.5	1801	10	BC078966	BC078966 Rattus no	495	222	12.3	100002	2	AC020372	AC020372 Drosophil
423	226.5	12.5	3870	10	BC036291	BC036291 Mus muscu	c 496	222	12.3	149801	2	CR382301	CR382301 Danio rer
424	226	12.5	5171	5	BC060500	BC060500 Xenopus l	497	222	12.3	156022	2	BX324195	BX324195 Danio rer
425	226	12.5	4638	3	CSU33058	U33058 Caenorhabdi	498	222	12.3	157314	2	CR352289	CR352289 Danio rer
426	226	12.5	4896	3	U88310	U88310 Caenorhabdi	499	222	12.3	168601	3	AC007471	AC007471 Drosophil
427	226	12.5	65649	3	AF003131	AF003131 Caenorhab	c 500	222	12.3	180916	2	CR381704	CR381704 Danio rer
428	226	12.5	294136	2	AC006901	AC006901 Caenorhab	501	222	12.3	201070	5	BX004830	BX004830 Zebrafish
429	226	12.5	299719	2	AC006858	AC006858 Caenorhab	502	222	12.3	271696	3	AE003835	AE003835 Drosophil
430	225.5	12.5	3328	10	MMU37708	U37708 Mus musculu	503	221.5	12.3	1112	9	AB094146	AB094146 Homo sapi
431	225.5	12.5	3352	10	MMU37709	U37709 Mus musculu	504	221.5	12.3	1112	10	AB092414	AB092414 Mus muscu
432	225	12.5	2607	6	AX179390	AX179390 Sequence	505	221.5	12.3	5314	5	BC074401	BC074401 Xenopus l
433	225	12.5	2607	6	AX259864	AX259864 Sequence	506	221	12.2	1308	3	AF456362	AF456362 Caenorhab
434	225	12.5	5586	6	CQ729937	CQ729937 Sequence	507	221	12.2	4525	9	AF289030	AF289030 Homo sapi
435	225	12.5	14327	9	HUMHSPG2B	M85289 Human hepar	508	221	12.2	5374	9	AF289030	AF289030 Homo sapi
c 436	225	12.5	3158	3	CBRG19K24	AC087734 Caenorhab	509	221	12.2	5374	6	CQ731799	CQ731799 Sequence
437	224.5	12.4	2404	6	CQ728038	CQ728038 Sequence	510	221	12.2	6187	9	AF023449	AF023449 Homo sapi
438	224.5	12.4	2611	10	AF115401	AF115401 Mus muscu	511	221	12.2	6413	9	AF023450	AF023450 Homo sapi
439	224.5	12.4	3960	6	CQ849821	CQ849821 Homo sapi	512	221	12.2	6435	5	AF461119	AF461119 Xenopus l
440	224.5	12.4	3960	9	AK126878	AK126878 Homo sapi	513	221	12.2	6649	9	AF217525	AF217525 Homo sapi
441	224.5	12.4	7642	6	CQ776627	CQ776627 Sequence	514	220.5	12.2	1011	10	AB183402	AB183402 Mus muscu
442	224.5	12.4	7642	6	AX818174	AX818174 Sequence	515	220.5	12.2	1287	10	AB183400	AB183400 Mus muscu

516	220.5	12.2	1329	6	BD261770	BD261770 12 human	589	218	12.1	6556	10	AF334385	AF334385 Rattus no
517	220.5	12.2	1329	9	CR457157	CR457157 Homo sapi	590	218	12.1	6829	10	AY005483	AY005483 Mus muscu
518	220.5	12.2	1338	10	AB183399	AB183399 Mus muscu	591	218	12.1	146352	2	CR548641	CR548641 Danio rer
519	220.5	12.2	1413	6	BD140567	BD140567 Polypteri	592	218	12.1	186279	5	BR950870	BR950870 Zebrafish
520	220.5	12.2	1413	6	AR429086	AR429086 Sequence	c 593	218	12.1	191779	2	CR376789	CR376789 Danio rer
521	220.5	12.2	1413	6	AR534977	AR534977 Sequence	594	217	12.0	3429	4	SSC459296	AJ459296 Sus scrofa
522	220.5	12.2	1413	6	AX375966	AX375966 Sequence	595	217	12.0	4410	3	AY118274	AY118274 Drosophila
523	220.5	12.2	1413	9	AY358334	AY358334 Homo sapi	596	217	12.0	41345	3	CEF1509	Z47068 Caenorhabdi
524	220.5	12.2	1448	9	BC035930	BC035930 Homo sapi	597	216.5	12.0	3057	6	CQ842487	CQ842487 Sequence
525	220.5	12.2	1450	10	AB064265	AB064265 Mus muscu	598	216.5	12.0	3057	9	AK125460	AK125460 Homo sapi
526	220.5	12.2	1508	6	BD261716	BD261716 12 human	599	216.5	12.0	4054	3	MSU50719	US0719 Manduca sex
527	220.5	12.2	1520	6	BD261709	BD261709 12 human	600	216.5	12.0	4430	10	BC062892	BC062892 Mus muscu
528	220.5	12.2	1548	6	AX136299	AX136299 Sequence	c 601	216	12.0	260998	2	AC099089	AC099089 Rattus no
529	220.5	12.2	1548	6	BD123602	BD123602 Secretary	602	215.5	11.9	2957	6	CQ591957	CQ591957 Sequence
530	220.5	12.2	1548	9	AK075502	AK075502 Homo sapi	603	215.5	11.9	3264	3	AY119465	AY119465 Drosophila
531	220.5	12.2	1548	6	BD247472	BD247472 Molecules	604	215.5	11.9	3397	7	AX780431	AX780431 Sequence
532	220.5	12.2	1598	6	AR278813	AR278813 Sequence	605	215.5	11.9	3397	9	AF312678	AF312678 Homo sapi
533	220.5	12.2	1817	10	AF539424	AF539424 Mus muscu	606	215.5	11.9	3498	10	RNU81035	U81035 Rattus norv
534	220.5	12.2	1862	6	AX399846	AX399846 Sequence	607	215.5	11.9	3853	3	DRNRGAA	M28331 Drosophila
535	220.5	12.2	1935	6	BD247473	BD247473 Molecules	608	215.5	11.9	4041	6	CQ573942	CQ573942 Sequence
536	220.5	12.2	1935	6	AR278814	AR278814 Sequence	609	215.5	11.9	4044	9	BC002377	BC002377 Homo sapi
537	220.5	12.2	1958	10	BC057125	BC057125 Mus muscu	610	215.5	11.9	4044	9	BC014626	BC014626 Homo sapi
538	220.5	12.2	2024	10	AB052293	AB052293 Mus muscu	611	215.5	11.9	4433	3	AY058284	AY058284 Drosophila
539	220.5	12.2	2340	6	CQ870000	CQ870000 Sequence	c 612	215.5	11.9	5026	6	CQ591956	CQ591956 Sequence
540	220.5	12.2	4444	10	AF434663	AF434663 Mus muscu	613	215.5	11.9	8574	3	DMNRG2	AF050085 Drosophila
541	220	12.2	2845	6	CQ716675	CQ716675 Sequence	614	215.5	11.9	8883	10	AY273816	AY273816 Rattus no
542	220	12.2	4717	6	AX463544	AX463544 Sequence	615	215.5	11.9	20510	6	CQ573941	CQ573941 Sequence
543	220	12.2	4759	6	AX463530	AX463530 Sequence	616	215.5	11.9	62442	2	AC018325	AC018325 Drosophila
544	220	12.2	5287	9	AB050468	AB050468 Homo sapi	c 617	215.5	11.9	71320	2	AC020124	AC020124 Drosophila
545	220	12.2	5719	6	CQ869705	CQ869705 Sequence	618	215.5	11.9	166512	3	AC099010	AC099010 Drosophila
546	219.5	12.2	991	5	AF364047	AF364047 Gallus ga	c 619	215.5	11.9	174287	3	AC007977	AC007977 Drosophila
547	219.5	12.2	1247	5	BC078527	BC078527 Xenopus l	620	215.5	11.9	174367	3	AC023696	AC023696 Drosophila
548	219.5	12.2	1258	9	AF005070	AF005070 Homo sapi	621	215.5	11.9	185405	3	AC023743	AC023743 Drosophila
549	219.5	12.2	2259	6	BD204924	BD204924 Homo sapi	c 622	215.5	11.9	270766	3	AE003615	AE003615 Drosophila
550	219.5	12.2	3512	9	AF132811	AF132811 Homo sapi	623	215.5	11.9	299686	3	AE003444	AE003444 Drosophila
551	219.5	12.2	3534	9	AF027558	AF027558 Homo sapi	624	215	11.9	1332	3	AF456363	AF456363 Caenorhab
552	219.5	12.2	4002	9	BC075829	BC075829 Homo sapi	625	215	11.9	3213	6	CQ847970	CQ847970 Sequence
553	219.5	12.2	4277	6	AX376372	AX376372 Sequence	626	215	11.9	4236	5	HSU33635	U33635 Human colon
554	219.5	12.2	4277	6	AX454572	AX454572 Sequence	627	215	11.9	5067	5	AF304131	AF304131 Danio rer
555	219.5	12.2	4277	6	AX491050	AX491050 Sequence	628	214.5	11.9	4956	2	AF041082	AF041082 Rattus no
556	219.5	12.2	4277	6	AX696989	AX696989 Sequence	c 629	214	11.8	77635	2	DMBR40010	AL122024 Drosophila
557	219.5	12.2	4277	9	AY358328	AY358328 Homo sapi	630	213.5	11.8	1121	6	CQ727036	CQ727036 Sequence
558	219.5	12.2	4291	6	BD204923	BD204923 Novel mol	631	213.5	11.8	1242	9	AY046418	AY046418 Homo sapi
559	219.5	12.2	6789	9	HSU0171	Z95705 Human DNA s	632	213.5	11.8	1614	6	BD177640	BD177640 MBGP1 pol
560	219	12.1	756	6	CQ729341	CQ729341 Sequence	633	213.5	11.8	1614	6	E37854	E37854 MBGP1 polyP
561	219	12.1	2638	6	AX833755	AX833755 Sequence	634	213.5	11.8	1614	6	AX003003	AX003003 Sequence
562	219	12.1	2638	9	AK095729	AK095729 Homo sapi	635	213.5	11.8	1680	9	BC033819	BC033819 Homo sapi
563	219	12.1	3210	5	AB015205	AB015205 Xenopus l	636	213.5	11.8	1685	6	BD172296	BD172296 Secreted
564	219	12.1	3690	9	AF549455	AF549455 Homo sapi	637	213.5	11.8	1685	6	BD172615	BD172615 Secreted
565	219	12.1	4129	6	CQ849703	CQ849703 Sequence	638	213.5	11.8	1685	6	BD172934	BD172934 Secreted
566	219	12.1	4129	9	AK126745	AK126745 Homo sapi	639	213.5	11.8	1685	6	BD173253	BD173253 Secreted
567	219	12.1	4762	9	AF381545	AF381545 Homo sapi	640	213.5	11.8	1685	6	BD175287	BD175287 Secretary
568	219	12.1	4805	9	AF730707	AF730707 Homo sapi	641	213.5	11.8	1685	6	AR410665	AR410665 Sequence
569	219	12.1	4822	6	E12950	E12950 cDNA GA3-43	642	213.5	11.8	1685	6	AR439029	AR439029 Sequence
570	219	12.1	4822	10	D78572	D78572 Mus musculu	643	213.5	11.8	1685	6	AR473049	AR473049 Sequence
571	219	12.1	4832	6	CQ869702	CQ869702 Sequence	644	213.5	11.8	1685	6	AR527035	AR527035 Sequence
572	219	12.1	5035	5	AY090737	AY090737 Homo sapi	645	213.5	11.8	1685	6	AR528625	AR528625 Sequence
573	219	12.1	12255	5	AJ584653	AJ584653 Gallus ga	646	213.5	11.8	1685	6	AR566068	AR566068 Sequence
574	218.5	12.1	1425	6	CQ725721	CQ725721 Sequence	647	213.5	11.8	1685	6	AX454458	AX454458 Sequence
575	218.5	12.1	4015	9	BC030141	BC030141 Homo sapi	648	213.5	11.8	1685	6	AX464214	AX464214 Sequence
576	218.5	12.1	4020	6	CQ870598	CQ870598 Homo sapi	649	213.5	11.8	1685	6	AX490936	AX490936 Sequence
577	218.5	12.1	6922	10	MMU17793	Y17793 Mus musculu	650	213.5	11.8	1685	6	BD075436	BD075436 Secretary
c 578	218.5	12.1	152686	2	AC018913	AC018913 Homo sapi	651	213.5	11.8	1685	9	AY358332	AY358332 Homo sapi
579	218	12.1	1689	9	AB056375	AB056375 Macaca fa	652	213.5	11.8	1718	6	BD247477	BD247477 Molecules
580	218	12.1	1884	6	CQ734341	CQ734341 Sequence	653	213.5	11.8	1718	6	AR278800	AR278800 Sequence
581	218	12.1	2350	6	CQ878954	CQ878954 Sequence	654	213.5	11.8	2496	6	BD191411	BD191411 Secreted
582	218	12.1	3958	9	AF531872	AF531872 Homo sapi	655	213.5	11.8	3557	9	AF363367	AF363367 Homo sapi
583	218	12.1	4191	6	CQ789354	CQ789354 Sequence	656	213.5	11.8	4155	6	AB040929	AB040929 Homo sapi
584	218	12.1	4191	9	AF531868	AF531868 Homo sapi	657	213.5	11.8	4594	9	AB040929	AB040929 Homo sapi
585	218	12.1	4191	9	HSU40271	U40271 Homo sapien	658	213.5	11.8	5384	5	AF337036	AF337036 Danio rer
586	218	12.1	4193	6	CQ715771	CQ715771 Sequence	659	213.5	11.8	5384	5	AF337036	AF337036 Danio rer
587	218	12.1	4238	9	BC071557	BC071557 Homo sapi	660	213	11.8	177	6	AX030585	AX030585 Sequence
588	218	12.1	6267	10	AF315558	AF315558 Mus muscu	661	213	11.8	851	5	BR932255	BR932255 Gallus ga

662	213	11.8	1605	6	CQ599856	Sequence	735	209	11.6	3402	6	AX080803	Sequence
663	213	11.8	1892	5	AB117614	Xenopus l	736	209	11.6	3402	6	AX191426	Sequence
664	213	11.8	2043	6	CQ717926	Sequence	737	209	11.6	3402	6	AX403231	Sequence
665	213	11.8	4381	10	AK173340	Mus muscu	738	209	11.6	3402	9	AY358303	Homo sapi
666	213	11.8	4470	5	AF538326	Danio rer	739	208.5	11.5	2811	10	AF487347	Mus muscu
667	212.5	11.8	2650	10	AF102134	Mus muscu	740	208.5	11.5	3448	10	MUSNGP	L01991
668	212.5	11.8	2732	10	MWBIG2A	M.musculus	741	208.5	11.5	3678	3	BT014656	Drosophil
669	212.5	11.8	4071	9	AF531869	Homo sapi	742	208.5	11.5	4956	6	BD085989	Method of
670	212.5	11.8	4631	9	HSU72391	Human neoge	743	208.5	11.5	4956	9	AF040990	Homo sapi
671	212.5	11.8	5021	6	CQ729613	Sequence	744	208.5	11.5	5667	6	CQ0606753	Sequence
672	212	11.7	177	6	AR030586	Sequence	745	208	11.5	6592	6	CQ598305	Sequence
673	212	11.7	3752	10	AY061639	Rattus no	746	208	11.5	152024	2	CR407703	Danio rer
674	212	11.7	4609	10	RNU35371	U35371	747	207.5	11.5	2220	6	AX748214	Sequence
675	211.5	11.7	2818	3	DROPARS2A	M7165 D.melanog	748	207.5	11.5	2220	9	AK093583	Homo sapi
676	211.5	11.7	2901	3	BT014661	Drosophil	749	207.5	11.5	185751	10	AC122038	Mus muscu
677	211.5	11.7	3070	3	DROFAS2B	BT014661 Drosophil	750	207.5	11.5	247498	10	AC135238	Mus muscu
678	211.5	11.7	3132	10	MWNSK22	M7166 D.melanog	751	207	11.5	2735	6	CQ728959	Sequence
679	211.5	11.7	3257	10	MWNSK21	X86445 M.musculus	752	207	11.5	2846	6	AX834922	Sequence
680	211.5	11.7	3414	6	CQ579258	X86444 M.musculus	753	207	11.5	2846	9	AK097633	Homo sapi
681	211.5	11.7	3798	10	AF388037	CQ579258 Sequence	754	207	11.5	5175	6	CQ585188	Sequence
682	211.5	11.7	4376	10	BC078631	AF388037 Mus muscu	755	207	11.5	36654	2	AC017551	Drosophil
683	211.5	11.7	4460	2	AC020249	BC078631 Mus muscu	756	207	11.5	177736	3	AC005714	Drosophil
684	211.5	11.7	5297	6	AX587800	AC020249 Drosophil	757	207	11.5	191467	3	AC008348	Drosophil
685	211.5	11.7	5297	6	AX771417	AX587800 Sequence	758	207	11.5	307323	3	AE003457	Drosophil
686	211.5	11.7	5297	9	HSU61262	AX771417 Sequence	759	206.5	11.4	980	9	BC013797	Homo sapi
687	211.5	11.7	5506	6	AR447897	U61262 Human neoge	760	206	11.4	3762	3	AF456361	Caenorhab
688	211.5	11.7	6168	3	DMSGG0007	AR447897 Sequence	761	205.5	11.4	708	5	CB385737	Gallus ga
689	211.5	11.7	165928	3	AC023725	AL033125 Drosophil	762	205.5	11.4	1542	6	BD193028	207 human
690	211.5	11.7	172784	3	AC105352	AC023725 Drosophil	763	205.5	11.4	1542	6	CQ822024	Sequence
691	211.5	11.7	295177	3	AE003430	AC105352 Drosophil	764	205.5	11.4	2067	10	AY210400	Mus muscu
692	211	11.7	1273	6	AR278799	AE003430 Drosophil	765	205.5	11.4	2539	6	CQ782770	Sequence
693	211	11.7	2377	10	AF195662	AR278799 Sequence	766	205.5	11.4	2539	6	BD127305	Primer fo
694	211	11.7	3366	10	AY059393	AF195662 Mus muscu	767	205.5	11.4	2539	9	AK074825	Homo sapi
695	211	11.7	5563	9	AF069601	AY059393 Homo sapi	768	205.5	11.4	4128	10	RNU11031	Rattus norv
696	211	11.7	5719	9	AF069601	AF069601 Homo sapi	769	205.5	11.4	4465	10	MMU543322	Mus muscu
697	211	11.7	20435	9	HSJA72535	AF069601 Homo sapi	770	205.5	11.4	5071	10	AK129207	Procamb
698	210.5	11.7	1837	6	CQ869997	AJ002535 Homo sapi	771	205.5	11.4	53424	3	AB055861	Sequence
699	210.5	11.7	3231	6	CQ724644	AJ002535 Homo sapi	772	205	11.4	1299	6	CQ728323	Sequence
700	210.5	11.7	5913	6	CQ869760	CQ724644 Sequence	773	205	11.4	1820	6	BD247476	Molecules
701	210	11.6	577	6	AR496051	CQ869760 Sequence	774	205	11.4	1820	6	AR278798	Sequence
702	210	11.6	577	6	AR511333	AR496051 Sequence	775	205	11.4	2096	9	AF062733	Homo sapi
703	210	11.6	4078	6	AF509585	AR511333 Sequence	776	204.5	11.3	2096	6	CQ579750	Sequence
704	210	11.6	5193	4	AF509585	AF509585 Sus scrof	777	204.5	11.3	2111	5	AF035677	Gallus ga
705	210	11.6	5193	6	AX698036	AF509585 Sequence	778	204.5	11.3	4641	10	RNU568726	U68726 Rattus norv
706	210	11.6	5193	6	AX698038	AX698036 Sequence	779	204.5	11.3	6860	5	AF304130	Danio rer
707	210	11.6	5745	9	AX339601	AX698038 Sequence	780	204.5	11.3	83495	3	AC087076	Caenorhab
708	210	11.6	5770	9	AF069602	AX339601 Homo sapi	781	204	11.3	1038	5	BC083011	Xenopus l
709	210	11.6	5896	9	BC064695	AF069602 Homo sapi	782	204	11.3	4517	10	MMDCCTSG	U07644 Gallus gall
710	210	11.6	5926	6	AR482482	BC064695 Homo sapi	783	204	11.3	4784	5	GDU07644	U07644 Gallus gall
711	210	11.6	5926	6	AX329738	AR482482 Sequence	784	204	11.3	5211	6	CQ870291	Sequence
712	210	11.6	5926	6	AX330278	AX329738 Sequence	785	204	11.3	5892	6	CQ588164	Sequence
713	210	11.6	5926	6	AX333040	AX330278 Sequence	786	204	11.3	20686	2	AC017508	Drosophil
714	210	11.6	5926	6	AX337264	AX333040 Sequence	787	204	11.3	149752	9	AC004616	Homo sapi
715	210	11.6	5926	6	AX375038	AX337264 Sequence	788	204	11.3	174920	3	AC010701	Drosophil
716	210	11.6	5926	6	AX410725	AX375038 Sequence	789	204	11.3	294272	3	AE003595	Drosophil
717	210	11.6	5926	9	HSU48959	AX410725 Sequence	790	203.5	11.3	4435	5	AF388035	Xenopus l
718	210	11.6	5992	10	BC058610	U48959 Homo sapien	791	203.5	11.3	5824	6	AF338581	Sequence
719	209.5	11.6	7644	6	CQ727360	BC058610 Mus muscu	792	203.5	11.3	6811	9	AF334384	Homo sapi
720	209.5	11.6	17193	6	CQ585358	CQ727360 Sequence	793	203.5	11.3	6834	9	AB032958	Homo sapi
721	209.5	11.6	58651	2	AC017558	CQ585358 Sequence	794	203.5	11.3	6899	9	AF491813	Homo sapi
722	209.5	11.6	69992	3	AC005421	AC017558 Drosophil	795	203	11.2	2749	5	DRE574916	Danio rer
723	209.5	11.6	189315	3	AC008319	AC005421 Drosophil	796	203	11.2	2774	5	BC053245	Sequence
724	209.5	11.6	306696	3	AE003586	AC008319 Drosophil	797	203	11.2	4248	6	AX054979	Danio rer
725	209	11.6	1248	6	CQ725953	AE003586 Drosophil	798	203	11.2	4775	3	CEU70618	Sequence
726	209	11.6	1450	6	AX287596	CQ725953 Sequence	799	203	11.2	6021	10	AY237726	Mus muscu
727	209	11.6	1489	9	AK172829	AX287596 Sequence	800	203	11.2	18524	6	CQ730656	Sequence
728	209	11.6	1565	9	AF279689	AK172829 Homo sapi	801	202.5	11.2	2697	6	CQ728585	Sequence
729	209	11.6	3080	6	AX287610	AF279689 Homo sapi	802	202.5	11.2	3801	9	AF531870	Homo sapi
730	209	11.6	3180	9	HSR277437	AX287610 Sequence	803	202.5	11.2	4340	3	AV118645	Drosophil
731	209	11.6	3180	9	AX287608	AJ277437 Homo sapi	804	202.5	11.2	9487	6	CQ717135	Sequence
732	209	11.6	3145	6	CQ870633	AX287608 Sequence	805	202.5	11.2	9645	6	CQ875263	Sequence
733	209	11.6	3305	9	BC036769	CQ870633 Sequence	806	202.5	11.2	9645	9	AF245505	Homo sapi
734	209	11.6	3402	6	AR252460	BC036769 Homo sapi	807	202.5	11.2	35347	3	CFT09B9	Caenorhabdi
						AR252460 Sequence							

808	202	11.2	2472	6	CQ592467	CQ592467 Sequence	881	197	10.9	5292	10	AB093285	AB093285 Mus muscu
809	202	11.2	2844	5	AY143173	AY143173 Gallus ga	882	197	10.9	43940	3	AY686597	AY686597 Drosophil
810	202	11.2	2847	5	BC052773	BC052773 Mus muscu	883	196.5	10.9	1559	5	CR354016	CR354016 Gallus ga
811	202	11.2	3822	3	AF041053	AF041053 Caenorhab	884	196.5	10.9	3284	6	AX443486	AX443486 Sequence
812	202	11.2	5604	5	AF394058	AF394058 Danio rer	885	196.5	10.9	3651	10	RNU1036	U1036 Rattus norv
813	202	11.2	5680	5	AY082380	AY082380 Danio rer	886	196.5	10.9	4041	5	GNEUPASC	X52224 G.gallus nr
814	202	11.2	6300	5	AY029280	AY029280 Danio rer	887	196.5	10.9	5822	10	RATANKIND	L1002 Rat ankryn
815	201.5	11.2	1161	6	AX645013	AX645013 Sequence	888	196.5	10.9	6218	9	AB002341	AB002341 Homo sapi
816	201.5	11.2	1307	6	AX512897	AX512897 Sequence	889	196.5	10.9	6219	6	CQ716062	CQ716062 Sequence
817	201.5	11.2	1514	6	AX645011	AX645011 Sequence	890	196.5	10.9	6254	6	BD190781	BD190781 Secreted
818	201.5	11.2	2176	9	AF363368	AF363368 Homo sapi	891	196.5	10.9	6254	6	AX099489	AX099489 Sequence
819	201.5	11.2	2859	6	CQ576375	CQ576375 Sequence	892	196.5	10.9	6384	6	AX448063	AX448063 Sequence
820	201.5	11.2	10242	6	CQ600663	CQ600663 Sequence	893	196.5	10.9	6384	6	AX531706	AX531706 Sequence
821	201.5	11.2	10801	10	AF215896	AF215896 Mus muscu	894	196.5	10.9	168144	2	CR792456	CR792456 Danio rer
822	201.5	11.2	12603	6	CQ598875	CQ598875 Sequence	895	196	10.9	10664	6	CQ870296	CQ870296 Sequence
823	201.5	11.2	13041	3	DME487018	AY487018 Drosophil	896	196	10.9	2351	5	RNOS36020	AY536020 Rattus no
824	201	11.1	3400	5	FSCTRKA	L11311 Torpedo cal	897	196	10.9	7631	5	GGFMVLYCK	X52876 G.gallus nr
825	201	11.1	3405	5	GG535114	AY535114 Gallus ga	898	196	10.9	96468	2	AC006902	AC006902 Caenorhab
826	201	11.1	4521	9	AK024462	AK024462 Homo sapi	899	195.5	10.8	479	6	AX665358	AX665358 Sequence
827	201	11.1	5130	9	AF230073	AF230073 Homo sapi	900	195.5	10.8	2898	6	CQ587259	CQ587259 Sequence
828	201	11.1	252070	2	AC098426	AC098426 Rattus no	901	195	10.8	2313	9	AK097802	AK097802 Homo sapi
829	200.5	11.1	1103	6	CQ728252	CQ728252 Sequence	902	195	10.8	3384	6	AX714308	AX714308 Sequence
830	200.5	11.1	4119	5	AX376856	AY376856 Danio rer	903	195	10.8	3384	9	AK056544	AK056544 Homo sapi
831	200.5	11.1	5414	10	WNEOGEN	Y09535 M.musculus	904	195	10.8	4381	6	CQ869962	CQ869962 Sequence
832	200.5	11.1	177476	9	AC010680	AC010680 Homo sapi	905	195	10.8	4569	9	AY509035	AY509035 Homo sapi
833	200.5	11.1	294540	9	HSA277892	AY277892 Homo sapi	906	195	10.8	5865	3	DMU71001	U71001 Drosophila
834	200	11.1	1967	6	AR156834	AR156834 Sequence	907	195	10.8	6279	6	CQ590850	CQ590850 Sequence
835	200	11.1	1967	6	BD269852	BD269852 The poly	908	195	10.8	6318	3	DMU71002	U71002 Drosophila
836	200	11.1	2193	10	MUSPCGBMA	J04055 Mouse basem	909	195	10.8	37091	6	CQ590849	CQ590849 Sequence
837	200	11.1	2274	10	MMU233947	AJ293947 Mus muscu	910	195	10.8	52726	2	AC017352	AC017352 Drosophil
838	200	11.1	2277	6	AX287593	AX287593 Sequence	911	195	10.8	189557	3	AC007356	AC007356 Drosophil
839	200	11.1	2339	10	BC058745	BC058745 Mus muscu	912	195	10.8	221235	2	AC096965	AC096965 Rattus no
840	200	11.1	2359	10	AF321300	AF321300 Mus muscu	913	195	10.8	251435	2	AC128510	AC128510 Rattus no
841	199.5	11.0	2173	9	BC068457	BC068457 Homo sapi	914	195	10.8	264547	2	AC094432	AC094432 Rattus no
842	199.5	11.0	3727	6	CQ726408	CQ726408 Sequence	915	195	10.8	294169	3	AE003821	AE003821 Drosophil
843	199.5	11.0	4924	10	RNU68725	U68725 Rattus norv	916	194.5	10.8	3211	3	BT001692	BT001692 Drosophil
844	199.5	11.0	5443	10	BC054540	BC054540 Mus muscu	917	194.5	10.8	173690	2	AC011307	AC011307 Homo sapi
845	199.5	11.0	7855	9	AK122586	AK122586 Homo sapi	918	194.5	10.8	178137	9	AC011302	AC011302 Homo sapi
846	199	11.0	2943	10	AY167411	AY167411 Rattus no	919	194	10.7	3783	6	AR177819	AR177819 Sequence
847	199	11.0	3226	9	AF190637	AF190637 Homo sapi	920	194	10.7	3783	10	MNMCAML1	X12875 Mouse mrna
848	199	11.0	4285	6	AR140634	AR140634 Sequence	921	194	10.7	5038	10	BC056988	BC056988 Mus muscu
849	199	11.0	4285	9	AF035835	AF035835 Homo sapi	922	194	10.7	216540	5	BX322647	BX322647 Zebrafish
850	199	11.0	4287	6	CQ721176	CQ721176 Sequence	923	193.5	10.7	826	6	CQ780202	CQ780202 Sequence
851	199	11.0	4871	5	AF337035	AF337035 Danio rer	924	193.5	10.7	826	6	CQ781611	CQ781611 Sequence
852	198.5	11.0	4285	6	CQ607487	CQ607487 Sequence	925	193.5	10.7	826	6	BD124911	BD124911 Primer fo
853	198.5	11.0	6645	10	AK131182	AK131182 Mus muscu	926	193.5	10.7	826	6	BD126320	BD126320 Primer fo
854	198.5	11.0	6729	9	AF304304	AF304304 Homo sapi	927	193.5	10.7	2499	6	CQ583689	CQ583689 Sequence
855	198.5	11.0	48870	2	AC017807	AC017807 Drosophil	928	193.5	10.7	4486	10	MMU543321	MMU543321 Mus muscu
856	198.5	11.0	155666	3	AC007854	AC007854 Drosophil	929	193.5	10.7	4944	10	BC055053	BC055053 Mus muscu
857	198.5	11.0	168471	3	AC006170	AC006170 Drosophil	930	193.5	10.7	5608	10	AK122252	AK122252 Mus muscu
858	198.5	11.0	231562	3	AE003767	AE003767 Drosophil	931	193.5	10.7	5925	6	AX921879	AX921879 Sequence
859	198	11.0	3233	6	CQ721186	CQ721186 Sequence	932	193	10.7	2687	3	DME312133	DME312133 Drosophil
860	198	11.0	3260	9	HSRNCAD22	X59350 H.sapiens m	933	193	10.7	3858	5	BC057728	BC057728 Xenopus l
861	198	11.0	4844	6	CQ728171	CQ728171 Sequence	934	193	10.7	4579	3	DME312134	DME312134 Drosophil
862	198	11.0	199446	10	AL125069	AL125069 Mus muscu	935	193	10.7	4846	5	XLU10986	XLU10986 Xenopus lae
863	198	11.0	202887	10	AL928789	AL928789 Mouse dna	936	193	10.7	4901	9	HSM803665	AL832357 Homo sapi
864	198	11.0	255090	2	AC073798	AC073798 Mus muscu	937	193	10.7	5099	3	DME312135	AJ312135 Drosophil
865	197.5	10.9	1416	5	EX932904	EX932904 Gallus ga	938	193	10.7	5194	3	BT010247	BT010247 Drosophil
866	197.5	10.9	1861	10	AF061260	AF061260 Mus muscu	939	193	10.7	7606	3	DFOLARM	M27700 D.melanog
867	197.5	10.9	2256	6	HUMDCC	M32292 Human color	940	193	10.7	7928	6	AX039412	AX039412 Sequence
868	197.5	10.9	3525	6	CQ715490	CQ715490 Sequence	941	192.5	10.7	2481	6	AR237560	AR237560 Sequence
869	197.5	10.9	4305	6	CQ613728	CQ613728 Sequence	942	192.5	10.7	2715	6	AR237555	AR237555 Sequence
870	197.5	10.9	4344	6	AX054981	AX054981 Sequence	943	192.5	10.7	2724	6	AR237562	AR237562 Sequence
871	197.5	10.9	4608	6	AR153583	AR153583 Sequence	944	192.5	10.7	2958	6	AR237557	AR237557 Sequence
872	197.5	10.9	4608	9	HSDDCG	X76132 H.sapiens D	945	192.5	10.7	2976	6	AR237558	AR237558 Sequence
873	197.5	10.9	4715	3	AX121698	AX121698 Drosophil	946	192.5	10.7	3192	6	BD270852	BD270852 Polistat
874	197.5	10.9	4726	3	AF210316	AF210316 Drosophil	947	192.5	10.7	3192	6	AR230355	AR230355 Sequence
875	197.5	10.9	4955	9	AB018239	AB018239 Homo sapi	948	192.5	10.7	3210	6	AR237553	AR237553 Sequence
876	197.5	10.9	5013	6	CQ870298	CQ870298 Sequence	949	192.5	10.7	3219	6	AR237561	AR237561 Sequence
877	197.5	10.9	5019	6	CQ870300	CQ870300 Sequence	950	192.5	10.7	3453	6	AR237556	AR237556 Sequence
878	197	10.9	2462	6	AX746553	AX746553 Sequence	951	192.5	10.7	3874	6	AR237568	AR237568 Sequence
879	197	10.9	2462	9	AK090639	AK090639 Homo sapi	952	192.5	10.7	3942	5	CHKRVO	L08960 Chicken cel
880	197	10.9	3894	6	BD085988	BD085988 Method of	953	192.5	10.7	3943	5	GGNRCAW	X58482 Chicken mrn

1100	185.5	10.3	2974	6	AX558324	Sequence	1173	182	10.1	3475	3	AF303661	AF303661
1101	185.5	10.3	2974	6	AX677147	Sequence	1174	182	10.1	3906	5	AY056466	AY056466
1102	185.5	10.3	2974	6	AX805532	Sequence	1175	182	10.1	6320	6	CQ598304	CQ598304
1103	185.5	10.3	2974	6	HUMCEAF	M29540 Human carc	1176	182	10.1	65758	2	AC019956	AC019956
1104	185.5	10.3	3036	6	CQ800159	Sequence	1177	182	10.1	173641	3	AC009739	AC009739
1105	185.5	10.3	3036	6	HUMANTCE	M17303 Human carc	1178	182	10.1	266426	3	AE003841	AE003841
1106	185.5	10.3	6215	6	AX556709	Sequence	1179	181.5	10.0	1364	3	MOTP4A	MOTP4A
1107	185.5	10.3	105000	9	BS000599	BS000599 Pan trogl	1180	181.5	10.0	3009	6	AX060540	AX060540
1108	185.5	10.3	173078	9	AC146249	AC146249 Pan trogl	1181	181.5	10.0	3146	10	AF026465	AF026465
1109	185.5	10.2	1719	5	BC950396	BC950396 Gallus ga	1182	181.5	10.0	3198	10	BC053057	BC053057
1110	185.5	10.2	2092	6	HSCRAASP	X16455 Human mRNA	1183	181.5	10.0	3379	6	AX359721	AX359721
1111	185.5	10.2	2106	6	AX133657	Sequence	1184	181.5	10.0	3430	6	AX359719	AX359719
1112	185.5	10.2	2106	6	AX192349	Sequence	1185	181.5	10.0	4122	5	DRNADML11	DRNADML11
1113	185.5	10.2	2370	10	AF249056	AF249056 Rattus no	1186	181	10.0	420	6	AX665356	AX665356
1114	185.5	10.2	2370	10	AF480411	AF480411 Mus muscu	1187	181	10.0	1764	6	CQ728797	CQ728797
1115	185.5	10.2	3585	10	BC063072	BC063072 Mus muscu	1188	181	10.0	1859	6	AX179640	AX179640
1116	185.5	10.2	4146	6	BD085987	BD085987 Method of	1189	181	10.0	1952	6	CQ095169	CQ095169
1117	185.5	10.2	4992	6	CQ869959	Sequence	1190	181	10.0	1952	6	CQ133915	CQ133915
1118	185.5	10.2	5259	10	AF060570	AF060570 Mus muscu	1191	181	10.0	1952	6	CQ172446	CQ172446
1119	185.5	10.2	135055	2	AC010056	AC010056 Drosophill	1192	181	10.0	1952	6	CQ201614	CQ201614
1120	185.5	10.2	135055	2	AC011909	AC011909 Drosophill	1193	181	10.0	1952	6	CQ217152	CQ217152
1121	185.5	10.2	184266	2	AX571737	AX571737 Danio rer	1194	181	10.0	1952	6	CQ255729	CQ255729
1122	184.5	10.2	198	6	AR030587	AR030587 Sequence	1195	181	10.0	1952	6	CQ292826	CQ292826
1123	184.5	10.2	198	6	AR030588	AR030588 Sequence	1196	181	10.0	1952	6	CQ329804	CQ329804
1124	184.5	10.2	1391	6	AR322160	AR322160 Sequence	1197	181	10.0	2944	6	AX747451	AX747451
1125	184.5	10.2	1391	6	HUMRAGE	M91211 Human recep	1198	181	10.0	2944	9	AX092284	AX092284
1126	184.5	10.2	2139	5	BC073724	BC073724 Xenopus l	1199	181	10.0	3153	9	HSM804421	HSM804421
1127	184.5	10.2	3015	6	CQ842363	CQ842363 Sequence	1200	181	10.0	3261	3	AF456360	AF456360
1128	184.5	10.2	3015	6	AK123850	AK123850 Homo sapi	1201	181	10.0	3570	9	HSM803401	HSM803401
1129	184.5	10.2	9282	9	AY603755	AY603755 Homo sapi	1202	181	10.0	4591	9	HSM803659	HSM803659
1130	184.5	10.2	1524	6	CQ827992	CQ827992 Sequence	1203	181	10.0	4988	9	HSM806135	HSM806135
1131	184.5	10.2	1818	9	AY017369	AY017369 Homo sapi	1204	181	10.0	5929	9	HSM806135	HSM806135
1132	184.5	10.2	2013	10	RATMAG	M14871 Rat myelin-	1205	181	10.0	11008	3	AF078161	AF078161
1133	184.5	10.2	2348	10	RATMAG	M23357 Rat 1B236/m	1206	181	10.0	113063	2	AC010946	AC010946
1134	184.5	10.2	2468	10	RATMAG	M23357 Rat 1B236/m	1207	181	10.0	122493	2	AC023270	AC023270
1135	184.5	10.2	2475	6	AX700174	AX700174 Sequence	1208	181	10.0	202505	2	AP000912	AP000912
1136	184.5	10.2	2475	10	RATMAG	M16800 Rat 1B236/m	1209	180.5	10.0	2547	3	HV059448	HV059448
1137	184.5	10.2	2934	6	CQ828004	CQ828004 Sequence	1210	180.5	10.0	3729	10	AF168466	AF168466
1138	184.5	10.2	4640	3	DM2TRK	X63453 D.melanogas	1211	180.5	10.0	3943	10	AF172256	AF172256
1139	184.5	10.2	4645	6	CQ591393	CQ591393 Sequence	1212	180.5	10.0	4052	5	AY376855	AY376855
1140	184.5	10.2	4645	6	CQ847776	CQ847776 Sequence	1213	180.5	10.0	4239	6	E40576	E40576
1141	184.5	10.2	4775	3	BT015249	BT015249 Drosophill	1214	180.5	10.0	4239	6	E40577	E40577
1142	184.5	10.2	5505	5	AF487829	AF487829 Danio rer	1215	180.5	10.0	4603	10	AF191090	AF191090
1143	184.5	10.2	7789	6	AX746187	AX746187 Sequence	1216	180	10.0	1776	6	AX521472	AX521472
1144	183.5	10.2	1357	3	MSU11879	MSU11879 Manduca sex	1217	180	10.0	2106	6	AX393888	AX393888
1145	183.5	10.2	2728	6	CQ413817	CQ413817 Sequence	1218	180	10.0	2350	11	BV177759	BV177759
1146	183.5	10.2	3631	6	BD170702	BD170702 NF-kappa	1219	180	10.0	2656	6	BD157949	BD157949
1147	183.5	10.2	5303	6	CQ071561	CQ071561 Homo sapi	1220	180	10.0	2656	6	AX277406	AX277406
1148	183.5	10.2	6999	6	CQ874027	CQ874027 Sequence	1221	180	10.0	2656	6	AX879647	AX879647
1149	183.5	10.2	6999	9	AX310398	AX310398 Homo sapi	1222	180	10.0	2656	9	AX022708	AX022708
1150	183.5	10.2	822	5	BX931320	BX931320 Gallus ga	1223	180	10.0	6445	5	AX556703	AX556703
1151	183.5	10.1	2748	6	CQ869976	CQ869976 Sequence	1224	179.5	9.9	921	5	CR352648	CR352648
1152	183.5	10.1	69145	3	AF260530	AF260530 Drosophill	1225	179.5	9.9	1086	10	RNO401157	RNO401157
1153	183.5	10.1	79405	10	AL928721	AL928721 Mouse DNA	1226	179.5	9.9	1515	6	CQ603762	CQ603762
1154	182.5	10.1	1565	5	AF364048	AF364048 Gallus ga	1227	179.5	9.9	2118	6	CQ859389	CQ859389
1155	182.5	10.1	2118	6	CQ859385	CQ859385 Sequence	1228	179.5	9.9	2526	5	AY197498	AY197498
1156	182.5	10.1	2783	6	CQ580170	CQ580170 Sequence	1229	179.5	9.9	2532	5	AF389400	AF389400
1157	182.5	10.1	2931	10	MMU06483	MMU06483 Mus muscu	1230	179.5	9.9	2784	3	AX112938	AX112938
1158	182.5	10.1	3252	3	AF188751	AF188751 Caenorhab	1231	179.5	9.9	156150	5	BX322540	BX322540
1159	182.5	10.1	4188	3	AY051656	AY051656 Drosophill	1232	179.5	9.9	174574	2	BX927363	BX927363
1160	182.5	10.1	4734	10	RATFUT1	D28498 Rattus norv	1233	179	9.9	900	6	AX1702	AX1702
1161	182.5	10.1	4901	9	HSM807328	AF647184 Homo sapi	1234	179	9.9	930	6	BD023445	BD023445
1162	182.5	10.1	5201	3	AF275903	AF275903 Drosophill	1235	179	9.9	1374	6	AX1700	AX1700
1163	182.5	10.1	5923	5	AY603753	AY603753 Danio rer	1236	179	9.9	1374	6	BD023443	BD023443
1164	182.5	10.1	6374	6	AX497861	AX497861 Sequence	1237	179	9.9	1851	10	BC021876	BC021876
1165	182.5	10.1	1904	6	CQ721212	CQ721212 Sequence	1238	179	9.9	2029	10	MMU89915	MMU89915
1166	182.5	10.1	1969	9	AX050301	AX050301 Homo sapi	1239	179	9.9	2429	10	MUSMAGX	MUSMAGX
1167	182.5	10.1	2275	9	AX094545	AX094545 Homo sapi	1240	179	9.9	2700	6	AX497857	AX497857
1168	182.5	10.1	2350	6	AX335887	AX335887 Sequence	1241	179	9.9	2967	9	BC042054	BC042054
1169	182.5	10.1	2350	6	AX658213	AX658213 Sequence	1242	179	9.9	3022	9	BC067107	BC067107
1170	182.5	10.1	2350	9	HUMMAG	M29273 Human myeli	1243	179	9.9	3887	9	BC070119	BC070119
1171	182.5	10.1	2400	9	BC053347	BC053347 Homo sapi	1244	179	9.9	5494	6	CQ721268	CQ721268
1172	182.5	10.1	3464	6	AX359697	AX359697 Sequence	1245	178.5	9.9	1401	9	AK000845	AK000845

1246	178.5	9.9	2558	9	HSW801204	1319	175	9.7	2224	5	CR848573	CR848573	Xenopus t
1247	178.5	9.9	3236	9	AK095256	1320	175	9.7	5754	9	HSM805275	AL834247	Homo sapi
1248	178.5	9.9	3705	10	AF125521	c1321	175	9.7	117951	9	AL359821	AL359821	Human DNA
1249	178.5	9.9	3970	10	AF127255	174.5	9.7	9.7	4094	6	CQ714181	CQ714181	Sequence
1250	178.5	9.9	5820	10	AF161715	c1322	174	9.6	785	6	AR496309	AR496309	Sequence
1251	178.5	9.9	6847	6	CQ714785	c1324	174	9.6	785	6	AR511591	AR511591	Sequence
c1252	178.5	9.9	140127	2	AC141742	1325	174	9.6	868	5	BR933478	BR933478	Gallus ga
1253	178	9.9	1580	10	AF205078	1326	174	9.6	1034	5	CR387777	CR387777	Gallus ga
1254	178	9.9	2107	10	AY271309	1327	174	9.6	1744	5	BR935017	BR935017	Gallus ga
1255	178	9.9	2684	10	BC076588	1328	174	9.6	2716	5	BC056023	BC056023	Xenopus l
1256	178	9.9	3581	10	AK173081	1329	174	9.6	3128	3	AY113638	AY113638	Drosophil
1257	177.5	9.8	1752	4	AB039957	1330	174	9.6	3550	6	AX133825	AX133825	Sequence
1258	177.5	9.8	2525	3	AY052120	1331	174	9.6	3562	6	AX179300	AX179300	Sequence
1259	177.5	9.8	2763	5	PMFGR3	1332	174	9.6	3698	10	AY169782	AY169782	Mus muscu
1260	177.5	9.8	3749	10	AF525412	1333	174	9.6	4023	9	AF129167	AF129167	Chloroceb
1261	177.5	9.8	4980	3	AY060637	1334	174	9.6	5831	3	AY047563	AY047563	Drosophil
1262	177.5	9.8	5164	6	CQ572346	1335	174	9.6	14985	9	HSTITIN	XG9490 H. sapiens m	
1263	177.5	9.8	7080	10	AY353236	1336	174	9.6	16799	2	AC020355	AC020355	Drosophil
1264	177.5	9.8	7158	6	CQ714120	1337	174	9.6	23546	6	CQ573465	CQ573465	Sequence
1265	177.5	9.8	20448	6	CQ599466	1338	174	9.6	23546	6	CQ847884	CQ847884	Sequence
c1266	177.5	9.8	24971	6	CQ599465	1339	174	9.6	68727	3	AC004516	AC004516	Drosophil
1267	177.5	9.8	27060	3	AB055927	c1340	174	9.6	71023	2	AC004426	AC004426	Drosophil
c1268	177.5	9.8	53757	2	AC017325	1341	174	9.6	97698	2	AC019670	AC019670	Drosophil
1269	177.5	9.8	70398	3	DME271740	1342	174	9.6	113320	2	AC010662	AC010662	Drosophil
1270	177.5	9.8	121584	2	AC008232	1343	174	9.6	166417	10	AC127685	AC127685	Mus muscu
c1271	177.5	9.8	144056	3	AC091222	1344	174	9.6	193262	3	AC007579	AC007579	Drosophil
1272	177.5	9.8	194006	3	AC010063	c1345	174	9.6	260367	3	AE003808	AE003808	Drosophil
c1273	177.5	9.8	315108	3	AE003473	1346	173.5	9.6	1962	10	AK131121	AK131121	Mus muscu
1274	177	9.8	1129	5	AF337034	1347	173.5	9.6	2550	6	AR008527	AR008527	Sequence
1275	177	9.8	2899	10	BC049361	1348	173.5	9.6	2550	6	AR014315	AR014315	Sequence
1276	177	9.8	2959	9	BC064925	1349	173.5	9.6	2550	6	AR068074	AR068074	Sequence
1277	177	9.8	3757	9	AF151909	1350	173.5	9.6	2550	6	186161	186161	Sequence 10
1278	177	9.8	3768	9	AB102655	1351	173.5	9.6	2550	6	186871	186871	Sequence 10
1279	177	9.8	6726	6	AB037718	1352	173.5	9.6	2550	6	AX746327	AX746327	Sequence
1280	177	9.8	7710	6	AC056397	1353	173.5	9.6	2550	6	AX816907	AX816907	Sequence
c1281	177	9.8	153114	2	BR927068	1354	173.5	9.6	2550	6	BD064497	BD064497	ICAM-4 an
1282	177	9.8	158241	3	AC115483	1355	173.5	9.6	2565	6	AX365516	AX365516	Sequence
c1283	177	9.8	161682	3	AC092236	1356	173.5	9.6	2598	9	AK000681	AK000681	Homo sapi
c1284	177	9.8	180190	2	CR626902	1357	173.5	9.6	2764	6	CQ767791	CQ767791	Sequence
c1285	177	9.8	187746	2	AC087123	1358	173.5	9.6	2764	6	AX376050	AX376050	Sequence
c1286	177	9.8	193180	2	AC112588	1359	173.5	9.6	2764	9	AY358337	AY358337	Homo sapi
c1287	177	9.8	303885	3	DROSADH01	1360	173.5	9.6	2988	6	AR008519	AR008519	Sequence
c1288	177	9.8	304771	3	AE003641	1361	173.5	9.6	2988	6	AR014307	AR014307	Sequence
1289	176.5	9.8	905	6	AX136566	1362	173.5	9.6	2988	6	AR068066	AR068066	Sequence
1290	176.5	9.8	905	6	BD123806	1363	173.5	9.6	2988	6	186153	186153	Sequence 1
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1292	176.5	9.8	1655	9	BC013867	1365	173.5	9.6	2988	6	AX746318	AX746318	Sequence
1293	176.5	9.8	2178	6	AX224732	1366	173.5	9.6	2988	6	AX816898	AX816898	Sequence
1294	176.5	9.8	2667	9	BC013955	1367	173.5	9.6	2988	6	BD064489	BD064489	ICAM-4 an
1295	176.5	9.8	2920	6	AX833622	1368	173.5	9.6	3563	3	AY121627	AY121627	Drosophil
1296	176.5	9.8	2920	9	AK095512	1369	173.5	9.6	3660	5	CHKCC4	CHKCC4	Gallus gall
1297	176.5	9.8	3183	9	AF337818	1370	173.5	9.6	3983	6	CQ581133	CQ581133	Sequence
1298	176.5	9.8	4347	9	AB023209	1371	173	9.6	1367	3	AY515320	AY515320	Bombyx mo
1299	176.5	9.8	5482	10	NWEMRK2	1372	173	9.6	1369	3	AB115084	AB115084	Bombyx mo
1300	176.5	9.8	5773	9	AF464873	1373	173	9.6	1370	3	AY515322	AY515322	Bombyx mo
1301	176.5	9.8	7424	5	AF537107	1374	173	9.6	1440	5	BR934867	BR934867	Gallus ga
1302	176	9.7	843	6	CQ605682	1375	173	9.6	1451	5	BR936257	BR936257	Gallus ga
1303	176	9.7	1383	3	AY515323	1376	173	9.6	2307	10	AF247659	AF247659	Mus muscu
1304	176	9.7	2646	6	AX786890	1377	173	9.6	3189	9	AB081017	AB081017	Sequence
1305	176	9.7	2729	6	AX833631	1378	173	9.6	3768	9	AB102653	AB102653	Homo sapi
1306	176	9.7	2729	9	AK095529	1379	173	9.6	3774	6	AR036493	AR036493	Sequence
1307	176	9.7	3488	9	BC042432	1380	173	9.6	3774	6	AR081015	AR081015	Sequence
1308	176	9.7	3768	6	AB102654	1381	173	9.6	3774	6	AR081016	AR081016	Sequence
1309	176	9.7	3903	6	AX779837	1382	173	9.6	3888	6	AR177813	AR177813	Sequence
1310	176	9.7	3903	6	AX779838	1383	173	9.6	3888	6	AR177813	AR177813	Sequence
c1311	176	9.7	4443	6	CQ579749	1384	173	9.6	4522	6	CQ728130	CQ728130	Sequence
c1312	176	9.7	148432	3	AC004642	1385	173	9.6	4522	6	CQ728130	CQ728130	Sequence
c1313	176	9.7	154840	3	AC099018	1386	173	9.6	4523	9	HUMIGL1A	HUMIGL1A	Homo sapien
1314	176	9.7	157851	2	AC020509	c1387	173	9.6	255090	2	AC073798	AC073798	Mus muscu
c1315	176	9.7	303823	3	AE003462	1388	172.5	9.6	2019	10	BC025840	BC025840	Mus muscu
1316	175.5	9.7	224166	2	AC110955	1389	172.5	9.6	2273	9	AB072038	AB072038	Homo sapi
1317	175	9.7	711	9	AF529206	1390	172.5	9.6	6164	3	HMU92813	HMU92813	Hirudo medi
1318	175	9.7	2190	9	AX328482	1391	172	9.5	839	5	CR523669	CR523669	Gallus ga

1392	172	9.5	862	6	I08155	108155 Sequence 1	1465	169.5	9.4	3112	9	HSN803530	AL832223 Homo sapi
1393	172	9.5	862	6	HUMCEALV	M17191 Human carci	1466	169.5	9.4	3112	9	HSN807351	BX547207 Homo sapi
1394	172	9.5	2107	6	I07278	I07278 Sequence 25	1467	169.5	9.4	4017	6	AX481481	AX481481 Sequence
1395	172	9.5	2107	6	BD015200	T1isa cel	1468	169.5	9.4	4017	9	AF063657	AF063657 Homo sapi
1396	172	9.5	2116	6	AX380711	Sequence cel	1469	169.5	9.4	6602	4	AV136512	AV136512 Canis fam
1397	172	9.5	2116	9	HSCD22AG	Sequence C	1470	169	9.4	1339	6	I08161	I08161 Sequence 12
1398	172	9.5	2239	10	BC008528	BC008528 Mus muscu	1471	169	9.4	1339	6	I08164	I08164 Sequence 5
1399	172	9.5	3774	6	AX658201	AX658201 Sequence	1472	169	9.4	1339	6	BD260118	BD260118 Matrix-re
1400	172	9.5	3774	9	HSN803687	HSN803687 Homo sapi	1473	169	9.4	1339	6	I08159	I08159 Sequence 8
1401	172	9.5	4683	9	HSN803687	HSN803687 Homo sapi	1474	169	9.4	3173	6	I08162	I08162 Sequence 1
1402	172	9.5	5436	9	HSN803309	HSN803309 Homo sapi	1475	169	9.4	3173	9	HSTM2CEA	X14831 Human mRNA
1403	172	9.5	5449	9	HSN807783	HSN807783 Homo sapi	1476	169	9.4	3736	5	BC077548	BC077548 Xenopus l
1404	172	9.5	5707	9	AF328296	AF328296 Homo sapi	1477	169	9.4	3815	5	XELX1RGFR	M55163 Xenopus lae
1405	172	9.5	16114	3	AB062881	AB062881 Mytilus g	1478	169	9.4	4102	3	DMIRCRGHA	Z21641 D.melanogas
1406	172	9.5	267762	2	AC073817	AC073817 Mus muscu	1479	169	9.4	4102	3	DROIRRECRP	L11040 Drosophila
1407	171.5	9.5	2352	6	AR030849	AR030849 Sequence	1480	169	9.4	4200	3	AY508722	AY508722 Podocoryn
1408	171.5	9.5	2352	6	I82808	I82808 Sequence 17	1481	169	9.4	5406	10	HSN807786	BX647640 Homo sapi
1409	171.5	9.5	2448	9	AV358135	AV358135 Homo sapi	1482	169	9.4	5580	5	AY744917	AY744917 Petromyzo
1410	171.5	9.5	2791	3	AY069421	AY069421 Drosophill	1483	169	9.4	5697	5	AY744918	AY744918 Petromyzo
1411	171.5	9.5	4014	6	AR397397	AR397397 Sequence	1484	168.5	9.3	1743	5	BX950651	BX950651 Gallus ga
1412	171.5	9.5	6227	3	AF017083	AF017083 Hirudo me	1485	168.5	9.3	2604	3	AF419623	AF419623 Drosophill
1413	171.5	9.5	7680	6	AX489880	AX489880 Sequence	1486	168.5	9.3	2975	3	AY089606	AY089606 Drosophill
1414	171.5	9.5	7680	6	AX926525	AX926525 Sequence	1487	168.5	9.3	6604	10	AV351699	AV351699 Mus muscu
1415	171.5	9.5	7680	6	AX951178	AX951178 Sequence	1488	168.5	9.3	6655	10	BC060237	BC060237 Mus muscu
1416	171.5	9.5	7680	6	AX960056	AX960056 Sequence	1489	168.5	9.3	8188	10	AK129379	AK129379 Mus muscu
1417	171.5	9.5	7680	9	HSFLT	HSFLT Human flt m	1490	168	9.3	648	6	CQ582024	CQ582024 Sequence
1418	171.5	9.5	9295	6	CQ573225	CQ573225 Sequence	1491	168	9.3	2383	6	AR030850	AR030850 Sequence
1419	171.5	9.5	31595	6	AX780060	AX780060 Sequence	1492	168	9.3	2383	6	I82809	I82809 Sequence 18
1420	171.5	9.5	81940	9	HSPITIN2B	X90568 H.sapiens m	1493	168	9.3	4241	5	BC073428	BC073428 Xenopus l
1421	171	9.5	1265	9	HSTM3CEA	X16356 Human mRNA	1494	168	9.3	10961	6	CQ789656	CQ789656 Sequence
1422	171	9.5	1473	6	A43165	A43165 Sequence 31	1495	168	9.3	19994	9	HSTITINX5	X92412 H.sapiens t
1423	171	9.5	1473	6	AR079551	AR079551 Sequence	1496	167.5	9.3	842	6	AR506523	AR506523 Sequence
1424	171	9.5	1473	6	S71326	S71326 BGPC=biilar	1497	167.5	9.3	1815	5	CRANEUR	L25056 Carassius a
1425	171	9.5	1630	6	I08160	I08160 Sequence 10	1498	167.5	9.3	2828	6	CQ782716	CQ782716 Sequence
1426	171	9.5	1630	6	I08163	I08163 Sequence 3	1499	167.5	9.3	2828	6	BD127278	BD127278 Primer fo
1427	171	9.5	1636	9	BC014473	BC014473 Homo sapi	1500	167.5	9.3	2828	9	AK074780	AK074780 Homo sapi
1428	171	9.5	2197	9	HUMBGP1	J03858 Human bilia							
1429	171	9.5	3461	6	I08157	I08157 Sequence 4							
1430	171	9.5	3461	6	I08167	I08167 Sequence 10							
1431	171	9.5	3464	6	CQ834029	CQ834029 Sequence							
1432	171	9.5	3464	6	CQ875303	CQ875303 Sequence							
1433	171	9.5	3464	6	AX330303	AX330303 Sequence							
1434	171	9.5	3464	6	AX818143	AX818143 Sequence							
1435	171	9.5	3464	9	HSTM1CEA	X16354 Human mRNA							
1436	171	9.5	4455	3	AY128456	AY128456 Drosophill							
1437	171	9.5	8882	6	CQ583050	CQ583050 Sequence							
1438	171	9.5	28280	3	AB079865	AB079865 Bombyx mo							
1439	171	9.5	160000	3	AB090307	AB090307 Bombyx mo							
c1440	171	9.5	172828	9	AC009948	AC009948 Homo sapi							
1441	170.5	9.4	1113	5	AY197501	AY197501 Danio rer							
1442	170.5	9.4	1504	4	AY568565S1	AY568565 Bos tauru							
1443	170.5	9.4	1566	4	OCY13243	Y13243 Oryctolagus							
1444	170.5	9.4	2267	3	BT011127	BT011127 Drosophill							
1445	170.5	9.4	2855	6	AX747111	AX747111 Sequence							
1446	170.5	9.4	2655	9	AC091650	AC091650 Homo sapi							
1447	170.5	9.4	2877	9	BC034471	BC034471 Homo sapi							
1448	170.5	9.4	2882	9	BC028698	BC028698 Homo sapi							
1449	170.5	9.4	3902	3	AY060635	AY060635 Drosophill							
1450	170.5	9.4	8577	6	CQ612483	CQ612483 Sequence							
1451	170	9.4	1422	9	HUMCEAX	M18234 Human carci							
1452	170	9.4	1676	10	BC065309	BC065309 Rattus no							
1453	170	9.4	1802	5	BC080901	BC080901 Rattus t							
1454	170	9.4	1895	10	AF276998	AF276998 Rattus no							
1455	170	9.4	2226	6	CQ716446	CQ716446 Sequence							
1456	170	9.4	2520	9	BC025268	BC025268 Homo sapi							
1457	170	9.4	3446	9	HSN804897	HSN804897 Homo sapi							
1458	170	9.4	3634	5	XL024491	XL024491 Xenopus lae							
c1459	170	9.4	207692	2	CR790369	CR790369 Danio rer							
c1460	170	9.4	213785	2	CR788255	CR788255 Danio rer							
1461	169.5	9.4	1420	10	RATRECEP	L33413 Rat recepto							
1462	169.5	9.4	1615	5	BC055118	BC055118 Danio rer							
1463	169.5	9.4	1819	9	AY305302	AY305302 Homo sapi							
1464	169.5	9.4	2832	6	CQ580356	CQ580356 Sequence							

ALIGNMENTS

RESULT 1	AR439648	Sequence 1	1032 bp	DNA	linear	PAT 20-FEB-2004
AR439648	LOCUS	Sequence 1 from patent US 6664383.				
	DEFINITION	AR439648				
	ACCESSION	AR439648				
	VERSION	AR439648.1	GI:42665572			
	KEYWORDS	Unknown.				
	SOURCE	Unknown.				
	ORGANISM	Unclassified.				
	REFERENCE	1 (bases 1 to 1032)				
	AUTHORS	Fukushima,D., Shibayama,S. and Tada,H.				
	TITLE	Polypeptides, cDNA encoding the same and utilization thereof				
	JOURNAL	Patent: US 6664383-A 1 16-DEC-2003;				
	FEATURES	Location/Qualifiers				
	source	1..1032				
	ORIGIN	/organism="unknown"				
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Pred. No.:	6.44e-158	Length:	1032			
Score:	1806.00	Matches:	344			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			
US-10-017-084A-523 (1-344) x AR439648 (1-1032)						
Qy	1 MetlysthrileGlnProlysmethHisasnSerlleSertTroAlailepHethrGlyleu 20					
Db	1 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTTGGGCAATCTTTCACGGGGCTG 60					

QY 21 AlaalaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40
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QY 101 GluIleGlnAenValAspValTyAspGluGlyProTyThrCysSerValGlnThrAsp 120
Db 301 GAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACGAC 360
QY 121 AenHisProlysThrSerArgValHisLeuIleValGlnValSerProLySileValGlu 140
Db 361 AACCAACCACAGACCTTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTGTAG 420
QY 141 IleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIleAlaThr 160
Db 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCCTCACCTGATAGCAACT 480
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLySAlaValGlyPheVal 180
Db 481 GGTAGACACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
QY 181 SerGluAspGluTyLeuGluIleGlnGlyLeThrArgGluGlnSerGlyAspTyGlu 200
Db 541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
QY 201 CysSerAlaSerAenAspValAlaAlaProValValArgValLysValThrValAen 220
Db 601 TGCAGTGCCTCCAAATGACGTGGCGCCGCCCGTGGTACCGAGAGTAAGGTCAACGTGAAC 660
QY 221 TyrProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 661 TATCCACCATACTATTCAGAGCCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyTrpLysAspAspLys 260
Db 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCCCTCAGCAGAAATTCAGTGTGTAACAAGATGACAAA 780
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
Db 781 AGACTGATGTAAGGAAGAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
QY 281 IlePhePheAenValSerGluHisAspTyTrpGlyAenTyThrCysValAlaSerAenLys 300
Db 841 ATCTTCTCATGTCTCTGAACATGACTATGGGAATCTACCTTGGTGGCTTCCACACAG 900
QY 301 LeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 901 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 960
QY 321 AenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValIleHisLeu 340
Db 961 AACGGCACGTGAGAGGGGAGGCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 1020
QY 341 LeuLeuLysPhe 344
Db 1021 CTTCTCAATTT 1032

RESULT 2
CQ768055
LOCUS
DEFINITION Sequence 522 from Patent EPI386931.
1679 bp DNA linear PAT 04-MAR-2004

ACCESSION CQ768055
VERSION CQ768055.1 GI:45108887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.
AUTHORS Human neurotrophin Homologue
TITLE Patent: EP 1386931-A 522 04-FEB-2004;
JOURNAL Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..1679
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 1.19e-157 Length: 1679
Pred. No.: 1806.00 Matches: 344
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
US-10-017-084A-523 (1-344) x CQ768055 (1-1679)
QY 1 MetLysThrIleGlnProLySMetHisAenSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCATCCAGCCAAATAATGCACAAATCTATCTCTGGCAATCTTCCAGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGGCGACGGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATTTGAC 313
QY 61 AenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyAlaGlyAenAsp 80
Db 314 AACCGGGTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrSerIle 100
Db 374 AAGTGGTCCCTGGATCTCCGGGTGGTCTCTTGAGCAACACCCAAACGATGACGATC 433
QY 101 GluIleGlnAenValAspValTyAspGluGlyProTyThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACGAC 493
QY 121 AenHisProLySThrSerArgValHisLeuIleValGlnValSerProLySileValGlu 140
Db 494 AACCAACCACAGACCTTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTGTAG 553
QY 141 IleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCCTCACCTGATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLySAlaValGlyPheVal 180
Db 614 GGTAGACACAGACCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyLeuGluIleGlnGlyLeThrArgGluGlnSerGlyAspTyGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAenAspValAlaAlaProValValArgValLysValThrValAen 220
Db 734 TGCAGTGCCTCCAAATGACGTGGCGCCGCCCGTGGTACGGAGAGTAAGGTCAACCGTGAAC 793

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QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCACCACATACATTTCAAGAACCCAAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGCAATTCAGGTGTACAAGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAAATC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTAATTTGGTCCAGGCGCCGTGAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGSCAGTCGAGGAGGCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 3
AR528639 AR528639 1679 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 375 from patent US 6725730.
DEFINITION AR528639
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Bollinger,C.L., Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 375 27-APR-2004;
FEATURES Location/Qualifiers
source 1..1679
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AR528639 (1-1679)

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QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGCAACGTGACGTCGCGGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTTGATGTATGACAGAGGCCCTTACACCTGCTGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACAGAGCCCTACCGTTACTTTGGAGACACATCTCTCCAAAGCCGTTGGCTTTGTG 673
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QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValLysValThrValAsn 220
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QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCACCACATACATTTCAAGAACCCAAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGCAATTCAGGTGTACAAGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAAATC 973
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QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGSCAGTCGAGGAGGCGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 4
AX358872 AX358872 1679 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 125 from Patent WO0193983.
DEFINITION AX358872
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secretd and transmembrane polypeptides and nucleic acids encoding
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the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AX358872 (1-1679)

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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGCGCAGGAGATGCCCTTCCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGTCGCGCAGCGGAGAGCGCCACCTTCAGGTGCATTTGAC 313

Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyfAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373

Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyfSerIle 100
Db 374 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGGACAACACCCAAACGATCAGCATC 433

Qy 101 GluIleGlnAsnValAspValTyfAspGluGlyProTyfThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGATGTATGACGAGGCGCTTACACCTGCTGCTGCAGACAGAC 493

Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGATAG 553

Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTCTCAGATATCTCCATTATAGGGGAACAAATATTAGCTCACCCTGCATAGCAACT 613

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Qy 221 TyrProProTyfIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCCTCAGCAGAAATTCAGTGTGTAACAGGATGACAAA 913

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Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 5
AX362365
LOCUS AX362365 1679 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AX362365 (1-1679)

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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGCGCAGGAGATGCCCTTCCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGTCGCGCAGCGGAGAGCGCCACCTTCAGGTGCATTTGAC 313

Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyfAlaGlyAsnAsp 80
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Db 374 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGGACAACACCCAAACGATCAGCATC 433

Qy 101 GluIleGlnAsnValAspValTyfAspGluGlyProTyfThrCysSerValGlnThrAsp 120
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Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCATGTCAGGGGACTTACAG 733

Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 734 TGCAGTGGCTCCATGAGTGGCCGCGCGCTGGTACGGAGATTAAGGTCAACGTGAAC 793

Qy 221 TyrProProTyfIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db 374 AAGTGTGCTGGATCCTCGCGTGGCTCTTTCAGAGCAACACCCAAACGCGATACAGATC 433
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Db 434 GAGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuileValGlnValSerProLysleValGlu 140
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QY 141 IleSerSerAspIleSerleAenGluGlyAsnAsnIleSerleuThrCysleAlaThr 160
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QY 321 AenGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCACGTCGAGGAGGCGGCTCGCTGGCTGCTGCTGCTCTTCTTGTGCTTGCACCTG 1153
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Db 1154 CTCTCAATTT 1165

RESULT 6

AX403748
LOCUS AX403748 1679 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 103 from Patent WO0077037.
ACCESSION AX403748
VERSION AX403748.1 GI:21437184

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

TITLE

The same

JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;

Genentech Inc. (US)

FEATURES

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Alignment Scores:

Pred. No.: 1..19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-10-017-084A-523 (1-344) x AX403748 (1-1679)

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Db 254 GCTATGGACACGTGACGCTCCGGCAGGGGAGAGCCGCCCTCAGGTGCATATTGAC 313
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QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db 1154 CTTCTCAAAATTT 1165

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DEFINITION Sequence 55 from Patent WO0208284.
ACCESSION AX454470
VERSION AX454470.1 GI:21713859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, K.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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/organism="Homo sapiens"
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ORIGIN
Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
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Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

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Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATATTAGCCTCACCTGCATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTrrArgHisIleSerProLysAlaValGlyPheVal 180
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LOCUS AX464242 1679 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 375 from Patent WO0140466.
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
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Gao, W. Q., Gerritsen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L., Sherwood, S., Smith, V., Stewart, T. A., Tumas, D., Watanabe, C. K., Wood, W. L. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

Patent: WO 0140466-A 375 07-JUN-2001; sale

Genentech Inc. (US)

Location/Qualifiers

1. .1679

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ORIGIN

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Score:	1806.00	344
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Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
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US-10-017-084A-523 (1-344) X AX464242 (1-1679)

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VERSION AV358331.1 GI:37181786
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1679)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
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Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAATACACTTGGTGGCTTCTCTCAAAACTC 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy 341 LeuLeuLysPhe 344
Db 1154 CTTTCAAAATTT 1165

RESULT 11
AR439649
LOCUS AR439649 1693 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2 from patent US 6664383.
ACCESSION AR439649
VERSION AR439649.1 GI:42665573
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1693)
AUTHORS Fukushima,D., Shibayama,S. and Tada,H.
TITLE Polypeptides, cDNA encoding the same and utilization thereof
JOURNAL Patent: US 6664383-A 2 16-DEC-2003;
FEATURES
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-017-084A-523 (1-344) x AR439649 (1-1693)

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DEFINITION Mus musculus neurotrophin, mRNA (cDNA clone MGC:30504
IMAGE:4480983), complete cds.
ACCESSION BC023307
VERSION BC023307.1 GI:23958300
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1615)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altekar, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shchepochko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length

TITLE

human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1615)
Strausberg, R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it
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Query Match: 91.22% Indels: 3
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US-10-017-084A-523 (1-344) x BC023307 (1-1615)

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: June 16, 2005, 10:23:02 ; Search time 643 Seconds
(without alignments)
3167.016 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
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ID AAZ47892 standard; cDNA; 1032 BP.
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PN WO958668-A1.
PD 18-NOV-1999.
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
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PD 21-DEC-2000.
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PN WO200200690-A2.
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PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
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PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
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PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
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PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
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PA (GETH) GENENTECH INC.
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PD 14-NOV-2002.
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PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
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DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA04211 standard; cDNA; 1679 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
FN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA65657 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADA76325 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ABT44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26

ID ADA61598 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 27
ID ADB19383 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 28
ID ADB27924 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 29
ID ADA86403 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 30
ID ADB15967 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 31
ID ADA47753 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 32
ID ADA67548 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 33
ID ADB30555 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 34
ID ADA85851 standard; cDNA; 1679 BP.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 35
ID ADA97063 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 36
ID ADA79367 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 37
ID ADA87506 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 38
ID ADB16708 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 39
ID ADA91800 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 40
ID ADB14863 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 41
ID ADA25061 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 42
ID ADA47275 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.

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PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 43
ID ADB1824 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 44
ID ADA94039 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 45
ID ADB1935 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 46
ID ADB13247 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 47
ID ACD98611 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 48
ID ACD30038 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 49
ID ADAL2722 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 50
ID ADA74501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068798-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 51
ID ADB24734 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 52
ID ADA82258 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 53
ID ADA75221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 54
ID ADA85299 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 55
ID ADA84747 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 56
ID ADB30003 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 57
ID ADA80531 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 58
ID ADA75773 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 59
ID ADA46998 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 60
ID ADB25294 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 61
ID ADA93470 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 62
ID ADB26820 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 63
ID ADB31107 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 64
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 65
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 66
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 67
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082890-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 68
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 69
ID ADA95959 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 70
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 71
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 72
ID ACD82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 73
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 74
ID ADA77532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 75
ID ADB18272 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADA8058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADA8610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
FN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.
FN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADA66996 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADB22857 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADB23630 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADA92352 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
```

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PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 92
ID ADB15415 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 93
ID ADB83615 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 94
ID ADB80721 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003080668-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 95
ID ADB73262 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200309368-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 96
ID ADB38667 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 97
ID ADB78344 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 98
ID ADB38115 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 99
ID ADB66587 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082689-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 100
ID ADB84992 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 101
ID ADB89667 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 102
ID ADB90399 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 103
ID ADB39500 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 104
ID ADB78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 105
ID ADB74028 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 106
ID ADB87164 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 107
ID ADB84746 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 108
ID ADB47123 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 109
ID ADB83861 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 110
ID ADB86730 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 111
ID ADB73016 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 112
ID ADB76744 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 113
ID ADB77335 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 114
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 115
ID ADB35596 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 116
ID ADB33940 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 117
ID ADB35044 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 118
ID ADB36148 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 119
ID ADB46543 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 120
ID ADC44170 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 121
ID ADC61930 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 122
ID ADC63894 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 123
ID ADC66994 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 124			
ID ADC69118 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003064407-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 125			
ID ADC63178 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003068648-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 126			
ID ADC68243 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003069178-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 127			
ID ADC11563 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003072745-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 128			
ID ADC67618 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003073131-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 129			
ID ADC62554 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003073624-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 130			
ID ADC36854 standard; cDNA; 1679 BP.			
DE Human PRO polynucleotide #63.			
PN US2003088065-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 131			
ID ADC42187 standard; cDNA; 1679 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.			
PN US2003104998-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 132			
ID ADC21844 standard; cDNA; 1679 BP.			
DE Human PRO polynucleotide #63.			
PN US2003096969-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 133			
ID ADC50416 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003092106-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 134			
ID ADC71963 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003092107-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 135			
ID ADC59942 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003092105-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 136			
ID ADC49875 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003088064-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 137			
ID ADC49074 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003088070-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 138			
ID ADC49591 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003088071-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 139			
ID ADC47452 standard; cDNA; 1679 BP.			
DE Novel human secreted and transmembrane protein PRO3337 cDNA.			
PN US2003088072-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

RESULT 140
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 141
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 142
ID ADC60494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 143
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 144
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 145
ID ADC54594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 146
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 147
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 148
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

ID ADC5956 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 149
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
FN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 150
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 151
ID ADD03200 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 152
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 153
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 154
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 155
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 156
ID ADC78072 standard; cDNA; 1679 BP.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 157
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 158
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 159
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 160
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 161
ID ADD10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 162
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 163
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 164
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 165
ID ADD11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 166
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 167
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 168
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 169
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 170
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 171
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 172
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 173
ID ADD37097 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 174
ID ADD51777 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 175
ID ADD02576 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 176
ID ADD50516 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 177
ID ADD02010 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 178
ID ADD54192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 179
ID ADD050270 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 180
ID ADD51281 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 181
ID ADE49556 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 182
ID ADD92509 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200319030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 183
ID ADD91405 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200319055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 184
ID ADE04019 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200319057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 185
ID ADE32316 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 186
ID ADE22248 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 187
ID ADD79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 188
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADE16724 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADD7339 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADE42008 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADE17825 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADD91957 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ADE33420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ADE33972 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ADD80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ADD93061 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ADD72697 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ADE19481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 200
ID ADE18929 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 201
ID ADE43125 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ADD95914 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 203
ID ADE22800 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 204
ID ADD78918 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 205
ID ADE33972 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADD80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

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Query Match: 100.00% Indels: 0
RESULT 205
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID AD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADE4088 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 213
ID ADE47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADF97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADG53119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADG80013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
```

ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 222

ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 223

ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 224

ID ADI61199 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 225

ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 226

ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 227

ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 228

ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 229

ID ADH81386 standard; cDNA; 1679 BP.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 230

ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 231

ID ACA66903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 232

ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 233

ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 234

ID ACD68655 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003045697-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 235

ID ACA67181 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 236

ID ADM82555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 237

ID ADNI5954 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

```
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 238
ID ADN16583 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 239
ID ADN15402 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 240
ID ADN14850 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 241
ID ADC48828 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 242
ID ADC61112 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 243
ID ADE20999 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 244
ID ADE05843 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 245
ID ADD76560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003100087-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 246
ID ADD75072 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 247
ID ADD75618 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 248
ID ADD85050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 249
ID ADD86876 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 250
ID ADE20753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 251
ID ADE39050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 252
ID ADD87924 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 253
ID ADD86328 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

ID ADE05597 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 255
ID ADD73582 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 256
ID ADE75776 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 257
ID ADE48856 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 258
ID ADD78422 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 259
ID ADE41305 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 260
ID ADE23352 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 261
ID ADE21245 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 262
ID ADD77360 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 263
ID ADE20507 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 264
ID ADD75572 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100664-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 265
ID ADD74088 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 266
ID ADD74334 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 267
ID ADD76064 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 268
ID ADD85556 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 269
ID ADE23904 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0


```
ID ADD77852 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 284
ID ADD85310 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 285
ID ADD73842 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 286
ID ADD74580 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 287
ID ADD77108 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 288
ID ADD85802 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 289
ID ADE05351 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 290
ID ADD74826 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 291
ID ADF61597 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 292
ID ADF40289 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 293
ID ADF46085 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 294
ID ADE94706 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 295
ID ADE93117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 296
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 297
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 298
ID ADF24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 299
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
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PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 300
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 301
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 303
ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 304
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 305
ID ADE92264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 306
ID AD890565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 307
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 308
ID ADF3216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 309
ID ADF25582 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 310
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 311
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 312
ID ADF46709 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 313
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 314
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 315
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 316
ID ADG02291 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 317
ID ADG22077 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 318
ID ADG20147 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 319
ID ADF98053 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 320
ID ADG24270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 321
ID ADF98624 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 322
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 323
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 324
ID ADG16761 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 325
ID ADG05220 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 326
ID ADG19487 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 327
ID ADG11255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 328
ID ADG13324 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 329
ID ADG08381 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 330
ID ADG15551 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 331
ID ADG12034 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 332
ID ADF96949 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207371-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 333
ID ADG06134 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207374-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 334
ID ADG23718 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 335
ID ADG04007 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 336
ID ADG24908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 337
ID ADF94591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 338
ID ADG07205 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 339
ID ADG07757 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

Query Match: 100.00% Indels: 0
RESULT 340
ID ADG06687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 341
ID ADG5252 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 342
ID ADG60916 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 343
ID ADG62020 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 344
ID ADG82221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 345
ID ADG57460 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 346
ID ADG56908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 347
ID ADG55804 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 348
ID ADG58564 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 349
ID ADG70930 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 350
ID ADH39031 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 351
ID ADG58012 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 352
ID ADG53596 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 353
ID ADG71482 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 354
ID ADG50695 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 355
ID ADG81669 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 356
ID ADH30631 standard; cDNA; 1679 BP.

DE Human PRO polynucleotide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 357
ID ADG63633 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 358
ID ADH1998 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 359
ID ADG50071 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 360
ID ADG51943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 361
ID ADG52420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 362
ID ADG54148 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 363
ID ADG49447 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 364
ID ADG81117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

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PN US2003194793-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 365
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 366
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 367
ID ADG48823 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 368
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 369
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 370
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 371
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 372
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
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PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 373
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 374
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 375
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 376
ID ADG62719 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 377
ID ADI81164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 378
ID ADI33591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 379
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 380
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EPI386931-A1.
PD 04-FEB-2004.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 381
ID ADG09907 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 382
ID ADI15378 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 383
ID ADG09255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 384
ID ADI14710 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 385
ID ADI29846 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 386
ID ADI18305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 387
ID ADM27243 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 388
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 389
ID ADJ77481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 390
ID ADK82833 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 391
ID ADK66601 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 392
ID ADJ65603 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 393
ID ADM27739 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 394
ID ADI17521 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 395
ID ADL07355 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 396
ID ADM42463 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 397
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 397
ID AD28325 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 398
ID AD195807 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 399
ID AD196359 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 400
ID AA247893 standard; cDNA; 1693 BP.
DE Human protein encoding cDNA SEQ ID NO:3.
FN WO9958668-A1.
PD 18-NOV-1999.
PA (ONVOY) ONO PHARM CO LTD.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 401
ID AA88790 standard; cDNA; 1603 BP.
DE Human SECX cDNA Clone 11753149.0.6.
FN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 402
ID ADD18288 standard; DNA; 1603 BP.
DE Human molecule (MOL) protein MOL10 DNA sequence.
FN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 403
ID AA88791 standard; cDNA; 2012 BP.
DE Human SECX cDNA Clone 11753149.0.37.
FN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 404
ID ADD18290 standard; DNA; 2012 BP.
DE Human molecule (MOL) protein MOL11 DNA sequence.
FN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0

Query Match: 99.61% Indels: 0
RESULT 405
ID ABK49272 standard; cDNA; 1873 BP.
DE Human Kruppel associated DNA binding protein 42 cDNA.
FN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Percent Similarity: 89.32% Conservative: 0
Best Local Similarity: 89.32% Mismatches: 1
Query Match: 97.23% Indels: 41
RESULT 406
ID AAI59655 standard; cDNA; 1690 BP.
DE Human polynucleotide SEQ ID NO 3644.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 97.01% Indels: 3
RESULT 407
ID AD121360 standard; cDNA; 1690 BP.
DE Novel human expressed sequence tag, EST #59.
FN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 97.01% Indels: 3
RESULT 408
ID ABT17393 standard; DNA; 1061 BP.
DE Human IG gene related nucleic acid SEQ ID No 19.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 409
ID AAI57869 standard; cDNA; 1678 BP.
DE Human polynucleotide SEQ ID NO 72.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 410
ID ABT17390 standard; DNA; 1839 BP.
DE Human IG gene related nucleic acid SEQ ID No 16.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 411
ID ABX76448 standard; DNA; 1839 BP.
DE Lung cancer-associated polynucleotide #312.
FN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 412
ID ADG63208 standard; DNA; 1839 BP.
DE Human neurotrophin DNA.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2

RESULT 413
 ID ADN19137 standard; cDNA; 1839 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 97.31%
 Best Local Similarity: 96.41%
 Query Match: 92.22%
 Conservatives: 3
 Mismatches: 8
 Indels: 2
 RESULT 414
 ID ADI21817 standard; cDNA; 2884 BP.
 DE Novel human protein cDNA #76.
 PN WO2003025148-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 97.31%
 Best Local Similarity: 96.41%
 Query Match: 92.22%
 Conservatives: 3
 Mismatches: 8
 Indels: 2
 RESULT 415
 ID ADQ22984 standard; DNA; 3987 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 97.31%
 Best Local Similarity: 96.41%
 Query Match: 92.22%
 Conservatives: 3
 Mismatches: 8
 Indels: 2
 RESULT 416
 ID ADQ24601 standard; DNA; 3987 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 97.31%
 Best Local Similarity: 96.41%
 Query Match: 92.22%
 Conservatives: 3
 Mismatches: 8
 Indels: 2
 RESULT 417
 ID ADG63210 standard; DNA; 1068 BP.
 DE Human neurotrophin DNA +33bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Percent Similarity: 94.20%
 Best Local Similarity: 93.33%
 Query Match: 91.36%
 Conservatives: 3
 Mismatches: 8
 Indels: 13
 RESULT 418
 ID ABT17391 standard; DNA; 1094 BP.
 DE Human IG gene related nucleic acid SEQ ID No 17.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 94.20%
 Best Local Similarity: 93.33%
 Query Match: 91.36%
 Conservatives: 3
 Mismatches: 8
 Indels: 13
 RESULT 419
 ID ADI35771 standard; DNA; 2129 BP.
 DE Human neurotrophin DNA.
 PN US2003100485-A1.
 PD 29-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 94.20%
 Best Local Similarity: 93.33%
 Query Match: 91.36%
 Conservatives: 3
 Mismatches: 8
 Indels: 13
 RESULT 420
 ID ADG63212 standard; DNA; 1104 BP.
 DE Human neurotrophin DNA +69bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Percent Similarity: 91.04%
 Best Local Similarity: 90.20%
 Query Match: 91.03%
 Conservatives: 3
 Mismatches: 8
 Indels: 25
 RESULT 421

ID ABT17392 standard; DNA; 1130 BP.
 DE Human IG gene related nucleic acid SEQ ID No 18.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 91.04%
 Best Local Similarity: 90.20%
 Query Match: 91.03%
 Conservatives: 3
 Mismatches: 8
 Indels: 25
 RESULT 422
 ID AA247894 standard; cDNA; 939 BP.
 DE Human protein encoding cDNA SEQ ID NO:5.
 PN WO9558668-A1.
 PD 18-NOV-1999.
 PA (ONOV) ONO PHARM CO LTD.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 90.92%
 Conservatives: 0
 Mismatches: 0
 Indels: 0
 RESULT 423
 ID ADG63214 standard; DNA; 1140 BP.
 DE Human neurotrophin DNA +108bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Percent Similarity: 88.08%
 Best Local Similarity: 87.26%
 Query Match: 90.70%
 Conservatives: 3
 Mismatches: 8
 Indels: 37
 RESULT 424
 ID ADE07017 standard; DNA; 3298 BP.
 DE Novel coding sequence (useful for identifying genetic disorders) #83.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 82.89%
 Best Local Similarity: 71.39%
 Query Match: 71.79%
 Conservatives: 39
 Mismatches: 57
 Indels: 1
 RESULT 425
 ID AAQ51015 standard; cDNA; 3069 BP.
 DE Rat opioid receptor gene.
 PN WO321309-A1.
 PD 28-OCT-1993.
 PA (LEEN) LEE N M.
 PA (LOHH) LOH H H.
 PA (LIPP) LIPPMAN D.
 Percent Similarity: 82.01%
 Best Local Similarity: 71.39%
 Query Match: 71.23%
 Conservatives: 36
 Mismatches: 60
 Indels: 1
 RESULT 426
 ID ABT17408 standard; DNA; 1071 BP.
 DE Human IG gene related nucleic acid SEQ ID No 34.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 83.28%
 Best Local Similarity: 72.24%
 Query Match: 70.21%
 Conservatives: 37
 Mismatches: 54
 Indels: 3
 RESULT 427
 ID ABT17407 standard; DNA; 1080 BP.
 DE Human IG gene related nucleic acid SEQ ID No 33.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 83.28%
 Best Local Similarity: 72.24%
 Query Match: 70.21%
 Conservatives: 37
 Mismatches: 54
 Indels: 3
 RESULT 428
 ID ABT17409 standard; DNA; 1478 BP.
 DE Human IG gene related nucleic acid SEQ ID No 35.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 83.28%
 Best Local Similarity: 72.24%
 Query Match: 70.21%
 Conservatives: 37
 Mismatches: 54
 Indels: 3

RESULT 429
ID ABT17406 standard; DNA; 3110 BP.
DE Human IG gene related nucleic acid SEQ ID No 32.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 430
ID ADG63206 standard; DNA; 3110 BP.
DE Opioid-binding protein/cell adhesion molecule-like DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 431
ID AAQ51017 standard; cDNA; 2179 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Percent Similarity: 81.31%
Best Local Similarity: 71.22%
Query Match: 69.77%
Conservative: 34
Mismatches: 59
Indels: 4
RESULT 432
ID AAQ51016 standard; cDNA; 2337 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Percent Similarity: 81.31%
Best Local Similarity: 71.22%
Query Match: 69.71%
Conservative: 34
Mismatches: 59
Indels: 4
RESULT 433
ID AAA44536 standard; cDNA; 832 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1111.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 99.56%
Best Local Similarity: 99.11%
Query Match: 64.95%
Conservative: 1
Mismatches: 1
Indels: 0
RESULT 434
ID ABT17404 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 30.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 435
ID AAL50356 standard; cDNA; 1411 BP.
DE Human limbic system associated membrane protein 36-85 coding sequence.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Percent Similarity: 72.62%
Best Local Similarity: 53.87%
Query Match: 51.63%
Conservative: 63
Mismatches: 85
Indels: 7
RESULT 436
ID ABT17402 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 28.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 437
ID ABX63560 standard; cDNA; 1195 BP.
DE Human cDNA #560 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 438
ID ADL12674 standard; cDNA; 1195 BP.
DE Human steroid-induced C3A liver cell cDNA #403.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 439
ID AAT42081 standard; cDNA to mRNA; 1014 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 73.54%
Best Local Similarity: 55.08%
Query Match: 51.30%
Conservative: 60
Mismatches: 81
Indels: 5
RESULT 440
ID AAT42080 standard; cDNA to mRNA; 1238 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 73.54%
Best Local Similarity: 55.08%
Query Match: 51.30%
Conservative: 60
Mismatches: 81
Indels: 5
RESULT 441
ID ABT17403 standard; DNA; 1075 BP.
DE Human IG gene related nucleic acid SEQ ID No 29.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 71.51%
Best Local Similarity: 53.71%
Query Match: 51.19%
Conservative: 60
Mismatches: 79
Indels: 17
RESULT 442
ID AAT42079 standard; cDNA to mRNA; 977 BP.
DE Human LAMP residues 8-332 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 74.06%
Best Local Similarity: 55.31%
Query Match: 51.14%
Conservative: 60
Mismatches: 78
Indels: 5
RESULT 443
ID AAT42116 standard; cDNA to mRNA; 1307 BP.
DE Rat LAMP clone 6c coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 68.97%
Best Local Similarity: 51.72%
Query Match: 50.55%
Conservative: 60
Mismatches: 80
Indels: 28
RESULT 444
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 75.50%
Conservative: 58

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Best Local Similarity: 56.29% Mismatches: 70
Query Match: 50.28% Indels: 4
RESULT 445
ID AAT42085 standard; cDNA to mRNA; 945 BP.
DE Rat LAMP residues 1-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 75.50% Conservative: 58
Best Local Similarity: 56.29% Mismatches: 70
Query Match: 50.22% Indels: 4
RESULT 446
ID AAT42083 standard; cDNA to mRNA; 930 BP.
DE Rat mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 74.12% Conservative: 59
Best Local Similarity: 55.21% Mismatches: 77
Query Match: 50.11% Indels: 4
RESULT 447
ID AAT42082 standard; cDNA to mRNA; 912 BP.
DE Human mature LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 74.68% Conservative: 59
Best Local Similarity: 55.52% Mismatches: 74
Query Match: 49.94% Indels: 4
RESULT 448
ID ABZ76264 standard; cDNA; 1757 BP.
DE Human GENSET cDNA clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST-) GENSET SA.
Percent Similarity: 72.14% Conservative: 61
Best Local Similarity: 53.25% Mismatches: 76
Query Match: 49.45% Indels: 14
RESULT 449
ID AAT42086 standard; cDNA to mRNA; 861 BP.
DE Human LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.09% Indels: 3
RESULT 450
ID AAT42087 standard; cDNA to mRNA; 861 BP.
DE Rat LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.03% Indels: 3
RESULT 451
ID AAH34425 standard; cDNA; 1153 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 68.68% Conservative: 60
Best Local Similarity: 51.44% Mismatches: 81
Query Match: 49.00% Indels: 29
RESULT 452
ID ADMA7274 standard; DNA; 617 BP.
DE Oestrogen regulated protein like NOVX 25b gene.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 56.59% Conservative: 4
Best Local Similarity: 55.39% Mismatches: 8

Query Match: 48.37% Indels: 138
RESULT 453
ID AA234325 standard; DNA; 503 BP.
DE Human EST DNA42301.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 454
ID AAC78591 standard; cDNA; 503 BP.
DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 455
ID ACA63893 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein DNA42301.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 456
ID ACA72057 standard; DNA; 503 BP.
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 457
ID ABX92697 standard; cDNA; 503 BP.
DE Human PRO337 EST polynucleotide sequence.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 458
ID ACA66438 standard; cDNA; 503 BP.
DE Human secreted/transmembrane protein EST DNA42301.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 459
ID ADA25063 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 460
ID ACD30039 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
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RESULT 461
ID ADA12724 standard; cDNA; 503 BP.
DE Human secreted/transmembrane polypeptide PRO337 EST.
FN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 462
ID ACD29454 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #134.
FN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 463
ID ADB74030 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
FN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 464
ID ADB76746 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
FN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 465
ID ADC44172 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 466
ID ADC61932 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 467
ID ADC63896 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 468
ID ADC66996 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 469
ID ADC69120 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 470
ID ADC63180 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 471
ID ADC68245 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 472
ID ADC41565 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 473
ID ADC67620 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 474
ID ADC62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 475
ID ADC42189 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 476
ID ADE49558 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 477
ID ADE35612 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
FN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0

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PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 478
ID AD816726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 479
ID AD773341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 480
ID AD772699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 481
ID AD817350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 482
ID AD747364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 483
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 484
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 485
ID AD161201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 486
ID AC042858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 487
ID AD848858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 488
ID AD889959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 489
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 47.56%
RESULT 490
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 491
ID ADF46087 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 492
ID ADF24483 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 493
ID ADF40915 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 494
ID ADF23959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 495
ID ADF33842 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 496
ID ADF27309 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 497
ID ADF27945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 498
ID ADF41539 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 499
ID ADF33218 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 500
ID ADF25584 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 501
ID ADF26685 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 502
ID ADF34474 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 503
ID ADF46711 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 504
ID ADG50697 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 505
ID ADG50073 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 506
ID ADG51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 507
ID ADG51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 47.56% Indels: 0
RESULT 507
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 508
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 509
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 510
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 511
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 512
ID AD25746 standard; cDNA; 503 BP.
DE Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 513
ID ADM17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 514
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 515
ID ABT17405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID NO 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 74.55%
Best Local Similarity: 55.56%
Query Match: 47.12%
Conservative: 55
Mismatch: 71
Indels: 2
RESULT 516
ID AB082337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 517
ID AD128059 standard; cDNA; 1327 BP.
DE ECMCAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 518
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 519
ID ABK33336 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 520
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 521
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 522
ID ACA04534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 523

ID ACA68497 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 524

ID ACA65675 standard; cDNA; 4834 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO6004.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 525

ID ABT44226 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 526

ID ADA47301 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
FN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 527

ID ABT44509 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
FN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 528

ID ACB82176 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO 6004 cDNA.
FN US200304934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 529

ID ACD30291 standard; cDNA; 4834 BP.
DE Human cDNA encoding Pro6004.
FN US2003049302-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 530

ID ACD30291 standard; cDNA; 4834 BP.
DE Human cDNA encoding Pro6004.
FN US2003049302-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 531

ID ADB83491 standard; cDNA; 4834 BP.
DE Human membrane bound receptor/protein PRO6004 cDNA sequence.

DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 532

ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003086068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 533

ID ADB73138 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 534

ID ADB78220 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 535

ID ADB84868 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 536

ID ADB77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 537

ID ADB87040 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 538

ID ADB84622 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 539

ID ADB83737 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

PN US2003069397-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 540
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 541
ID ADC36730 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 542
ID ADC31720 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 543
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 544
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 545
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 546
ID ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 547
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105288-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 548
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 549
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 550
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 551
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 552
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 553
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 554
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indel: 2
RESULT 555
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.

Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 572
ID ADB21121 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 573
ID ADD77236 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 574
ID ADB20383 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 575
ID ADD75448 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 576
ID ADD73964 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 577
ID ADD74210 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 578
ID ADD75940 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 579
ID ADB85432 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 47.85%

Query Match: 45.57% Indels: 2
RESULT 580
ID ADB04981 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 581
ID ADD75194 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 582
ID ADD76738 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 583
ID ADD86506 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 584
ID ADB41224 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 585
ID ADD77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 586
ID ADD77482 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 587
ID ADD77728 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Mismatches: 105
Indels: 2
Query Match: 45.57%

RESULT 588
ID AD085186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 589
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 590
ID AD074456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 591
ID AD076984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 592
ID AD085678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 593
ID ADE05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 594
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 595
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 596
ID ADI33467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

ID ADG27068 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 597
ID ADG11131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 598
ID ADG11910 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 599
ID ADF94467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 600
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 601
ID AD338907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 602
ID ADG3658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 603
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

RESULT 604
ID ADI33467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2

```
DE Human PRO polynucleotide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 605
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 606
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 607
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200404179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 608
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US200404180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 609
ID ADS2049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS ) LG LIFE SCI LTD.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 610
ID ABN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 611
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBFB20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 66.87%
Best Local Similarity: 47.85%
Query Match: 45.40%
Indels: 2
Conservative: 62
Mismatch: 106
Indels: 2
RESULT 612
ID ABO82338 standard; cDNA; 1165 BP.
DE Human NOV12b encoding cDNA SEQ ID NO:25.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 68.45%
Best Local Similarity: 48.58%
Query Match: 45.35%
Indels: 2
Conservative: 63
Mismatch: 98
Indels: 2
RESULT 613
ID ABT17401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID NO:27.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 67.06%
Best Local Similarity: 47.48%
Query Match: 45.13%
Indels: 10
Conservative: 66
Mismatch: 101
Indels: 10
RESULT 614
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 615
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 616
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 617
ID ABX92783 standard; cDNA; 2840 BP.
DE cDNA encoding human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 618
ID ACA66524 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 619
ID ADA25149 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatch: 106
Indels: 2
RESULT 620
ID ACD30125 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
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PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 621
ID ADA12811 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane polypeptide PRO4993.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 622
ID ACD29540 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #139.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 623
ID ADB74117 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 624
ID ADB76833 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 625
ID ADC44259 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 626
ID ADC62019 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 627
ID ADC63983 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 628
ID ADC67083 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 629
ID ADC69207 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 630
ID ADC63267 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 631
ID ADC68332 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 632
ID ADC41652 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 633
ID ADC67707 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 634
ID ADC62643 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 635
ID ADC42276 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 636
ID ADE49645 standard; cDNA; 2840 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 637
 ID ADE35699 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203434-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 638
 ID ADE16813 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203435-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 639
 ID ADD73428 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203436-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 640
 ID ADD72786 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003194781-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 641
 ID ADE17437 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203433-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 642
 ID ADF47451 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003195333-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 643
 ID ADG53208 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003216561-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 644
 ID ADG60528 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003206915-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63

Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 645
 ID ADI61288 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003077700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 646
 ID ACD42944 standard; cDNA; 2840 BP.
 DE Novel human secreted and transmembrane protein PRO4993 cDNA.
 PN US2003050239-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 647
 ID ADE48945 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003104536-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 648
 ID ADE90046 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003130181-A1.
 PD 10-JUL-2003.
 PA (ASHK/) ASKENAZI A J.
 PA (BAKE/) BAKER K P.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GIRM/) GIRMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N P.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 649
 ID ADP61686 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003195345-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2

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RESULT 650
ID ADF40378 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 651
ID ADF46174 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 652
ID ADF24570 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 653
ID ADF41002 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 654
ID ADF23946 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 655
ID ADF33929 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 656
ID ADF27396 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 657
ID ADF28032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 658
ID ADF41626 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 659
ID ADF33305 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 660
ID ADF25671 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 661
ID ADF26772 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 662
ID ADF34561 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 663
ID ADF46798 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 664
ID ADG50784 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 665
ID ADG50160 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 666
ID ADG52032 standard; cDNA; 2840 BP.
```


DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003215908-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 667
 ID ADG49536 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003216305-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 668
 ID ADG48912 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003216360-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 669
 ID ADG51408 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2004005312-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 670
 ID ADG59352 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2004005657-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 671
 ID ADG62808 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2004006219-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 672
 ID ADM17610 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2004048332-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 673
 ID ADL07444 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2004063921-A1.
 PD 01-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87%
 Best Local Similarity: 66.87%
 Query Match: 106
 Indels: 2
 RESULT 674
 ID AAT42094 standard; cDNA to mRNA; 756 BP.
 DE Human LAMP residues 46-294 coding sequence.

PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 76.68%
 Best Local Similarity: 76.68%
 Query Match: 50
 Indels: 1
 RESULT 675
 ID AAT42095 standard; cDNA to mRNA; 756 BP.
 DE Rat LAMP residues 46-294 coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 76.68%
 Best Local Similarity: 76.68%
 Query Match: 58
 Indels: 1
 RESULT 676
 ID ADH71417 standard; DNA; 1030 BP.
 DE Human gene of the invention NOV11q SEQ ID NO:313.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 64.20%
 Best Local Similarity: 64.20%
 Query Match: 104
 Indels: 12
 RESULT 677
 ID ADH71411 standard; DNA; 1033 BP.
 DE Human gene of the invention NOV11n SEQ ID NO:307.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 64.20%
 Best Local Similarity: 64.20%
 Query Match: 104
 Indels: 12
 RESULT 678
 ID ADH71413 standard; DNA; 1035 BP.
 DE Human gene of the invention NOV11o SEQ ID NO:309.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 64.20%
 Best Local Similarity: 64.20%
 Query Match: 104
 Indels: 12
 RESULT 679
 ID ABS76364 standard; DNA; 1427 BP.
 DE DNA encoding human immunoglobulin superfamily protein IGSFP-9.
 PN WO200272794-A2.
 PD 19-SEP-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 64.20%
 Best Local Similarity: 64.20%
 Query Match: 44
 Indels: 12
 RESULT 680
 ID AAD47371 standard; DNA; 2653 BP.
 DE Human LP289 DNA.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 64.20%
 Best Local Similarity: 64.20%
 Query Match: 44
 Indels: 12
 RESULT 681
 ID ADH71395 standard; DNA; 976 BP.
 DE Human gene of the invention NOV11f SEQ ID NO:291.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 64.40%
 Best Local Similarity: 64.40%
 Query Match: 45
 Indels: 103
 RESULT 682
 ID ADH71389 standard; DNA; 976 BP.
 DE Human gene of the invention NOV11c SEQ ID NO:285.
 PN WO2003102155-A2.

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PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 45
Percent Similarity: 64.40%
Best Local Similarity: 50.46% Mismatches: 103
Query Match: 42.19% Indels: 12
RESULT 683
ID ADH71401 standard; DNA; 926 BP.
DE Human gene of the invention NOV11i SEQ ID NO:297.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 684
ID ADH71405 standard; DNA; 927 BP.
DE Human gene of the invention NOV11k SEQ ID NO:301.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 685
ID ADH71409 standard; DNA; 946 BP.
DE Human gene of the invention NOV11m SEQ ID NO:305.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 686
ID ADH71393 standard; DNA; 946 BP.
DE Human gene of the invention NOV11e SEQ ID NO:289.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 687
ID ADH71415 standard; DNA; 976 BP.
DE Human gene of the invention NOV11p SEQ ID NO:311.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 688
ID ADH71397 standard; DNA; 976 BP.
DE Human gene of the invention NOV11g SEQ ID NO:293.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 689
ID ABS71699 standard; DNA; 1017 BP.
DE DNA encoding human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 690
ID ADJ35978 standard; cDNA; 1017 BP.
DE Human NOVX cDNA #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M. Conservative: 41
(SHEN/) SHENOY S G. Mismatches: 94
(SPYT/) SPYTEK K A. Indels: 8
(ZERH/) ZERHUSEN B D.
(PATT/) PATTURAJAN M.
(GUOX/) GUO X.
(KEKU/) KEKUDA R.
(GANG/) GANGOLLI E A.
(SHIM/) SHIMKETS R A.
(TAUP/) TAUPIER R J.
(LILL/) LI L.
(PADI/) PADIGARU M.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
RESULT 691
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 692
ID ADJ35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M. Conservative: 41
(SHEN/) SHENOY S G. Mismatches: 94
(SPYT/) SPYTEK K A. Indels: 8
(ZERH/) ZERHUSEN B D.
(PATT/) PATTURAJAN M.
(GUOX/) GUO X.
(KEKU/) KEKUDA R.
(GANG/) GANGOLLI E A.
(SHIM/) SHIMKETS R A.
(TAUP/) TAUPIER R J.
(LILL/) LI L.
(PADI/) PADIGARU M.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
RESULT 693
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV11h SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 694
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV11b SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 41
Percent Similarity: 66.11%
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 695
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11a SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. Conservative: 43
Percent Similarity: 63.89% Mismatches: 105
Best Local Similarity: 50.82% Indels: 12
Query Match: 42.08%
RESULT 696
ID ADH71421 standard; DNA; 1271 BP.

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DE Human gene of the invention NOV11s SEQ ID NO:317.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 63.89% Conservative: 43
Best Local Similarity: 50.62% Mismatches: 105
Query Match: 42.08% Indels: 12
RESULT 697
ID ABS71700 standard; DNA; 1136 BP.
DE DNA encoding human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 65.78% Conservative: 40
Best Local Similarity: 52.49% Mismatches: 95
Query Match: 41.92% Indels: 8
RESULT 698
ID ADH71403 standard; DNA; 1171 BP.
DE Human gene of the invention NOV11j SEQ ID NO:299.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 65.78% Conservative: 40
Best Local Similarity: 52.48% Mismatches: 95
Query Match: 41.92% Indels: 8
RESULT 699
ID ADH71419 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11r SEQ ID NO:315.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 63.89% Conservative: 44
Best Local Similarity: 50.31% Mismatches: 105
Query Match: 41.92% Indels: 12
RESULT 700
ID ADP28685 standard; DNA; 834 BP.
DE Human secreted protein encoding sequence SEQ ID #683.
PN WO200403732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 68.33% Conservative: 40
Best Local Similarity: 54.09% Mismatches: 84
Query Match: 41.67% Indels: 5
RESULT 701
ID ABK35606 standard; DNA; 1011 BP.
DE Gene encoding novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 65.12% Conservative: 44
Best Local Similarity: 50.50% Mismatches: 97
Query Match: 40.20% Indels: 8
RESULT 702
ID ABS71701 standard; DNA; 1169 BP.
DE DNA encoding human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.78% Conservative: 43
Best Local Similarity: 50.50% Mismatches: 98
Query Match: 39.92% Indels: 8
RESULT 703
ID ADH71407 standard; DNA; 1169 BP.
DE Human gene of the invention NOV11l SEQ ID NO:303.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.78% Conservative: 43
Best Local Similarity: 50.50% Mismatches: 98
Query Match: 39.92% Indels: 8
RESULT 704

ID ABA06475 standard; cDNA; 2813 BP.
DE Human cDNA SEQ ID NO: 141.
PN WO20015474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 70.45% Conservative: 53
Best Local Similarity: 50.38% Mismatches: 77
Query Match: 39.89% Indels: 1
RESULT 705
ID ABV83812 standard; cDNA; 2813 BP.
DE Human polynucleotide SEQ ID NO 141.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 70.45% Conservative: 53
Best Local Similarity: 50.38% Mismatches: 77
Query Match: 39.89% Indels: 1
RESULT 706
ID AAD47374 standard; DNA; 2601 BP.
DE Human LP319b DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIF) LILLY & CO ELI.
Percent Similarity: 65.12% Conservative: 44
Best Local Similarity: 50.50% Mismatches: 97
Query Match: 39.04% Indels: 9
RESULT 707
ID ACH15238 standard; cDNA; 437 BP.
DE Human adult brain cDNA #2450.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 1
Query Match: 38.21% Indels: 0
RESULT 708
ID ADH71391 standard; DNA; 760 BP.
DE Human gene of the invention NOV1ld SEQ ID NO:287.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 68.40% Conservative: 32
Best Local Similarity: 55.60% Mismatches: 74
Query Match: 38.07% Indels: 5
RESULT 709
ID ADL35982 standard; cDNA; 1168 BP.
DE Human NOVX cDNA #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZSER/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Percent Similarity: 64.24% Conservative: 43
Best Local Similarity: 50.00% Mismatches: 99
Query Match: 37.76% Indels: 10
RESULT 710
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.

PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 64.26%
Best Local Similarity: 51.89%
Indels: 19
Query Match: 36
Conservative: 36
Mismatch: 86
Indels: 19
RESULT 711
ID ADL35980 standard; cDNA; 1133 BP.
DE Human NOVX cDNA #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M.
PA (SHEN) SHENOY S G.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATT) PATTURAJAN M.
PA (GUOX) GUO X.
PA (KEKU) KEKUDA R.
PA (GANG) GANGOLLI E A.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (LILL) LI L.
PA (PADI) PADIGARU M.
Percent Similarity: 64.78%
Best Local Similarity: 51.16%
Indels: 11
Query Match: 37.71%
Conservative: 41
Mismatch: 98
Indels: 11
RESULT 712
ID AAS28811 standard; cDNA; 4656 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 69.81%
Best Local Similarity: 49.43%
Indels: 3
Query Match: 37.35%
Conservative: 54
Mismatch: 78
Indels: 3
RESULT 713
ID ADB31536 standard; cDNA; 4656 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 57.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 69.81%
Best Local Similarity: 49.43%
Indels: 3
Query Match: 37.35%
Conservative: 54
Mismatch: 78
Indels: 3
RESULT 714
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 59.57%
Best Local Similarity: 45.90%
Indels: 28
Query Match: 36.68%
Conservative: 45
Mismatch: 106
Indels: 28
RESULT 715
ID ABJ99899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 63.61%
Best Local Similarity: 44.08%
Indels: 14
Query Match: 36.10%
Conservative: 66
Mismatch: 109
Indels: 14
RESULT 716
ID AAC91321 standard; cDNA; 537 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN WO200073509-A2.
PD 07-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 97.54%
Best Local Similarity: 97.54%
Indels: 0
Query Match: 34.95%
Conservative: 0
Mismatch: 3
Indels: 0

RESULT 717
ID AAD47372 standard; DNA; 754 BP.
DE Human LP289 splice variant (LP343) DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 69.27%
Best Local Similarity: 55.96%
Indels: 5
Query Match: 33.58%
Conservative: 29
Mismatch: 62
Indels: 5
RESULT 718
ID AAS78035 standard; cDNA; 484 BP.
DE DNA encoding novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 90.30%
Best Local Similarity: 86.57%
Indels: 0
Query Match: 33.22%
Conservative: 5
Mismatch: 13
Indels: 0
RESULT 719
ID ADP28686 standard; DNA; 666 BP.
DE Human secreted protein encoding sequence SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 67.70%
Best Local Similarity: 53.98%
Indels: 5
Query Match: 33.19%
Conservative: 31
Mismatch: 68
Indels: 5
RESULT 720
ID ACH46276 standard; cDNA; 409 BP.
DE Human infant brain cDNA #339.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA) DRMANAC R T.
PA (LABA) LABAT I.
PA (STAC) STACHE-CRAIN B.
PA (DICK) DICKSON M C.
PA (JONE) JONES L W.
Percent Similarity: 95.87%
Best Local Similarity: 94.21%
Indels: 0
Query Match: 32.06%
Conservative: 2
Mismatch: 5
Indels: 0
RESULT 721
ID AAF93346 standard; cDNA; 452 BP.
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 32.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 722
ID AAS78034 standard; cDNA; 443 BP.
DE DNA encoding novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Indels: 11
Query Match: 31.53%
Conservative: 0
Mismatch: 3
Indels: 11
RESULT 723
ID ADQ83739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (WUTD) WU T D.
PA (ZHOU) ZHOU Y.
Percent Similarity: 64.96%
Best Local Similarity: 50.00%
Indels: 8
Query Match: 30.79%
Conservative: 35
Mismatch: 74
Indels: 8
RESULT 724
ID AAC19214 standard; cDNA; 333 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23289.
PN EP1033401-A2.

PD 06-SEP-2000.
 PA (GEST) GENSET.
 Percent Similarity: 95.50%
 Best Local Similarity: 94.53%
 Query Match: 30.18%
 Indels: 1
 RESULT 725
 ID AAS78003 standard; cDNA; 2883 BP.
 DE DNA encoding novel human diagnostic protein #13807.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 56.58%
 Best Local Similarity: 45.55%
 Query Match: 29.10%
 Indels: 50
 RESULT 726
 ID ADE08816 standard; DNA; 2883 BP.
 DE Novel DNA-related contig nucleotide sequence #60.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 56.58%
 Best Local Similarity: 45.55%
 Query Match: 29.10%
 Indels: 50
 RESULT 727
 ID AAF93597 standard; cDNA; 585 BP.
 DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
 PN WO200107611-A2.
 PD 01-FEB-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 71.58%
 Best Local Similarity: 50.53%
 Query Match: 27.16%
 Indels: 4
 RESULT 728
 ID ABS52769 standard; cDNA; 408 BP.
 DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
 PN WO200246475-A2.
 PD 13-JUN-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 75.00%
 Best Local Similarity: 55.88%
 Query Match: 22.18%
 Indels: 1
 RESULT 729
 ID ADG63283 standard; DNA; 540 BP.
 DE Human OBCAM gene exon 2.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Percent Similarity: 78.38%
 Best Local Similarity: 69.37%
 Query Match: 21.68%
 Indels: 13
 RESULT 730
 ID AAC02777 standard; cDNA; 352 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 2775.
 PN EPI033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Percent Similarity: 82.80%
 Best Local Similarity: 73.12%
 Query Match: 19.03%
 Indels: 1
 RESULT 731
 ID ABL25337 standard; DNA; 1242 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 42.93%
 Best Local Similarity: 27.99%
 Query Match: 18.74%
 Indels: 63
 RESULT 732
 ID ABL17651 standard; DNA; 948 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4426.
 PN WO200171042-A2.
 PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
 Percent Similarity: 50.17%
 Best Local Similarity: 31.86%
 Query Match: 18.44%
 Indels: 22
 RESULT 733
 ID ABL1515 standard; cDNA; 2010 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 47.64%
 Best Local Similarity: 28.72%
 Query Match: 16.97%
 Indels: 30
 RESULT 734
 ID ABX71182 standard; cDNA; 913 BP.
 DE Novel human cDNA sequence #407.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 66.13%
 Best Local Similarity: 46.77%
 Query Match: 16.75%
 Indels: 1
 RESULT 735
 ID ABL04261 standard; cDNA; 1110 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7265.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 44.37%
 Best Local Similarity: 29.69%
 Query Match: 16.47%
 Indels: 27
 RESULT 736
 ID ABL04260 standard; cDNA; 3426 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 44.37%
 Best Local Similarity: 29.69%
 Query Match: 16.47%
 Indels: 27
 RESULT 737
 ID ABX56303 standard; DNA; 8243 BP.
 DE Human NOV25b CG93858-02 DNA SEQ ID 85.
 PN WO200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 42.47%
 Best Local Similarity: 30.14%
 Query Match: 16.47%
 Indels: 63
 RESULT 738
 ID ADX60477 standard; DNA; 8546 BP.
 DE Angiogenesis differentially expressed gene GS-N52.
 PN FR2836687-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Percent Similarity: 42.12%
 Best Local Similarity: 29.79%
 Query Match: 16.09%
 Indels: 63
 RESULT 739
 ID ADX60778 standard; DNA; 8546 BP.
 DE Angiogenesis differentially expressed gene GS-N52.
 PN FR2836686-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Percent Similarity: 42.12%
 Best Local Similarity: 29.79%
 Query Match: 16.09%
 Indels: 63
 RESULT 740
 ID ADP73100 standard; DNA; 8546 BP.
 DE Angiogenesis inhibitor human DNA sequence, GS-N52.

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PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 741
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 742
ID ADO08272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GORM/) GORMAN L.
PA (GERL/) GERLACH V.
PA (GUOX/) GUOX X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPIT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERRHUSEN B D.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 743
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 744
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 745
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR283687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 746
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR283686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 747
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 748
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 749
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 750
ID ADH72101 standard; DNA; 2153 BP.
DE Human gene of the invention NOV43a SEQ ID NO:997.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 751
ID ADO08270 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUOX X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
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PA (LILL/) LI L.
 PA (LIUX/) LIU X.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLER C E.
 PA (MILL/) MILLER I.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SPYT/) SPYTEK K A.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERR/) ZERRHUSEN B D.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 752
 ID ACD03633 standard; cDNA; 2916 BP.
 DE Novel human GPCR related protein NOV9b cDNA.
 PN WO200299116-A2.
 PD 12-DEC-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 43.97%
 Best Local Similarity: 30.50%
 Query Match: 15.97%
 RESULT 753
 ID AAS68120 standard; cDNA; 3910 BP.
 DE DNA encoding novel human diagnostic protein #3924.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 754
 ID AAI72024 standard; cDNA; 4073 BP.
 DE Human thrombospondin protein, BTL012, coding sequence.
 PN WO200174852-A2.
 PD 11-OCT-2001.
 PA (FARB) BAYER CORP.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 755
 ID ADL33996 standard; cDNA; 5877 BP.
 DE Human G-coupled protein receptor-related gene #44.
 PN US2004006205-A1.
 PD 08-JAN-2004.
 PA (LILL/) LI L.
 PA (GERL/) GERLACH V.
 PA (LIUX/) LIU X.
 PA (MILL/) MILLER C E.
 PA (SPYT/) SPYTEK K A.
 PA (ZERR/) ZERRHUSEN B D.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (ZHON/) ZHONG H.
 PA (SMIT/) SMITHSON G.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOGF F L.
 PA (VOSS/) VOSS E Z.
 PA (VERN/) VERNET C A.
 PA (MACD/) MACDOUGALL J R.
 PA (RAST/) RASTELLI L.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (MEZE/) MEZES P S.
 PA (FURT/) FURTAK K.
 PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.
 PA (SHIM/) SHIMKETS R A.
 PA (TAUP/) TAUPIER R J.
 PA (EDIN/) EDINGER S.
 PA (MAZU/) MAZUR A.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 756
 ID ADE16057 standard; DNA; 5935 BP.
 DE G-coupled protein receptor related polypeptide DNA, SEQ ID NO 87.
 PN WO200283841-A2.
 PD 24-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 757
 ID ABX56304 standard; DNA; 6343 BP.
 DE Human gene of the invention NOV43d SEQ ID NO:1003.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 758
 ID ADH72107 standard; DNA; 6343 BP.
 DE Human gene of the invention NOV43d SEQ ID NO:1003.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 759
 ID ABQ86156 standard; DNA; 16908 BP.
 DE Novel human gene. SEQ ID 27.
 PN WO200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Percent Similarity: 43.36%
 Best Local Similarity: 31.12%
 Query Match: 15.97%
 RESULT 760
 ID ADQ22570 standard; DNA; 18248 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 43.77%
 Best Local Similarity: 30.25%
 Query Match: 15.92%
 RESULT 761
 ID ADM93822 standard; DNA; 2916 BP.
 DE DNA encoding human NOV protein #21.
 PN US2004009480-A1.
 PD 15-JAN-2004.
 PA (ANDE/) ANDERSON D W.
 PA (BAUM/) BAUMGARTNER J C.
 PA (BOLD/) BOLDOGF F L.
 PA (CASM/) CASMAN S J.
 PA (EDIN/) EDINGER S R.
 PA (GANG/) GANGOLLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUOX/) GUO X S.
 PA (HJAL/) HJALT T.
 PA (KEKU/) KEKUDA R.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.

PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATURAJAN M.
PA (PENA/) PENA C E A.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERRH/) ZERRHUSEN B D.
Percent Similarity: 43.01%
Best Local Similarity: 30.07%
Query Match: 15.86%
RESULT 762
ID ABL12455 standard; cDNA; 1710 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31847.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 43.10%
Best Local Similarity: 26.15%
Query Match: 15.75%
RESULT 763
ID AD953259 standard; DNA; 3170 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.52%
Best Local Similarity: 25.51%
Query Match: 15.37%
RESULT 764
ID AD124496 standard; cDNA; 2960 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
RESULT 765
ID ADA53985 standard; cDNA; 3309 BP.
DE Human coding sequence, SEQ ID 1553.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
RESULT 766
ID AAH98595 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 452.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
RESULT 767
ID AAH98610 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 467.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
RESULT 768
ID AAD14203 standard; DNA; 8513 BP.
DE MESVR/EGFP/IRESNCAPro(ori) vector.

PN WO200155371-A1.
PD 02-AUG-2001.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
RESULT 769
ID ADD25618 standard; DNA; 2633 BP.
DE Binding domain-immunoglobulin fusion protein-associated DNA #93.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE CRAFT INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.23%
RESULT 770
ID AD131624 standard; cDNA; 2633 BP.
DE Human cDNA #950.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.23%
RESULT 771
ID ADL12516 standard; cDNA; 5807 BP.
DE Human steroid-induced C3A liver cell cDNA #245.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.17%
RESULT 772
ID AAD56185 standard; DNA; 6801 BP.
DE Human LRRCAPS DNA #2.
PN WO2003035831-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 39.58%
Best Local Similarity: 29.17%
Query Match: 15.17%
RESULT 773
ID ADH48823 standard; DNA; 7097 BP.
DE NOV45B coding sequence, SEQ ID 107.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.99%
Best Local Similarity: 29.00%
Query Match: 15.14%
RESULT 774
ID ADH48821 standard; DNA; 4321 BP.
DE NOV45A coding sequence, SEQ ID 105.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.74%
Best Local Similarity: 28.97%
Query Match: 15.03%
RESULT 775
ID AAL62047 standard; cDNA; 3360 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.84%
Best Local Similarity: 24.83%
Query Match: 15.01%
RESULT 776
ID ABL23499 standard; DNA; 2190 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21970.
PN WO200171042-A2.

PA (PILA/) PILARSKY C. Conservative: 32
Percent Similarity: 38.70%
Best Local Similarity: 28.79%
Query Match: 14.87%
Indels: 51
RESULT 792
ID ADR66267 standard; DNA; 6847 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 121 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 38.70%
Best Local Similarity: 28.79%
Query Match: 14.87%
Indels: 51
RESULT 793
ID ADR66768 standard; DNA; 6847 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 61 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 38.70%
Best Local Similarity: 28.79%
Query Match: 14.87%
Indels: 51
RESULT 794
ID ADR81722 standard; DNA; 6939 BP.
DE Leukaemia-related DNA sequence #2278.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 38.70%
Best Local Similarity: 28.79%
Query Match: 14.87%
Indels: 51
RESULT 795
ID ADR81721 standard; DNA; 6939 BP.
DE Leukaemia-related DNA sequence #2277.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 38.70%
Best Local Similarity: 28.79%
Query Match: 14.87%
Indels: 51
RESULT 796
ID ABL17650 standard; DNA; 3060 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4423.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
PA (SCHO/) SCHOCH C.
Percent Similarity: 44.74%
Best Local Similarity: 28.53%
Query Match: 14.78%
Indels: 62
RESULT 797
ID ABS70409 standard; cDNA; 6814 BP.
DE Human bone remodelling gene #66.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.39%
Best Local Similarity: 28.48%
Query Match: 14.78%
Indels: 62

Query Match: 14.59%
Indels: 51
RESULT 798
ID ABX63089 standard; cDNA; 4978 BP.
DE Human cDNA #89 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 43.15%
Best Local Similarity: 26.03%
Query Match: 14.56%
Indels: 33
RESULT 799
ID AAX5767 standard; cDNA; 4188 BP.
DE Drosophila Robo 1 polypeptide encoding cDNA.
PN WO9925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 42.16%
Best Local Similarity: 26.14%
Query Match: 14.45%
Indels: 50
RESULT 800
ID AAX57350 standard; cDNA; 4188 BP.
DE Drosophila sp. ROBO1 cDNA.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 42.16%
Best Local Similarity: 26.14%
Query Match: 14.45%
Indels: 50
RESULT 801
ID ABL10471 standard; cDNA; 2113 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25895.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.34%
Best Local Similarity: 26.18%
Query Match: 14.42%
Indels: 73
RESULT 802
ID ABL22881 standard; DNA; 4355 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20116.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.16%
Best Local Similarity: 26.14%
Query Match: 14.40%
Indels: 50
RESULT 803
ID ABX13540 standard; DNA; 93801 BP.
DE Human RGS11 DNA.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Percent Similarity: 42.96%
Best Local Similarity: 29.60%
Query Match: 14.34%
Indels: 26
RESULT 804
ID ADQ89963 standard; DNA; 103052 BP.
DE Antagonist of cell cycle progression nucleotide sequence #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Percent Similarity: 42.96%
Best Local Similarity: 29.60%
Query Match: 14.34%
Indels: 26
RESULT 805
ID ADM74170 standard; DNA; 1140 BP.
DE Human NOV3A gene sequence SeqID9.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.38%
Best Local Similarity: 27.38%
Query Match: 14.31%
Indels: 61

RESULT 806		
ID	AZ06640 standard; cDNA; 1335 BP.	
DE	Beta-secretase polynucleotide.	
PN	US5942400-A.	
PD	24-AUG-1999.	
PA	(ELAN-) ELAN PHARM INC.	
Percent Similarity:	42.33%	Conservative: 58
Best Local Similarity:	26.63%	Mismatches: 137
Query Match:	14.17%	Indels: 76
RESULT 807		
ID	AAC85809 standard; cDNA; 1335 BP.	
DE	Beta-secretase cDNA.	
PN	US6221645-B1.	
PD	24-APR-2001.	
PA	(ELAN-) ELAN PHARM INC.	
Percent Similarity:	42.33%	Conservative: 58
Best Local Similarity:	26.63%	Mismatches: 137
Query Match:	14.17%	Indels: 76
RESULT 808		
ID	ABL114207 standard; cDNA; 2131 BP.	
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 37103.	
PN	WO200171042-A2.	
PD	27-SEP-2001.	
PA	(PEKE) PE CORP NY.	
Percent Similarity:	39.78%	Conservative: 53
Best Local Similarity:	24.93%	Mismatches: 131
Query Match:	14.17%	Indels: 84
RESULT 809		
ID	ADM74176 standard; DNA; 918 BP.	
DE	Human NOV3D gene sequence Segid15.	
PN	WO2004015079-A2.	
PD	19-FEB-2004.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	43.38%	Conservative: 53
Best Local Similarity:	27.08%	Mismatches: 123
Query Match:	14.04%	Indels: 61
RESULT 810		
ID	ABT17377 standard; DNA; 1216 BP.	
DE	Human IG Gene related nucleic acid SEQ ID No 3.	
PN	WO200299040-A2.	
PD	12-DEC-2002.	
PA	(EXEL-) EXELIXIS INC.	
Percent Similarity:	43.60%	Conservative: 55
Best Local Similarity:	26.83%	Mismatches: 124
Query Match:	14.04%	Indels: 61
RESULT 811		
ID	ABT17376 standard; DNA; 1242 BP.	
DE	Human IG gene related nucleic acid SEQ ID No 2.	
PN	WO200299040-A2.	
PD	12-DEC-2002.	
PA	(EXEL-) EXELIXIS INC.	
Percent Similarity:	43.06%	Conservative: 57
Best Local Similarity:	26.91%	Mismatches: 137
Query Match:	14.04%	Indels: 65
RESULT 812		
ID	ADI19787 standard; DNA; 2113 BP.	
DE	Human NOV12 DNA.	
PN	US2004002134-A1.	
PD	01-JAN-2004.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	43.06%	Conservative: 57
Best Local Similarity:	26.91%	Mismatches: 137
Query Match:	14.04%	Indels: 65
RESULT 813		
ID	AAF27862 standard; cDNA; 2116 BP.	
DE	Human NOV12 cDNA.	
PN	WO200075321-A2.	
PD	14-DEC-2000.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	43.06%	Conservative: 57
Best Local Similarity:	26.91%	Mismatches: 137
Query Match:	14.04%	Indels: 65
RESULT 814		
ID	AAF27862 standard; cDNA; 2116 BP.	
DE	Human NOV12 cDNA.	
PN	WO200075321-A2.	
PD	14-DEC-2000.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	43.06%	Conservative: 57
Best Local Similarity:	26.91%	Mismatches: 137
Query Match:	14.04%	Indels: 65

DE Neurotrophin-like protein splice variant coding sequence.
PN WO200357175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.97%
Best Local Similarity: 27.36%
Query Match: 14.01%
Conservative: 51
Mismatch: 132
Indels: 40
RESULT 823
ID ADO47371 standard; DNA; 2196 BP.
DE Human neurotrophin-like protein-related gene SeqID6.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 43.97%
Best Local Similarity: 27.36%
Query Match: 14.01%
Conservative: 51
Mismatch: 132
Indels: 40
RESULT 824
ID ABL09371 standard; cDNA; 2658 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22595.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.56%
Best Local Similarity: 26.49%
Query Match: 13.87%
Conservative: 54
Mismatch: 122
Indels: 71
RESULT 825
ID ABL54189 standard; cDNA; 1124 BP.
DE Neurotrophin-like protein partial coding sequence.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 826
ID ADO47367 standard; DNA; 1124 BP.
DE Human neurotrophin-like protein-related gene SeqID2.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 827
ID ADO47370 standard; cDNA; 1377 BP.
DE Human neurotrophin-like protein-related cDNA SeqID5.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 828
ID ABL54190 standard; cDNA; 1699 BP.
DE Neurotrophin-like protein coding sequence.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 829
ID ADO47368 standard; cDNA; 1699 BP.
DE Human neurotrophin-like protein-related cDNA SeqID3.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 830
ID ADS09923 standard; DNA; 1699 BP.
DE Human therapeutic DNA - SEQ ID 160.

PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 831
ID ADO47384 standard; DNA; 2868 BP.
DE Human neurotrophin-like protein-related DNA SeqID12.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 832
ID AAL62046 standard; cDNA; 3257 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-34 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 833
ID ADO47382 standard; DNA; 3312 BP.
DE Human neurotrophin-like protein-related gene SeqID17.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 834
ID ADS09924 standard; DNA; 3312 BP.
DE Human therapeutic DNA - SEQ ID 161.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 835
ID ADS10423 standard; DNA; 3386 BP.
DE Human therapeutic DNA - SEQ ID 660.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 836
ID AAS76287 standard; cDNA; 3868 BP.
DE DNA encoding novel human diagnostic protein #12091.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 837
ID ADH72133 standard; DNA; 4141 BP.
DE Human gene of the invention NOV46f SEQ ID NO:1029.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 44.89%
Best Local Similarity: 27.74%
Query Match: 13.84%
Conservative: 47
Mismatch: 123
Indels: 28
RESULT 838
ID ABX70427 standard; DNA; 4169 BP.
DE DNA encoding human GPCR related protein NOV13a.
PN WO200279398-A2.

PA	(PATT//)	PATTURAJAN M.	
PA	(BURG//)	BURGESS C E.	
PA	(VERN//)	VERNET C A M.	
PA	(LILL//)	LI L.	
PA	(GORM//)	GORMAN L.	
PA	(MALY//)	MALYANKAR U M.	
PA	(BOLD//)	BOLDOG F L.	
PA	(GUOX//)	GUO X.	
PA	(SHEN//)	SHENY S G.	
PA	(PADI//)	PADIGARU M.	
PA	(TAUP//)	TAUPIER R J.	
PA	(MILL//)	MILLER C E.	
PA	(CASW//)	CASMAN S J.	
PA	(PENA//)	PENA C E A.	
PA	(GANG//)	GANGOLLI E A.	
PA	(GUSE//)	GUSEV V Y.	
PA	(SMIT//)	SMITHSON G.	
PA	(ZERH//)	ZERHUSEN B D.	
PA	(GERL//)	GERLACH V.	
PA	(POCH//)	POCHART P F.	
PA	(FERN//)	FERNANDES E R.	
PA	(SHIM//)	SHIMKETS R A.	
PA	(RAST//)	RASTELLI L.	
PA	(SPAD//)	SPADERNA S K.	
PA	(LARO//)	LAROCHEILLE W J.	
PA	(ZHON//)	ZHONG M.	
PA	(KHRA//)	KHRAMTSOV N V.	
PA	(VOSS//)	VOSS E Z.	
PA	(HERR//)	HERRMANN J L.	
Percent Similarity:		44.99%	
Best Local Similarity:		27.74%	
Query Match:		13.84%	
RESULT 843			
ID	ABD33040	standard; cDNA; 3588 BP.	
DE	Human cancer-associated cDNA HR22-025.1.		
PN	WO2004074320-A2.		
PD	02-SEP-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 844			
ID	AA164283	standard; DNA; 4548 BP.	
DE	Human transient axonal glycoprotein (tag-1) DNA.		
PN	WO200188546-A2.		
PD	22-NOV-2001.		
PA	(UNMI)	UNIV MICHIGAN.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 845			
ID	ABD33041	standard; cDNA; 6137 BP.	
DE	Human cancer-associated cDNA HR22-025.2.		
PN	WO2004074320-A2.		
PD	02-SEP-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 846			
ID	AQD23368	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(PROT-)	PROTEIN DESIGN LABS INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 847			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 848			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 849			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 850			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 851			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 852			
ID	AQ24513	standard; DNA; 7625 BP.	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.		
PN	WO2004048938-A2.		
PD	10-JUN-2004.		
PA	(SAGR-)	SAGRES DISCOVERY INC.	
Percent Similarity:		40.70%	
Best Local Similarity:		26.67%	
Query Match:		13.82%	
RESULT 853			

PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 40.70%
Best Local Similarity: 26.67%
Query Match: 13.82%
Indels: 59
RESULT 848
ID ADO28580 standard; cDNA; 7650 BP.
DE Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.70%
Best Local Similarity: 26.67%
Query Match: 13.82%
Indels: 59
RESULT 849
ID ADA53286 standard; cDNA; 1880 BP.
DE Human coding sequence, SEQ ID 854.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 44.31%
Best Local Similarity: 26.46%
Query Match: 13.76%
Indels: 55
RESULT 850
ID ABL24131 standard; DNA; 1404 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23866.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.08%
Best Local Similarity: 27.41%
Query Match: 13.73%
Indels: 78
RESULT 851
ID ABK94709 standard; DNA; 3314 BP.
DE Neurodegenerative disease associated polynucleotide #18.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 852
ID ABK94710 standard; DNA; 3335 BP.
DE Neurodegenerative disease associated polynucleotide #19.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 853
ID AAQ74440 standard; cDNA; 3360 BP.
DE Human contactin cDNA (EMBL Accession #221488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT) BECTON DICKINSON CO.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 854
ID ABL64109 standard; DNA; 3360 BP.
DE Breast cancer related gene sequence SEQ ID NO:2446.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 855
ID ABL63715 standard; DNA; 3360 BP.
DE Breast cancer related gene sequence SEQ ID NO:2052.
PN WO200194629-A2.
PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 856
ID ABK94708 standard; DNA; 3360 BP.
DE Neurodegenerative disease associated polynucleotide #17.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 857
ID ADE71112 standard; DNA; 3360 BP.
DE Contactin gene, SEQ ID 66.
PN WO200307089-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 858
ID ADJ75287 standard; DNA; 3360 BP.
DE Marker Gene SEQ ID NO:539.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 859
ID AAT07313 standard; cDNA; 3395 BP.
DE Human contactin coding sequence.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 860
ID ADO28658 standard; cDNA; 3427 BP.
DE Human CONT encoding cDNA SEQ ID NO:87.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Indels: 49
RESULT 861
ID ADR66243 standard; DNA; 4015 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 97 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERW/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 39.04%
Best Local Similarity: 27.03%
Query Match: 13.62%
Indels: 57
RESULT 862
ID ADR66585 standard; DNA; 4015 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 97 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERW/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 39.04%

Best Local Similarity: 27.03% Mismatches: 146
Query Match: 13.62% Indels: 57
RESULT 863
ID AAG67246 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 864
ID AAS71723 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 865
ID AAG64445 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 866
ID AAS64798 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #602.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 867
ID ABK90037 standard; cDNA; 7764 BP.
DE Human OCP cDNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 868
ID ABK90051 standard; cDNA; 7770 BP.
DE Coding sequence of human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 869
ID ADL02243 standard; cDNA; 7770 BP.
DE Human OCP cDNA #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 870
ID AAT15929 standard; cDNA; 2178 BP.
DE Neural cell adhesion molecule splice variant cDNA.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Percent Similarity: 41.98% Conservative: 57
Best Local Similarity: 24.38% Mismatches: 109
Query Match: 13.37% Indels: 83

Query Match: 13.37% Indels: 31
RESULT 871
ID AAT15928 standard; cDNA; 2450 BP.
DE Neural cell adhesion molecule full-length DNA.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Percent Similarity: 41.98% Conservative: 57
Best Local Similarity: 24.38% Mismatches: 109
Query Match: 13.37% Indels: 31
RESULT 872
ID ADJ76119 standard; cDNA; 3843 BP.
DE Marker gene SEQ ID NO:1371.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 41.85% Conservative: 55
Best Local Similarity: 24.28% Mismatches: 133
Query Match: 13.37% Indels: 49
RESULT 873
ID ADA53434 standard; cDNA; 3870 BP.
DE Human coding sequence, SEQ ID 1002.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 44.33% Conservative: 48
Best Local Similarity: 27.84% Mismatches: 109
Query Match: 13.37% Indels: 53
RESULT 874
ID ADI24497 standard; cDNA; 4723 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:47.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 41.67% Conservative: 55
Best Local Similarity: 24.69% Mismatches: 158
Query Match: 13.37% Indels: 31
RESULT 875
ID AB211468 standard; cDNA; 6599 BP.
DE Human polynucleotide SEQ ID NO 350.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.60% Conservative: 44
Best Local Similarity: 26.71% Mismatches: 131
Query Match: 13.34% Indels: 28
RESULT 876
ID ADM43986 standard; cDNA; 6599 BP.
DE Novel human arginine-rich protein cDNA #350.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 42.60% Conservative: 44
Best Local Similarity: 26.71% Mismatches: 131
Query Match: 13.34% Indels: 28
RESULT 877
ID AAD04326 standard; cDNA; 2766 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_2 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 878
ID AAD04325 standard; cDNA; 2771 BP.
DE Human cell adhesion molecule homologue (CAM-H) DNA #2.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.

Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 879
ID AAD04327 standard; DNA; 2771 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_1 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 880
ID AAD04328 standard; DNA; 3060 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_2 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 881
ID AAD04324 standard; DNA; 3065 BP.
DE Human cell adhesion molecule homologue (CAM-H) DNA #1.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 882
ID ADJ56383 standard; cDNA; 6829 BP.
DE C elegans cDNA differentially expressed in MYCN activated cells SeqID189.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Percent Similarity: 38.39% Conservative: 32
Best Local Similarity: 28.48% Mismatches: 148
Query Match: 13.18% Indels: 52
RESULT 883
ID ABS54189 standard; cDNA; 8180 BP.
DE Human osteoclast protein (OCP) cDNA 5+3 corrected.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 884
ID ADJ02228 standard; cDNA; 8180 BP.
DE Human OCP cDNA #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 885
ID ABK90038 standard; cDNA; 8262 BP.
DE Human 5+3 corrected OCP cDNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75

RESULT 886
ID AAI72586 standard; cDNA; 8262 BP.
DE Human OCP cDNA.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 887
ID ABS54187 standard; cDNA; 8262 BP.
DE Human osteoclast protein (OCP) cDNA.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 888
ID ADJ02226 standard; cDNA; 8262 BP.
DE Human OCP cDNA #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 889
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 77.78% Conservative: 14
Best Local Similarity: 58.33% Mismatches: 16
Query Match: 13.12% Indels: 0
RESULT 890
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 77.78% Conservative: 14
Best Local Similarity: 58.33% Mismatches: 16
Query Match: 13.12% Indels: 0
RESULT 891
ID ADR07797 standard; cDNA; 2451 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1303.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 40.83% Conservative: 34
Best Local Similarity: 29.07% Mismatches: 133
Query Match: 13.07% Indels: 39
RESULT 892
ID ADH71831 standard; DNA; 2902 BP.
DE Human gene of the invention NOV29af SEQ ID NO:727.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.59% Conservative: 46
Best Local Similarity: 27.06% Mismatches: 127
Query Match: 13.04% Indels: 75
RESULT 893
ID ADH71817 standard; DNA; 2902 BP.

Percent Similarity: 39.45% Conservative: 42
 Best Local Similarity: 24.91% Mismatches: 132
 Query Match: 12.93% Indels: 43
 RESULT 908
 ID ADR82853 standard; cDNA; 1427 BP.
 DE Human PRO polynucleotide #38.
 PN US2004043927-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 39.45% Conservative: 42
 Best Local Similarity: 24.91% Mismatches: 132
 Query Match: 12.93% Indels: 43
 RESULT 909
 ID ADR67151 standard; DNA; 3904 BP.
 DE Human bladder cancer associated nucleotide sequence.
 PN WO2004076613-A2.
 PD 10-SEP-2004.
 PA (HERR/) HERR A.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (STAU/) STAU E.
 PA (PILA/) PILARSKY C.
 PA (SPEC/) SPECHT T.
 Percent Similarity: 39.45% Conservative: 42
 Best Local Similarity: 24.91% Mismatches: 132
 Query Match: 12.93% Indels: 43
 RESULT 910
 ID ABI22880 standard; DNA; 8410 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20113.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 38.84% Conservative: 49
 Best Local Similarity: 23.85% Mismatches: 121
 Query Match: 12.93% Indels: 79
 RESULT 911
 ID ADH71829 standard; DNA; 2902 BP.
 DE Human gene of the invention NOV29ae SEQ ID NO:725.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.71% Conservative: 47
 Best Local Similarity: 26.84% Mismatches: 126
 Query Match: 12.87% Indels: 75
 RESULT 912
 ID ADH71815 standard; DNA; 2902 BP.
 DE Human gene of the invention NOV29x SEQ ID NO:711.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.71% Conservative: 47
 Best Local Similarity: 26.84% Mismatches: 126
 Query Match: 12.87% Indels: 75
 RESULT 913
 ID ADH71819 standard; DNA; 7831 BP.
 DE Human gene of the invention NOV29z SEQ ID NO:715.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 914
 ID ABS51089 standard; cDNA; 7876 BP.
 DE cDNA encoding human NOV12a protein.
 PN WO200250277-A2.
 PD 27-JUN-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 915
 ID ADJ83054 standard; DNA; 7876 BP.

DE Human NOVX NOV12a DNA.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLEY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 916
 ID ADH71843 standard; DNA; 7876 BP.
 DE Human gene of the invention NOV29al SEQ ID NO:739.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 917
 ID ADH71769 standard; DNA; 7876 BP.
 DE Human gene of the invention NOV29a SEQ ID NO:665.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 918
 ID ADH71839 standard; DNA; 7876 BP.
 DE Human gene of the invention NOV29aj SEQ ID NO:735.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 919
 ID ADH71847 standard; DNA; 7876 BP.
 DE Human gene of the invention NOV29an SEQ ID NO:743.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 40.35% Conservative: 46
 Best Local Similarity: 26.90% Mismatches: 132
 Query Match: 12.85% Indels: 72
 RESULT 920
 ID ADH71853 standard; DNA; 7876 BP.
 DE Human gene of the invention NOV29aq SEQ ID NO:749.
 PN WO2003102155-A2.
 PD 11-DEC-2003.

PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 921		
ID	ADH71841 standard; DNA; 7876 BP.	
DE	Human gene of the invention NOV29ak SEQ ID NO:737.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 922		
ID	ADH71845 standard; DNA; 7876 BP.	
DE	Human gene of the invention NOV29am SEQ ID NO:741.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 923		
ID	ADH71849 standard; DNA; 7876 BP.	
DE	Human gene of the invention NOV29ao SEQ ID NO:745.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 924		
ID	ADH71835 standard; DNA; 7876 BP.	
DE	Human gene of the invention NOV29ah SEQ ID NO:731.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 925		
ID	ADH71851 standard; DNA; 7876 BP.	
DE	Human gene of the invention NOV29ap SEQ ID NO:747.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 926		
ID	ADH71837 standard; DNA; 7877 BP.	
DE	Human gene of the invention NOV29ai SEQ ID NO:733.	
PN	WO2003102155-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 927		
ID	ABS51094 standard; cDNA; 8270 BP.	
DE	cDNA encoding human NOV12f protein.	
PN	WO200250277-A2.	
PD	27-JUN-2002.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72
RESULT 928		
ID	ADJ83064 standard; DNA; 8270 BP.	
DE	Human NOVX NOV12f DNA.	
PN	US2003170630-A1.	
PD	11-SEP-2003.	
PA	(ALSO/) ALSOBROOK J P.	
Percent Similarity:	40.35%	Conservative: 46
Best Local Similarity:	26.90%	Mismatches: 132
Query Match:	12.85%	Indels: 72

PA (TCHE/) TCHERNEV V T.			
PA (LIUX/) LIU X.			
PA (SPVT/) SPYTEK K A.			
PA (ZERR/) ZERHUSEN B D.			
PA (PATI/) PATURAJAN M.			
PA (LEPL/) LEPLEY D M.			
PA (BURG/) BURGESS C E.			
PA (SHIM/) SHIMKETS R A.			
PA (GROS/) GROSSE W M.			
PA (SZEK/) SZEKERES E S.			
PA (VERN/) VERNET C A M.			
PA (LILL/) LI L.			
PA (CASM/) CASMAN S J.			
PA (BOLD/) BOLDOG F L.			
PA (GORM/) GORMAN L.			
PA (GANG/) GANGOLLI E A.			
PA (FERN/) FERNANDES E R.			
PA (RIEG/) RIEGER D K.			
PA (EDIN/) EDINGER S R.			
PA (GUNT/) GUNTHER E.			
PA (MILL/) MILLET I.			
PA (SCIO/) SCIORE P.			
PA (ELLE/) ELLERMAN K.			
PA (MACD/) MACDOUGALL J R.			
PA (SMIT/) SMITHSON G.			
Percent Similarity:	40.35%		
Best Local Similarity:	26.90%		
Query Match:	12.85%		
RESULT 929			
ID ADH71821 standard; DNA; 8270 BP.			
DE Human gene of the invention NOV29aa SEQ ID NO:717.			
PN WO2003102155-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Percent Similarity:	40.35%		
Best Local Similarity:	26.90%		
Query Match:	12.85%		
RESULT 930			
ID ABX10231 standard; cDNA; 11796 BP.			
DE Human cDNA encoding protein NOV9.			
PN WO200285922-A2.			
PD 31-OCT-2002.			
PA (CURA-) CURAGEN CORP.			
PA (MILL-) MILLENNIUM PHARM INC.			
Percent Similarity:	39.55%		
Best Local Similarity:	28.30%		
Query Match:	12.85%		
RESULT 931			
ID AAV40528 standard; cDNA; 3442 BP.			
DE Homo sapiens DL185_1 clone secreted protein coding region.			
PN WO9830695-A2.			
PD 16-JUL-1998.			
PA (GEMY-) GENETICS INST INC.			
Percent Similarity:	42.01%		
Best Local Similarity:	26.74%		
Query Match:	12.79%		
RESULT 932			
ID ADQ38613 standard; DNA; 13650 BP.			
DE Human SNP containing myocardial infarction-associated gene			
PN WO2004058052-A2.			
PD 15-JUL-2004.			
PA (APPL-) APPLERA CORP.			
Percent Similarity:	38.91%		
Best Local Similarity:	26.05%		
Query Match:	12.79%		
RESULT 933			
ID ADQ38612 standard; DNA; 13711 BP.			
DE Human SNP containing myocardial infarction-associated gene			
PN WO2004058052-A2.			
PD 15-JUL-2004.			
PA (APPL-) APPLERA CORP.			
Percent Similarity:	38.91%		
Best Local Similarity:	26.05%		
Query Match:	12.79%		
RESULT 934			
ID ADQ38611 standard; DNA; 13711 BP.			
DE Human SNP containing myocardial infarction-associated gene			
PN WO2004058052-A2.			
PD 15-JUL-2004.			
PA (APPL-) APPLERA CORP.			
Percent Similarity:	38.91%		
Best Local Similarity:	26.05%		
Query Match:	12.79%		
RESULT 935			
ID ADQ38610 standard; DNA; 13711 BP.			
DE Human SNP containing myocardial infarction-associated gene			
PN WO2004058052-A2.			
PD 15-JUL-2004.			
PA (APPL-) APPLERA CORP.			
Percent Similarity:	38.91%		
Best Local Similarity:	26.05%		
Query Match:	12.79%		

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Query Match: 12.79% Indels: 42
RESULT 934
ID ADQ38614 standard; DNA; 13793 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 277.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.79% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 935
ID ADQ38611 standard; DNA; 14194 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 274.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.79% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 936
ID AAT87074 standard; cDNA; 2869 BP.
DE Rat Dmk receptor cDNA.
FN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.13%
Best Local Similarity: 25.16%
Query Match: 12.76% Indels: 51
Conservative: 45
Mismatch: 145
Indels: 51
RESULT 937
ID AAT90472 standard; cDNA; 2869 BP.
DE Rat muscle-specific kinase (MusK) cDNA.
FN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.13%
Best Local Similarity: 25.16%
Query Match: 12.76% Indels: 51
Conservative: 45
Mismatch: 145
Indels: 51
RESULT 938
ID ABQ33038 standard; cDNA; 8455 BP.
DE Mouse cancer-associated cDNA MK22-025.1.
FN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 38.78%
Best Local Similarity: 25.51%
Query Match: 12.76% Indels: 77
Conservative: 39
Mismatch: 103
Indels: 77
RESULT 939
ID ABQ32650 standard; cDNA; 10976 BP.
DE Human cancer-associated cDNA HR13-036.1.
FN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 36.96%
Best Local Similarity: 24.30%
Query Match: 12.76% Indels: 116
Conservative: 50
Mismatch: 134
Indels: 116
RESULT 940
ID AAT87073 standard; DNA; 2610 BP.
DE Human dmk receptor gene.
FN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.88%
Best Local Similarity: 26.17%
Query Match: 12.74% Indels: 55
Conservative: 44
Mismatch: 138
Indels: 55
RESULT 941
ID AAT90473 standard; cDNA; 2610 BP.
DE Human muscle-specific kinase (MusK) cDNA.
FN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.88%
Best Local Similarity: 26.17%
Query Match: 12.74% Indels: 55
Conservative: 44
Mismatch: 138
Indels: 55
Query Match: 12.79% Indels: 42
RESULT 942
ID ADQ89843 standard; DNA; 2610 BP.
DE Antagonist of cell cycle progression nucleotide sequence #137.
FN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Percent Similarity: 39.88%
Best Local Similarity: 26.17%
Query Match: 12.74% Indels: 55
Conservative: 44
Mismatch: 138
Indels: 55
RESULT 943
ID ADL13698 standard; DNA; 13182 BP.
DE Osteoarthritis-associated polymorphic nucleotide #230.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.74% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 944
ID ADL13697 standard; DNA; 13793 BP.
DE Osteoarthritis-associated polymorphic nucleotide #229.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.74% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 945
ID ADL35757 standard; DNA; 13793 BP.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) DNA.
FN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.74% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 946
ID AAS87452 standard; cDNA; 14586 BP.
DE DNA encoding novel human diagnostic protein #23256.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.74% Indels: 42
Conservative: 40
Mismatch: 148
Indels: 42
RESULT 947
ID ADM03329 standard; cDNA; 2004 BP.
DE Human cDNA of the invention SEQ ID NO:2014.
FN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 37.60%
Best Local Similarity: 27.58%
Query Match: 12.71% Indels: 78
Conservative: 36
Mismatch: 146
Indels: 78
RESULT 948
ID ACN42337 standard; cDNA; 6144 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1212.
FN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71% Indels: 49
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 949
ID ADL16583 standard; cDNA; 6487 BP.
DE Human 282P1G3 polynucleotide #16.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71% Indels: 49
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 950
```

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ID ADL16581 standard; cDNA; 6487 BP.
DE Human 282PiG3 polynucleotide #14.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 951
ID ADL16430 standard; cDNA; 6487 BP.
DE Human 282PiG3 polynucleotide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 952
ID ADL16587 standard; cDNA; 7329 BP.
DE Human 282PiG3 polynucleotide #17.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 953
ID ADL16432 standard; cDNA; 7329 BP.
DE Human 282PiG3 polynucleotide #5.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 954
ID ADL16589 standard; cDNA; 7329 BP.
DE Human 282PiG3 polynucleotide #19.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 955
ID ADL16601 standard; cDNA; 7527 BP.
DE Human 282PiG3 polynucleotide #25.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 956
ID ADL16436 standard; cDNA; 7527 BP.
DE Human 282PiG3 polynucleotide #7.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 957
ID ADL16599 standard; cDNA; 7527 BP.
DE Human 282PiG3 polynucleotide #23.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 958
ID ADL16442 standard; cDNA; 7570 BP.
DE Human 282PiG3 polynucleotide #10.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 959
ID ADL16617 standard; cDNA; 7570 BP.
DE Human 282PiG3 polynucleotide #32.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 960
ID ADL16619 standard; cDNA; 7570 BP.
DE Human 282PiG3 polynucleotide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 961
ID ADL16434 standard; cDNA; 7602 BP.
DE Human 282PiG3 polynucleotide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 962
ID ADL16593 standard; cDNA; 7602 BP.
DE Human 282PiG3 polynucleotide #20.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 963
ID ADL16595 standard; cDNA; 7602 BP.
DE Human 282PiG3 polynucleotide #22.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 964
ID ADL16576 standard; cDNA; 7650 BP.
DE Human 282PiG3 polynucleotide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 965
ID ADL16582 standard; cDNA; 7650 BP.
DE Human 282PiG3 polynucleotide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatch: 139
Indels: 49
RESULT 966
ID ADL16612 standard; cDNA; 7650 BP.
DE Human 282PiG3 polynucleotide #30.
```



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Query Match: 12.43% Indels: 49
RESULT 997
ID ADL15033 standard; DNA; 7642 BP.
DE Human neural cell adhesion molecule DNA for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 998
ID ADJ75061 standard; DNA; 7642 BP.
DE Marker Gene SEQ ID NO:313.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 999
ID ADN04061 standard; cDNA; 7642 BP.
DE Antiprosclerotic cDNA sequence #230.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 1000
ID ADQ19765 standard; DNA; 7642 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2584.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 1001
ID ADQ23905 standard; DNA; 7642 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6725.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 1002
ID ADRI14750 standard; DNA; 7642 BP.
DE Nucleotide sequence of human MAPCAX orthologue #8.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 1003
ID ADI61707 standard; cDNA; 7647 BP.
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 334247.2.
PN US668288-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 39.42%
Best Local Similarity: 25.32%
Query Match: 12.43% Indels: 49
Conservative: 44
Mismatches: 140
Indels: 49
RESULT 1004
ID AAS66304 standard; cDNA; 1464 BP.
DE DNA encoding novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 25.32%
Query Match: 12.40% Indels: 82
Conservative: 41
Mismatches: 137
Indels: 82
RESULT 1005
ID AAS90766 standard; cDNA; 1464 BP.
DE DNA encoding novel human diagnostic protein #26570.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 25.50%
Query Match: 12.40% Indels: 82
Conservative: 41
Mismatches: 137
Indels: 82
RESULT 1006
ID AAS72490 standard; cDNA; 1802 BP.
DE DNA encoding novel human diagnostic protein #8294.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 25.50%
Query Match: 12.40% Indels: 82
Conservative: 41
Mismatches: 137
Indels: 82
RESULT 1007
ID AAS66206 standard; cDNA; 2214 BP.
DE DNA encoding novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 25.50%
Query Match: 12.40% Indels: 82
Conservative: 41
Mismatches: 137
Indels: 82
RESULT 1008
ID AAK94785 standard; cDNA; 2500 BP.
DE Human full-length cDNA, SEQ ID NO: 3892.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.90%
Best Local Similarity: 23.89%
Query Match: 12.40% Indels: 68
Conservative: 44
Mismatches: 127
Indels: 68
RESULT 1009
ID ADL31859 standard; cDNA; 2500 BP.
DE Full length human cDNA clone SeqID 3892.
PN EP139543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 37.90%
Best Local Similarity: 23.89%
Query Match: 12.40% Indels: 68
Conservative: 44
Mismatches: 127
Indels: 68
RESULT 1010
ID AAX37725 standard; cDNA; 3598 BP.
DE Human PRO335 DNA fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1011
ID AAX52264 standard; DNA; 3662 BP.
DE Protein PRO335 cDNA clone DNA41388-1234.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1012
ID AA252206 standard; cDNA; 3662 BP.
DE Human PRO335 protein encoding cDNA, UNQ287V.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1013
ID AA252206 standard; cDNA; 3662 BP.
DE Human PRO335 protein encoding cDNA, UNQ287V.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatches: 148
Indels: 146
```


ID ADC78601 standard; cDNA; 3662 BP.
DE Human PRO335 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.90%
Best Local Similarity: 23.89%
Query Match: 12.40%
Conservative: 44
Mismatch: 127
Indels: 68
RESULT 1014

ID AAF72422 standard; cDNA; 3662 BP.
DE Human PRO335 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1015

ID AA500161 standard; cDNA; 3662 BP.
DE Human cDNA clone DNA41388-1234 encoding PRO335 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1016

ID ACA60239 standard; cDNA; 3662 BP.
DE Human cDNA for secreted/transmembrane protein PRO335.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1017

ID ADC07639 standard; cDNA; 3662 BP.
DE Novel human secreted and transmembrane protein PRO335 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1018

ID ABX71687 standard; cDNA; 3662 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO335.
PN US200213240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1019

ID ACH07019 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane polypeptide PRO335 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1020

ID ABX96256 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #52.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1021

ID ACA05577 standard; cDNA; 3662 BP.

DE cDNA encoding human secreted protein PRO335.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1022

ID ACD20244 standard; cDNA; 3662 BP.
DE Human secreted / transmembrane polypeptide PRO335 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1023

ID ACA55047 standard; cDNA; 3662 BP.
DE Novel human secreted and transmembrane protein PRO335 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1024

ID ACD19882 standard; cDNA; 3662 BP.
DE Human secreted / transmembrane polypeptide PRO335 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1025

ID ADS29494 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1026

ID ADA18350 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003039571-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1027

ID ACD67029 standard; cDNA; 3662 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO335.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1028

ID ACD83190 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1029

ID ADA16325 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.

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PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1030
ID ADA42470 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1031
ID ACD23368 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1032
ID ADA16749 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1033
ID ADA13178 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1034
ID ADA42046 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1035
ID ADA17393 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1036
ID ADA42896 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1037
ID ACD23730 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
PN US2003064923-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1038
ID ADB77815 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1039
ID ADB74951 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1040
ID ADC28597 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1041
ID ADC39797 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1042
ID ADC40311 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1043
ID ADC19135 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1044
ID ADC34435 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1045
ID ADC29490 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003049676-A1.
PD 13-MAR-2003.
```


Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1062
ID ADE79791 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1063
ID ADE73467 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1064
ID ADE74002 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1065
ID ADE99556 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1066
ID ADE98675 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1067
ID ADE99102 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1068
ID ADG40572 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1069
ID ADF73966 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.

DE Human secreted/transmembrane protein cDNA, #54.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1070
ID ADF73542 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1071
ID ADG92385 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1072
ID ADG92812 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1073
ID ADH20601 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1074
ID ADH07456 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1075
ID ADH60001 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1076
ID ADH07029 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.

PA (GODD/) GODDARD A. 33.03% Conservative: 54
 PA (GODO/) GODOWSKI P. J. 33.03% Mismatches: 148
 PA (GURN/) GURNEY A. L. 20.73% Indels: 146
 PA (MATH/) MATHER J. P. 12.40%
 PA (WILL/) WILLIAMS P. M. 33.03% Conservative: 54
 PA (WOOD/) WOOD W. I. 20.73% Mismatches: 148
 Percent Similarity: 12.40% Indels: 146
 Best Local Similarity: 33.03%
 Query Match: 20.73%
 RESULT 1077
 ID AD118771 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003152959-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1078
 ID AD137750 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003096340-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1079
 ID ADH97550 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003190610-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1080
 ID AD165918 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003148371-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1081
 ID ADH60661 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2004023331-A1.
 PD 05-FEB-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P. J.
 PA (GURN/) GURNEY A. L.
 PA (MATH/) MATHER J. P.
 PA (WILL/) WILLIAMS P. M.
 PA (WOOD/) WOOD W. I.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1082
 ID ADJ99718 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1083
 ID ADL08911 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003186358-A1.

PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1084
 ID ADM25252 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003096233-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1085
 ID ADM30002 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2003190611-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1086
 ID ADO06324 standard; cDNA; 3662 BP.
 DE Human PRO polynucleotide #52.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1087
 ID ADR11176 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146
 RESULT 1088
 ID ADR18085 standard; cDNA; 3662 BP.
 DE Human secreted/transmembrane protein cDNA, #54.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D. L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M. E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P. J.
 PA (GRIM/) GRIMALDI C. J.
 PA (GURN/) GURNEY A. L.
 PA (HILL/) HILLAN K. J.
 PA (KLJA/) KLJAVIN I. J.
 PA (MATH/) MATHER J. P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N. P.
 PA (ROYM/) ROY M. A.
 PA (STEW/) STEWART T. A.
 PA (TUNA/) TUNAS D.
 PA (WILL/) WILLIAMS P. M.
 PA (WOOD/) WOOD W. I.
 Percent Similarity: 33.03% Conservative: 54
 Best Local Similarity: 20.73% Mismatches: 148
 Query Match: 12.40% Indels: 146

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RESULT 1089
ID AD703761 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
FN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1090
ID ADS74724 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane cDNA #54.
FN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1091
ID AAX37743 standard; cDNA; 3807 BP.
DE Human PRO326 DNA fragment #2.
FN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1092
ID AAX52266 standard; DNA; 4053 BP.
DE Protein PRO326 cDNA clone DNA37140-1234.
FN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1093
ID AA252208 standard; cDNA; 4053 BP.
DE Human PRO326 protein encoding cDNA, UNQ287.
FN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1094
ID AAF72424 standard; cDNA; 4053 BP.
DE Human PRO326 cDNA.
FN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1095
ID AAC84422 standard; cDNA; 4053 BP.
DE Human PRO326 polypeptide encoding cDNA.
FN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1096
ID AAS00163 standard; cDNA; 4053 BP.
DE Human cDNA clone DNA37140-1234 encoding PRO326 (UNQ287).
FN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1097
ID AAS21419 standard; cDNA; 4053 BP.
DE Human cDNA sequence encoding for PRO326 polypeptide.
FN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1098
ID ACA60241 standard; cDNA; 4053 BP.
DE Human cDNA for secreted/transmembrane protein PRO326.
FN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1099
ID ACD07641 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1100
ID ACA03778 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1101
ID ABX71689 standard; cDNA; 4053 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO326.
FN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1102
ID ACH07021 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane polypeptide PRO326 cDNA.
FN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 12.40% Indels: 146
RESULT 1119
ID ADA15943 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1120
ID ADA87482 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1121
ID ADA18354 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
FN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1122
ID ACB67031 standard; cDNA; 4053 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO326.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1123
ID ADA67524 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1124
ID ADB30531 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1125
ID ADA85927 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1126
ID ADA97039 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1127
ID ADA79343 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1128
ID ADA87482 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1129
ID ADB16684 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1130
ID ACB83192 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
FN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1131
ID ADA16329 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
FN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1132
ID ADA91776 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1133
ID ADB14839 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1134
ID ADB18800 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1135
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ID ADA94015 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1136

ID ADB19911 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1137

ID ADB13223 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1138

ID ACD98599 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1139

ID ADA74477 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1140

ID ADA42474 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1141

ID ADB24710 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1142

ID ADA82234 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1143

ID ADA75197 standard; cDNA; 4053 BP.

DE Human PRO polynucleotide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1144

ID ADA85275 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1145

ID ADA84723 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1146

ID ACD23370 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1147

ID ADB29979 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1148

ID ADA80507 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1149

ID ADA75749 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1150

ID ADA46974 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1151

ID ADB25270 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.

PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1152
ID ADA93446 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1153
ID ADB26796 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1154
ID ADB31083 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1155
ID ADA61011 standard; cDNA; 4053 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1156
ID ADB24158 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1157
ID ADA96487 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1158
ID ADA81059 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1159
ID ADA95935 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082759-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1160
ID ADB26244 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1161
ID ADB21729 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1162
ID ADA77508 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1163
ID ADB18248 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1164
ID ADA86931 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1165
ID ADA16753 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1166
ID ADA13182 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1167
ID ADA42050 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082540-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1168
ID ADA88034 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1169
ID ADA46422 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1170
ID ADAL7397 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1171
ID ADA42900 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1172
ID AD828452 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1173
ID ADB29004 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1174
ID ADA76956 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1175
ID ADA88586 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1176
ID ADA97591 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082886-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1177
ID ADB27348 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1178
ID ADB22281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1179
ID ADB23732 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1180
ID ADA66972 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1181
ID ADB22833 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1182
ID ADB23606 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1183
ID ADA92328 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1184
ID ADA88586 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 1184
ID ADB15391 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1185
ID ADB38643 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1186
ID ADB38091 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087347-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1187
ID ADB66563 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1188
ID ADB89643 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1189
ID ADB90375 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1190
ID ADB77819 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1191
ID ADB39476 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1192

ID ADB74955 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1193
ID ADB47099 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1194
ID ADB86706 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1195
ID ADB77311 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1196
ID ADB34468 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1197
ID ADB35572 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1198
ID ADB33916 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1199
ID ADB35020 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1200
ID ADB36124 standard; cDNA; 4053 BP.

DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1201
ID ADB46519 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1202
ID ADC28601 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1203
ID ADC39801 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1204
ID ADC40315 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1205
ID ADC19139 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1206
ID ADC34439 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1207
ID ADC29494 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1208
ID ADC29025 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.

PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1209
ID ADC40910 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1210
ID ADC19567 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1211
ID ADC34015 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1212
ID ADC13085 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1213
ID ADC50392 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1214
ID ADC71939 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1215
ID ADC59918 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1216
ID ADC52925 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087365-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1217
ID ADC57279 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1218
ID ADC60470 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1219
ID ADC50945 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1220
ID ADC65472 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1221
ID ADC54570 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1222
ID ADC53531 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1223
ID ADC59054 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1224
ID ADC55932 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087360-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1225
ID ADC58502 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1226
ID ADC12537 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1227
ID ADD03176 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1228
ID ADC90168 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1229
ID ADC69587 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1230
ID ADC48476 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1231
ID ADD10005 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 33.03%
Query Match: 12.40%
RESULT 1232
ID ADD04580 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.


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Query Match: 12.40% Indels: 146
RESULT 1249
ID ADD92485 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1250
ID ADD91381 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1251
ID ADE03995 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1252
ID ADE32292 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1253
ID ADE22224 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1254
ID ADD79448 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1255
ID ADE41984 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1256
ID ADE17801 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1257
ID ADD91933 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1258
ID ADE33396 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1259
ID ADE33948 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1260
ID ADE80000 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1261
ID ADD93037 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1262
ID ADE19457 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1263
ID ADE34926 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
FN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1264
ID ADE18905 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40% Indels: 146
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1265
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ID ADB43101 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1266

ID ADP95890 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1267

ID ADP95890 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1268

ID ADD78894 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1269

ID ADB32844 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1270

ID ADB42536 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1271

ID ADD80552 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1272

ID ADB89580 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1273

ID ADB40864 standard; cDNA; 4053 BP.

DE Human PRO polynucleotide #176.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1274

ID ADE04663 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1275

ID ADP92792 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1276

ID ADG21501 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1277

ID ADG23142 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1278

ID ADF97477 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1279

ID ADG80541 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1280

ID ADG79989 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1281

ID ADH59409 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.

PN US2003039972-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1282
ID ADH55281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1283
ID ADH55283 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1284
ID ADI38188 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1285
ID ADI64052 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1286
ID ADI65001 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1287
ID ADI63500 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1288
ID ADH81914 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1289
ID ADH81362 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207377-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1290
ID ACA59137 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1291
ID ACD24028 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1292
ID ACA58534 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1293
ID ACA67169 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1294
ID ADJ26456 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1295
ID ADM82531 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1296
ID ADN15930 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1297
ID ADN16559 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1298
ID ADN15378 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1299
ID ADN14826 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1300
ID ADC91088 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1301
ID ADE79371 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1302
ID ADD76536 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1303
ID ADD87900 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1304
ID ADD86304 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1305
ID ADE79795 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1306
ID ADE75752 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1307
ID ADE73471 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1308
ID ADE23328 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1309
ID ADE23880 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1310
ID ADE24523 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1311
ID ADD87348 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1312
ID ADE89214 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1313
ID ADE74006 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146

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Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1314
ID ADE18353 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein #176.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1315
ID ADE88662 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1316
ID ADE99560 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1317
ID ADE94682 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1318
ID ADE91093 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1319
ID ADE95234 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1320
ID ADE93344 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1321
ID ADE34925 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1322
ID ADE98679 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1323
ID ADE92240 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1324
ID ADE90541 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1325
ID ADE91688 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1326
ID ADE99106 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1327
ID ADG40576 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1328
ID ADF73970 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1329
ID ADG02267 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
```

PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1330
ID ADG22053 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1331
ID ADG20123 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1332
ID ADF98029 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1333
ID ADG24246 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1334
ID ADF98600 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1335
ID ADG03431 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1336
ID ADF99152 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1337
ID ADG16737 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207359-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1338
ID ADG05196 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1339
ID ADG19463 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1340
ID ADF73546 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1341
ID ADG13300 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1342
ID ADG08357 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1343
ID ADG15527 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1344
ID ADF96925 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1345
ID ADG06110 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207374-A1.
PD 06-NOV-2003.

Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1362
ID ADG57988 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1363
ID ADG53572 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1364
ID ADG71458 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1365
ID ADG81645 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1366
ID ADH30607 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1367
ID ADH11974 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1368
ID ADG52396 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1369
ID ADG54124 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146

RESULT 1370
ID ADG81093 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1371
ID ADG56332 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1372
ID ADH12598 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1373
ID ADG61444 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1374
ID ADH28531 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1375
ID ADG54676 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1376
ID ADG59716 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1377
ID ADH20605 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1378
ID ADH20605 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146

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ID ADH07460 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1379
ID ADH60005 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1380
ID ADH07033 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1381
ID ADH18140 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1382
ID ADH18775 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003152399-A1.
PD 14-AUG-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1383
ID ADH37754 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1384
ID ADG09883 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1385
ID ADH97554 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1386
ID ADH15354 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1387
ID ADG09231 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1388
ID ADH65922 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1389
ID ADH14686 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1390
ID ADH60665 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1391
ID ADH18281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indel: 146
RESULT 1392
ID ADJ99722 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
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PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1393
 ID ADJ08915 standard; cDNA; 4053 BP.
 DE Human secreted/transmembrane protein cDNA, #56.
 PN US2003186358-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1394
 ID ADJ25256 standard; cDNA; 4053 BP.
 DE Human secreted/transmembrane protein cDNA, #56.
 PN US2003096233-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1395
 ID ADJ63562 standard; cDNA; 4053 BP.
 DE Novel human secreted and transmembrane protein PRO326 cDNA.
 PN US2004039164-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1396
 ID ADJ30006 standard; cDNA; 4053 BP.
 DE Human secreted/transmembrane protein cDNA, #56.
 PN US2003190611-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1397
 ID ADJ77457 standard; cDNA; 4053 BP.
 DE Human PRO polynucleotide #176.
 PN US2004038336-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1398
 ID ADJ65579 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US2004038335-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1399
 ID ADJ27715 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1400
 ID ADJ42439 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US2004058424-A1.

PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1401
 ID ADJ06328 standard; cDNA; 4053 BP.
 DE Human PRO polynucleotide #54.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1402
 ID ADJ28301 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1403
 ID ADJ1180 standard; cDNA; 4053 BP.
 DE Human secreted/transmembrane protein cDNA, #56.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1404
 ID ADJ18089 standard; cDNA; 4053 BP.
 DE Human secreted/transmembrane protein cDNA, #56.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOVERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M B.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1405
 ID ADJ95783 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US200307659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Query Match: 12.40%
 RESULT 1406
 ID ADJ42439 standard; cDNA; 4053 BP.
 DE cDNA encoding human PRO polypeptide #176.
 PN US2004058424-A1.

RESULT 1406
ID ADI96335 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1407
ID ADT03765 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1408
ID ADS74728 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane cDNA #56.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHENNAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1409
ID ABA06424 standard; cDNA; 2667 BP.
DE Human cDNA SEQ ID NO: 90.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 37.92%
Best Local Similarity: 25.28%
Query Match: 12.38%
Conservative: 34
Mismatch: 123
Indels: 45
RESULT 1410
ID ABV83761 standard; cDNA; 2667 BP.
DE Human polynucleotide SEQ ID NO 90.
PN US2002090872-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 37.92%
Best Local Similarity: 25.28%
Query Match: 12.38%
Conservative: 34
Mismatch: 123
Indels: 45
RESULT 1411
ID ABX34664 standard; cDNA; 1213 BP.
DE Human mddt cDNA SEQ ID 225.

PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.94%
Best Local Similarity: 26.40%
Query Match: 12.35%
Conservative: 38
Mismatch: 123
Indels: 62
RESULT 1412
ID AA233346 standard; cDNA; 1417 BP.
DE Human secreted protein clone cw1000_2 nucleotide sequence SEQ ID NO:61.
PN WO9957132-A1.
PD 11-NOV-1999.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.25%
Best Local Similarity: 25.07%
Query Match: 12.35%
Conservative: 61
Mismatch: 153
Indels: 52
RESULT 1413
ID ADR28012 standard; cDNA; 3540 BP.
DE Long form full-length IGSF9 protein encoding cDNA.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.
PA (ROWE/) ROWE T.
Percent Similarity: 39.48%
Best Local Similarity: 24.78%
Query Match: 12.35%
Conservative: 51
Mismatch: 144
Indels: 66
RESULT 1414
ID ADP28247 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #245.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 40.81%
Best Local Similarity: 25.55%
Query Match: 12.29%
Conservative: 49
Mismatch: 142
Indels: 48
RESULT 1415
ID ADP28237 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #235.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 40.81%
Best Local Similarity: 25.55%
Query Match: 12.29%
Conservative: 49
Mismatch: 142
Indels: 48
RESULT 1416
ID ADH72193 standard; DNA; 3333 BP.
DE Human gene of the invention NOV51d SEQ ID NO:1089.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.25%
Best Local Similarity: 24.15%
Query Match: 12.29%
Conservative: 40
Mismatch: 111
Indels: 50
RESULT 1417
ID ABL23498 standard; DNA; 7171 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21967.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.66%
Best Local Similarity: 24.05%
Query Match: 12.29%
Conservative: 43
Mismatch: 115
Indels: 101
RESULT 1418
ID AAA43911 standard; cDNA; 971 BP.
DE Human secreted expressed sequence tag SEQ ID NO:486.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.34%
Best Local Similarity: 26.43%
Query Match: 12.24%
Conservative: 53
Mismatch: 128
Indels: 65
RESULT 1419

ID AAS86820 standard; cDNA; 2948 BP.
DE DNA encoding novel human diagnostic protein #22624.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 37.77% Conservative: 28
Best Local Similarity: 25.75% Mismatches: 107
Query Match: 12.24% Indels: 38
RESULT 1420
ID AAV31988 standard; cDNA; 6413 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity: 40.25% Conservative: 28
Best Local Similarity: 28.63% Mismatches: 122
Query Match: 12.24% Indels: 22
RESULT 1421
ID AAV31981 standard; cDNA; 6604 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity: 40.25% Conservative: 28
Best Local Similarity: 28.63% Mismatches: 122
Query Match: 12.24% Indels: 22
RESULT 1422
ID ADK71086 standard; DNA; 6649 BP.
DE Human MP21 polypeptide encoding DNA.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 40.25% Conservative: 28
Best Local Similarity: 28.63% Mismatches: 122
Query Match: 12.24% Indels: 22
RESULT 1423
ID ADR41293 standard; cDNA; 1153 BP.
DE Human CD-like molecule HATC207 cDNA, SEQ ID NO:92.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1424
ID AAR80677 standard; cDNA; 1329 BP.
DE Human secreted protein #11 nucleotide sequence SEQ ID #137.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1425
ID ADA27145 standard; cDNA; 1329 BP.
DE Human novel secreted protein from gene 11 cDNA #3.
PN US200305231-A1.
PD 20-MAR-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P B.
PA (KINN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1426
ID ADE86686 standard; cDNA; 1329 BP.

DE Novel human secreted protein #11 associated cDNA #1.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P B.
PA (KINN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1427
ID AAX80055 standard; cDNA; 1413 BP.
DE Human PRO355 nucleotide sequence.
PN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1428
ID AAA49563 standard; cDNA; 1413 BP.
DE Human PRO355 cDNA.
PN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1429
ID AAS45941 standard; cDNA; 1413 BP.
DE Human DNA encoding PRO polypeptide sequence #17.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1430
ID ACA89391 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003036141-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1431
ID ACA73401 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1432
ID ACA05716 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1433
ID ACA66550 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO protein #17.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1434
ID ACF20125 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040063-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1435
ID ACF19511 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040064-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1436
ID ACD21799 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1437
ID ACF12964 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036160-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1438
ID ACD25067 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1439
ID ACF00116 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003054474-A1.
PD 20-MAR-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1440
ID ABX96814 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1441
ID ACA72173 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1442
ID ACD04697 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032101-A1.

PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1443
ID ACD18158 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1444
ID ACD08165 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1445
ID ABX78468 standard; DNA; 1413 BP.
DE DNA encoding Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1446
ID ACA88599 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1447
ID ACA70041 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036134-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1448
ID ACD12263 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1449
ID ACC74178 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027275-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1450
ID ACD15806 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003027324-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1451
ID ACD25374 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036118-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1452
ID ACD17851 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036123-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1453
ID ACC88138 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036148-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1454
ID ACD21492 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003040060-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1455
ID ACD18559 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003044916-A1.
PD 06-MAR-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1456
ID ABX77102 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1457
ID ABX98169 standard; cDNA; 1413 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 33.
PN US2003036156-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1458
ID ACD13920 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032117-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1459
ID ACD09700 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036128-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1460
ID ACC88445 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.

PN US2003027266-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1461
ID ACD21185 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1462
ID ABX75557 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1463
ID ABX97760 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032102-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1464
ID ACA97236 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1465
ID ACA57699 standard; cDNA; 1413 BP.
DE Human PRO355 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1466
ID ACD14227 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032130-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1467
ID ACC91010 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1468
ID ACC88752 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036132-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1469
ID ACD06949 standard; cDNA; 1413 BP.

DE Human PRO polynucleotide #17.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1470
ID ACA67400 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1471
ID ACC81455 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032137-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1472
ID ACC89059 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027269-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1473
ID ACC86415 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027268-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1474
ID ACC89673 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027374-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1475
ID ACC92852 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1476
ID ACA72480 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1477
ID ACA88998 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003022297-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1478
ID ACA96877 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1479
ID ACA96877 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1480
ID ACA90873 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1481
ID ACA70655 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032111-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1482
ID ACA95165 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1483
ID ACC86108 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027263-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1484
ID ACC89980 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027271-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1485
ID ACD12588 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036125-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1486
ID ACF19818 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040068-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1487

ID ABX75933 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO355.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1488
ID ABX76762 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1489
ID ACA73094 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1490
ID ACA68637 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1491
ID ACA74481 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1492
ID ACA70348 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1493
ID ACD14534 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003040066-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1494
ID ABX89644 standard; cDNA; 1413 BP.
DE cDNA encoding novel secreted and transmembrane protein PRO355.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1495
ID ACA68206 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45

RESULT 1496
ID ABX98671 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1497
ID ACC81148 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032120-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1498
ID ACA95472 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1499
ID ACD04390 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1500
ID ACC87831 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 16, 2005, 12:21:54 ; Search time 212 Seconds
(without alignments)
2655.091 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTQPKMHSISWAIFGL.....RRAGCVMLPLLVLLHLKLF 344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOPECL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10017084 @CCN 1.1 69 @runat 14062005 151230 18877 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	1032	4	US-09-700-397-1
2	1806	100.0	1693	4	US-09-700-397-2
3	1642	90.9	939	4	US-09-700-397-5
4	931.5	51.6	1195	4	US-09-976-594-403
5	926.5	51.3	1014	2	US-08-414-657D-5
6	926.5	51.3	1018	3	US-09-135-080-7
7	926.5	51.3	1234	2	US-08-414-657D-3
8	926.5	51.3	1238	3	US-09-135-080-3
9	923.5	51.1	977	2	US-08-414-657D-1
10	923.5	51.1	977	3	US-09-135-080-1
11	908	50.3	924	2	US-08-414-657D-7
12	907	50.2	945	2	US-08-414-657D-8

13	902	49.9	912	2	US-08-414-657D-6	Sequence 6, Appli
14	886.5	49.1	861	2	US-08-414-657D-9	Sequence 9, Appli
15	885.5	49.0	861	2	US-08-414-657D-10	Sequence 10, Appli
16	796.5	44.1	756	2	US-08-414-657D-17	Sequence 17, Appli
17	795.5	44.0	756	2	US-08-414-657D-18	Sequence 18, Appli
18	742.5	41.1	1030	4	US-09-949-016-4587	Sequence 4587, Ap
19	545	30.2	333	4	US-09-513-999C-23289	Sequence 23289, A
20	344	19.0	352	4	US-09-513-999C-2775	Sequence 2775, Ap
21	339	18.8	113538	4	US-09-949-016-16329	Sequence 16329, A
22	302.5	16.7	913	4	US-09-774-528-410	Sequence 410, App
23	276	15.3	2599	4	US-09-949-016-4676	Sequence 4676, Ap
24	275	15.2	2633	4	US-09-023-655-950	Sequence 950, App
25	274	15.2	5807	4	US-09-976-594-245	Sequence 245, App
26	273.5	15.1	2118	4	US-09-270-767-11659	Sequence 11659, A
27	263.5	14.6	6814	3	US-09-484-970B-6	Sequence 66, Appli
28	256	14.2	1266	3	US-08-659-984A-2	Sequence 2, Appli
29	256	14.2	1266	3	US-08-660-531-2	Sequence 2, Appli
30	256	14.2	1335	2	US-08-659-984A-4	Sequence 4, Appli
31	256	14.2	1335	3	US-08-660-531-4	Sequence 4, Appli
32	249.5	13.8	4548	4	US-09-571-479C-5	Sequence 5, Appli
33	246.5	13.6	3318	4	US-09-949-016-4450	Sequence 4450, Ap
34	246.5	13.6	3360	1	US-08-408-093-5	Sequence 5, Appli
35	246.5	13.6	3360	1	US-08-408-420A-5	Sequence 5, Appli
36	246.5	13.6	3360	1	US-08-714-901-5	Sequence 5, Appli
37	246.5	13.6	3360	3	US-08-040-741-5	Sequence 5, Appli
38	241.5	13.4	4723	4	US-09-949-016-644	Sequence 644, App
39	241	13.3	6599	4	US-09-799-451-350	Sequence 350, App
40	237.5	13.2	4597	4	US-09-949-016-5173	Sequence 5173, Ap
41	237	13.1	219	2	US-08-414-657D-11	Sequence 11, Appli
42	237	13.1	219	2	US-08-414-657D-12	Sequence 12, Appli
43	230.5	12.8	2869	1	US-08-374-834-2	Sequence 2, Appli
44	230.5	12.8	2869	1	US-08-644-271-2	Sequence 2, Appli
45	230.5	12.8	2869	3	US-09-077-955-2	Sequence 2, Appli
46	230	12.7	2610	1	US-08-374-834-17	Sequence 17, Appli
47	230	12.7	2610	1	US-08-644-271-28	Sequence 28, Appli
48	230	12.7	2610	3	US-09-077-955-32	Sequence 32, Appli
49	225.5	12.5	1581	5	PCT-US95-084933-14	Sequence 14, Appli
50	225.5	12.5	2580	5	PCT-US95-08493-18	Sequence 18, Appli
51	225.5	12.5	2604	5	PCT-US95-08493-20	Sequence 20, Appli
52	225	12.5	2607	4	US-09-715-249-7	Sequence 7, Appli
53	224.5	12.4	7647	4	US-09-566-921-75	Sequence 75, Appli
54	224	12.4	3662	4	US-09-907-794A-289	Sequence 289, App
55	224	12.4	3662	4	US-09-905-125A-289	Sequence 289, App
56	224	12.4	3662	4	US-09-902-775A-289	Sequence 289, App
57	224	12.4	3662	4	US-09-906-700-289	Sequence 289, App
58	224	12.4	3662	4	US-09-903-603A-289	Sequence 289, App
59	224	12.4	3662	4	US-09-904-920A-289	Sequence 289, App
60	224	12.4	3662	4	US-09-903-084-289	Sequence 289, App
61	224	12.4	3662	4	US-09-903-381A-289	Sequence 289, App
62	224	12.4	3662	4	US-09-906-618-289	Sequence 289, App
63	224	12.4	4053	4	US-09-907-794A-293	Sequence 293, App
64	224	12.4	4053	4	US-09-905-125A-293	Sequence 293, App
65	224	12.4	4053	4	US-09-902-775A-293	Sequence 293, App
66	224	12.4	4053	4	US-09-906-700-293	Sequence 293, App
67	224	12.4	4053	4	US-09-903-603A-293	Sequence 293, App
68	224	12.4	4053	4	US-09-904-920A-293	Sequence 293, App
69	224	12.4	4053	4	US-09-909-064-293	Sequence 293, App
70	224	12.4	4053	4	US-09-905-381A-293	Sequence 293, App
71	224	12.4	4053	4	US-09-906-618-293	Sequence 293, App
72	220.5	12.2	1413	4	US-09-866-028-60	Sequence 60, Appli
73	220.5	12.2	1413	4	US-09-944-457-60	Sequence 60, Appli
74	220.5	12.2	1598	4	US-09-778-510-19	Sequence 19, Appli
75	220.5	12.2	1935	4	US-09-778-510-21	Sequence 21, Appli
76	219	12.1	4843	3	US-08-986-485-1	Sequence 1, Appli
77	213.5	11.8	1685	4	US-09-907-794A-83	Sequence 83, Appli
78	213.5	11.8	1685	4	US-09-905-125A-83	Sequence 83, Appli
79	213.5	11.8	1685	4	US-09-902-775A-83	Sequence 83, Appli
80	213.5	11.8	1685	4	US-09-906-700-83	Sequence 83, Appli
81	213.5	11.8	1685	4	US-09-903-603A-83	Sequence 83, Appli
82	213.5	11.8	1685	4	US-09-904-920A-83	Sequence 83, Appli
83	213.5	11.8	1685	4	US-09-909-064-83	Sequence 83, Appli
84	213.5	11.8	1685	4	US-09-905-381A-83	Sequence 83, Appli
85	213.5	11.8	1685	4	US-09-906-618-83	Sequence 83, Appli

86	213.5	11.8	1718	4	US-09-778-510-5	Sequence 5, Appli	159	173.5	9.6	2550	1	US-08-481-130-10	Sequence 10, Appli
87	213	11.8	177	2	US-08-414-657D-13	Sequence 13, Appli	160	173.5	9.6	2550	1	US-08-656-984A-10	Sequence 10, Appli
88	212	11.7	177	2	US-08-414-657D-14	Sequence 14, Appli	161	173.5	9.6	2550	1	US-08-485-604-10	Sequence 10, Appli
89	211.5	11.7	5506	4	US-09-576-594-530	Sequence 530, App	162	173.5	9.6	2550	2	US-08-487-595-10	Sequence 10, Appli
90	211	11.7	1273	4	US-09-778-510-3	Sequence 3, Appli	163	173.5	9.6	2988	1	US-08-245-295-1	Sequence 1, Appli
91	210	11.6	577	4	US-09-270-767-1011	Sequence 1011, Ap	164	173.5	9.6	2988	1	US-08-481-130-1	Sequence 1, Appli
92	210	11.6	577	4	US-09-270-767-16293	Sequence 16293, A	165	173.5	9.6	2988	1	US-08-656-984A-1	Sequence 1, Appli
93	210	11.6	4078	4	US-09-016-434-1120	Sequence 1120, Ap	166	173.5	9.6	2988	1	US-08-485-604-1	Sequence 1, Appli
94	210	11.6	5926	4	US-09-917-254-41	Sequence 41, Appli	167	173.5	9.6	2988	2	US-08-487-595-1	Sequence 1, Appli
95	209	11.6	3093	4	US-09-949-016-4183	Sequence 4183, Ap	168	173	9.6	3189	2	US-08-427-497E-3	Sequence 3, Appli
96	209	11.6	3145	4	US-09-949-016-1149	Sequence 1149, Ap	169	173	9.6	3774	2	US-08-341-843B-1	Sequence 1, Appli
97	205.5	11.4	1542	4	US-09-205-258-123	Sequence 123, App	170	173	9.6	3774	2	US-08-427-497E-1	Sequence 1, Appli
98	205	11.4	1820	4	US-09-778-510-1	Sequence 1, Appli	171	173	9.6	3774	2	US-08-427-497E-2	Sequence 2, Appli
99	203.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appli	172	173	9.5	3888	3	US-08-506-296B-13	Sequence 13, Appli
100	202	11.2	4059	4	US-09-799-451-560	Sequence 560, App	173	172	9.5	1630	3	US-08-468-856B-2	Sequence 2, Appli
101	201	11.1	3398	5	PCT-US95-08493-12	Sequence 12, Appli	174	172	9.5	1630	3	US-08-468-856A-2	Sequence 2, Appli
102	200	11.1	1967	3	US-09-383-586-22	Sequence 22, Appli	175	172	9.5	2116	4	US-09-023-655-1256	Sequence 1256, Ap
103	200	11.1	1967	4	US-09-823-038A-22	Sequence 22, Appli	176	172	9.5	3461	3	US-08-468-856B-6	Sequence 6, Appli
104	199	11.0	4285	3	US-09-040-774-1	Sequence 1, Appli	177	172	9.5	3461	3	US-08-468-856A-6	Sequence 6, Appli
105	198	11.0	6718	4	US-09-949-016-4632	Sequence 4632, Ap	178	171.5	9.5	2352	1	US-08-232-538-17	Sequence 17, Appli
106	197.5	10.9	4608	3	US-09-041-886-24	Sequence 24, Appli	179	171.5	9.5	2352	2	US-08-786-164-17	Sequence 17, Appli
107	197.5	10.9	5908	5	PCT-US94-05277-1	Sequence 1, Appli	180	171.5	9.5	4014	4	US-09-119-014D-5	Sequence 5, Appli
108	196.5	10.9	5905	4	US-09-949-016-5625	Sequence 5625, Ap	181	171.5	9.5	7680	4	US-09-953-318-3	Sequence 3, Appli
109	196.5	10.9	6218	4	US-09-949-016-706	Sequence 706, App	182	171	9.5	1473	2	US-08-602-725-31	Sequence 31, Appli
110	196.5	10.9	6384	4	US-09-976-594-724	Sequence 724, App	183	171	9.5	1473	4	US-09-949-016-245	Sequence 245, App
111	196.5	10.9	6384	4	US-09-919-039-379	Sequence 279, App	184	171	9.5	1475	4	US-09-949-016-1654	Sequence 1654, Ap
112	194	10.7	3783	3	US-08-506-236B-20	Sequence 20, Appli	185	170	9.4	862	3	US-08-468-856B-4	Sequence 4, Appli
113	192.5	10.7	2481	3	US-08-877-730-15	Sequence 15, Appli	186	170	9.4	862	3	US-08-468-859A-4	Sequence 4, Appli
114	192.5	10.7	2715	3	US-09-877-730-5	Sequence 5, Appli	187	169	9.4	1339	3	US-08-468-856B-3	Sequence 3, Appli
115	192.5	10.7	2724	3	US-09-877-730-19	Sequence 19, Appli	188	169	9.4	1339	3	US-08-468-859A-3	Sequence 3, Appli
116	192.5	10.7	2958	3	US-09-877-730-9	Sequence 9, Appli	189	168	9.3	2383	1	US-08-232-538-18	Sequence 18, Appli
117	192.5	10.7	2976	3	US-09-877-730-11	Sequence 11, Appli	190	168	9.3	2383	2	US-08-786-164-18	Sequence 18, Appli
118	192.5	10.7	3192	3	US-09-412-554A-1	Sequence 1, Appli	191	167.5	9.3	842	4	US-08-270-767-11483	Sequence 11483, A
119	192.5	10.7	3210	3	US-09-877-730-17	Sequence 17, Appli	192	167	9.2	2264	1	US-08-232-538-16	Sequence 16, Appli
120	192.5	10.7	3219	3	US-09-877-730-17	Sequence 17, Appli	193	167	9.2	2264	1	US-08-786-164-16	Sequence 16, Appli
121	192.5	10.7	3453	3	US-09-877-730-7	Sequence 7, Appli	194	167	9.2	2292	3	US-09-142-956B-1	Sequence 1, Appli
122	192.5	10.7	3874	3	US-09-877-730-31	Sequence 31, Appli	195	167	9.2	4071	3	US-09-098-707A-1	Sequence 1, Appli
123	192.5	10.7	3943	3	US-08-506-296B-27	Sequence 27, Appli	196	167	9.2	4071	3	US-09-483-539-1	Sequence 1, Appli
124	192	10.6	2094	4	US-09-270-767-13304	Sequence 13304, A	197	167	9.2	4236	2	US-08-810-116-7	Sequence 7, Appli
125	191	10.6	601	4	US-09-949-016-163724	Sequence 163724, A	198	167	9.2	4236	2	US-07-930-548A-7	Sequence 7, Appli
126	190	10.5	6055	4	US-09-563-318-10	Sequence 10, Appli	199	167	9.2	5830	4	US-09-967-655-3	Sequence 3, Appli
127	187.5	10.4	3991	3	US-08-506-296B-3	Sequence 3, Appli	200	167	9.2	5830	4	US-09-949-016-327	Sequence 327, App
128	186	10.3	3551	4	US-09-620-312D-760	Sequence 760, App	201	167	9.2	5831	4	US-09-949-016-3982	Sequence 3982, Ap
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130	185.5	10.3	1023	2	US-08-633-148-1	Sequence 1, Appli	203	166.5	9.2	1143	3	US-09-877-730-3	Sequence 3, Appli
131	185.5	10.3	1215	3	US-08-217-299-2	Sequence 2, Appli	204	166.5	9.2	1405	4	US-08-755-235-3	Sequence 3, Appli
132	185.5	10.3	2031	1	US-08-217-299-2	Sequence 2, Appli	205	166	9.2	2523	3	US-09-051-363-1	Sequence 1, Appli
133	185.5	10.3	2097	2	US-08-602-725-35	Sequence 35, Appli	206	165.5	9.2	1960	4	US-09-653-961-3	Sequence 3, Appli
134	185.5	10.3	2220	1	US-08-389-459A-16	Sequence 16, Appli	207	165.5	9.2	1962	4	US-09-653-961-5	Sequence 5, Appli
135	185.5	10.3	2220	3	US-08-987-867A-16	Sequence 16, Appli	208	165.5	9.2	2487	1	US-08-261-304-1	Sequence 1, Appli
136	185.5	10.3	2349	2	US-08-184-009-145	Sequence 145, App	209	165.5	9.2	2539	2	US-08-432-016-1	Sequence 1, Appli
137	185.5	10.3	2349	2	US-08-458-356-145	Sequence 145, App	210	165.5	9.2	2539	2	US-08-684-594-1	Sequence 1, Appli
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139	185.5	10.3	2349	4	US-09-535-370-145	Sequence 145, App	212	165.5	9.2	3306	4	US-09-023-655-1434	Sequence 1434, Ap
140	185.5	10.3	2349	4	US-09-663-667-144	Sequence 144, App	213	165.5	9.2	3583	4	US-09-949-016-857	Sequence 857, App
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142	185.5	10.3	2434	2	US-08-184-009-144	Sequence 144, App	215	165.5	9.2	4854	4	US-09-784-358-1	Sequence 1, Appli
143	185.5	10.3	2434	2	US-08-458-356-144	Sequence 144, App	216	165.5	9.2	5076	4	US-09-784-358-1	Sequence 1, Appli
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147	185.5	10.3	2974	4	US-09-949-016-613	Sequence 613, App	220	164.5	9.1	2539	4	US-09-023-655-1496	Sequence 1496, Ap
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149	184.5	10.2	198	2	US-08-414-657D-15	Sequence 15, Appli	222	164.5	9.1	2565	3	US-09-068-051A-31	Sequence 31, Appli
150	184.5	10.2	1391	4	US-09-638-649-4	Sequence 16, Appli	223	164.5	9.1	2793	3	US-03-336-536-68	Sequence 68, Appli
151	184.5	10.2	1391	4	US-09-638-648-4	Sequence 4, Appli	224	164	9.1	1378	4	US-09-068-051A-33	Sequence 33, Appli
152	182	10.1	2346	4	US-09-949-016-1979	Sequence 1979, Ap	225	164	9.1	1378	4	US-09-419-788-3	Sequence 23, Appli
153	182	10.1	2346	4	US-09-949-016-342	Sequence 342, App	226	164	9.1	1742	3	US-09-383-586-23	Sequence 23, Appli
154	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	227	164	9.1	1913	3	US-09-823-038A-23	Sequence 23, Appli
155	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	228	164	9.1	2418	4	US-09-057-860A-8	Sequence 8, Appli
156	174	9.6	785	4	US-09-270-767-1269	Sequence 1269, Ap	229	163.5	9.1	1950	4	US-09-949-016-1694	Sequence 1694, Ap
157	174	9.6	785	4	US-09-270-767-16551	Sequence 16551, A	230	163.5	9.1	2539	4	US-09-653-961-1	Sequence 1, Appli
158	173.5	9.6	2550	1	US-08-245-295-10	Sequence 10, Appli	231	163.5	9.1	2697	4	US-09-949-016-5335	Sequence 5335, Ap

232	163.5	9.1	4235	4	US-09-702-705-317	Sequence 317, App	305	159	8.8	6363	4	US-09-023-655-879	Sequence 879, App
233	163.5	9.1	4235	4	US-09-736-457-317	Sequence 317, App	306	158.5	8.8	4890	4	US-09-677-046A-3	Sequence 3, Appli
234	163.5	9.1	4235	4	US-09-614-124B-317	Sequence 317, App	307	158.5	8.8	4943	4	US-09-677-046A-7	Sequence 7, Appli
235	163.5	9.1	4235	4	US-09-671-325-317	Sequence 317, App	308	158.5	8.8	5220	4	US-09-677-046A-1	Sequence 1, Appli
236	163.5	9.1	4235	4	US-09-589-184-317	Sequence 317, App	309	158	8.7	2208	5	PCT-US93-00031-14	Sequence 14, Appli
237	163.5	9.1	4235	4	US-09-658-824-317	Sequence 317, App	310	157.5	8.7	1140	3	US-08-462-270-1	Sequence 1, Appli
238	163.5	9.1	5720	1	US-09-800-729-18	Sequence 18, Appli	311	157.5	8.7	5170	4	US-09-677-046A-5	Sequence 5, Appli
239	163	9.0	2775	1	US-08-481-130-25	Sequence 25, Appli	312	157	8.7	1421	3	US-09-188-930-254	Sequence 254, App
240	163	9.0	2775	1	US-08-656-984A-25	Sequence 25, Appli	313	157	8.7	1421	4	US-09-312-283C-254	Sequence 254, App
241	163	9.0	2775	2	US-08-485-604-25	Sequence 25, Appli	314	157	8.7	1822	4	US-09-397-243D-1	Sequence 1, Appli
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243	163	9.0	2927	1	US-08-481-130-27	Sequence 27, Appli	316	157	8.7	1857	4	US-09-905-125A-118	Sequence 118, App
244	163	9.0	2927	1	US-08-656-984A-27	Sequence 27, Appli	317	157	8.7	1857	4	US-09-902-775A-118	Sequence 118, App
245	163	9.0	2927	1	US-08-485-604-27	Sequence 27, Appli	318	157	8.7	1857	4	US-09-906-700-118	Sequence 118, App
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253	161	8.9	3554	4	US-09-905-125A-422	Sequence 422, App	326	156	8.6	1940	1	US-08-429-742-3	Sequence 3, Appli
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256	161	8.9	3554	4	US-09-903-603A-422	Sequence 422, App	329	155.5	8.6	2184	3	US-09-484-970B-161	Sequence 161, App
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258	161	8.9	3554	4	US-09-905-064-422	Sequence 422, App	331	155.5	8.6	3307	2	US-08-237-401A-5	Sequence 5, Appli
259	161	8.9	3554	4	US-09-905-381A-422	Sequence 422, App	332	155.5	8.6	3785	1	US-08-445-640-9	Sequence 9, Appli
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261	161	8.9	5470	2	US-08-443-861-1	Sequence 1, Appli	334	155.5	8.6	3785	3	US-08-447-314-9	Sequence 9, Appli
262	161	8.9	5470	3	US-08-193-829B-1	Sequence 1, Appli	335	155.5	8.6	3785	3	US-08-445-461-9	Sequence 9, Appli
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264	160.5	8.9	3159	3	US-08-986-485-3	Sequence 3, Appli	337	155	8.6	2431	3	US-08-985-526-35	Sequence 35, Appli
265	160.5	8.9	4111	4	US-09-375-248-1	Sequence 1, Appli	338	155	8.6	4006	4	US-09-949-016-4724	Sequence 4724, Ap
266	160.5	8.9	4195	1	US-08-340-011-1	Sequence 1, Appli	339	155	8.6	4006	4	US-09-949-016-4725	Sequence 4725, Ap
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268	160.5	8.9	4195	4	US-09-169-079-1	Sequence 1, Appli	341	155	8.6	5406	1	US-07-977-451-5	Sequence 5, Appli
269	160.5	8.9	4416	3	US-08-795-430-1	Sequence 1, Appli	342	155	8.6	5406	1	US-07-946-507-3	Sequence 3, Appli
270	160.5	8.9	4416	3	US-08-355-700-1	Sequence 1, Appli	343	155	8.6	5406	1	US-08-252-517-5	Sequence 5, Appli
271	160.5	8.9	4416	3	US-08-601-132-36	Sequence 36, Appli	344	155	8.6	5406	1	US-07-906-397A-5	Sequence 5, Appli
272	160.5	8.9	4416	4	US-08-671-573B-36	Sequence 36, Appli	345	155	8.6	5406	1	US-08-601-891-5	Sequence 5, Appli
273	160.5	8.9	4416	4	US-09-631-052B-36	Sequence 36, Appli	346	155	8.6	5406	2	US-08-021-324-5	Sequence 5, Appli
274	160.5	8.9	4416	1	US-09-534-376A-1	Sequence 1, Appli	347	155	8.6	5406	4	US-09-872-136B-5	Sequence 5, Appli
275	160.5	8.9	4425	1	US-08-222-616-31	Sequence 31, Appli	348	155	8.6	5406	5	PCT-US92-02750-7	Sequence 7, Appli
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278	160.5	8.9	4425	4	US-09-023-655-889	Sequence 889, App	351	154.5	8.6	5406	5	PCT-US92-09893-5	Sequence 5, Appli
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282	160.5	8.9	4795	3	US-08-901-710-3	Sequence 3, Appli	355	154.5	8.6	2600	2	US-08-427-497B-4	Sequence 4, Appli
283	160.5	8.9	9108	3	US-09-169-079-3	Sequence 3, Appli	356	154.5	8.6	2685	4	US-09-949-016-4734	Sequence 4734, Ap
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286	160	8.9	960	1	US-08-597-495B-23	Sequence 23, Appli	359	154	8.5	1009	3	US-08-462-270-3	Sequence 3, Appli
287	160	8.9	960	1	US-09-068-051A-23	Sequence 23, Appli	360	154	8.5	1009	3	US-09-173-151A-1	Sequence 1, Appli
288	160	8.9	2469	1	US-07-997-133-2	Sequence 2, Appli	361	153.5	8.5	1964	3	US-08-468-856B-7	Sequence 7, Appli
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290	160	8.9	2469	5	US-07-997-133-2	Sequence 2, Appli	363	153	8.5	571	4	US-09-270-767-1097	Sequence 1097, Ap
291	160	8.9	2662	2	US-08-451-822A-14	Sequence 14, Appli	364	153	8.5	571	4	US-09-270-767-16379	Sequence 16379, A
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294	160	8.9	2733	5	PCT-US96-00331-14	Sequence 14, Appli	367	152	8.4	3173	3	US-08-468-856B-1	Sequence 1, Appli
295	160	8.9	3944	4	US-09-949-016-1877	Sequence 1876, Ap	368	152	8.4	3173	3	US-08-468-856A-1	Sequence 1, Appli
296	160	8.9	3944	4	US-09-949-016-1877	Sequence 1877, Ap	369	152	8.4	3766	4	US-09-949-016-1651	Sequence 1651, Ap
297	160	8.9	3944	4	US-09-949-016-1878	Sequence 1878, Ap	370	152	8.4	3766	4	US-09-949-016-359	Sequence 359, App
298	160	8.9	3944	4	US-09-949-016-1879	Sequence 1879, Ap	371	151.5	8.4	1190	4	US-09-949-016-1720	Sequence 1720, Ap
299	160	8.9	3944	4	US-09-949-016-1880	Sequence 1880, Ap	372	151.5	8.4	2003	1	US-08-036-555B-21	Sequence 21, Appli
300	160	8.9	3944	4	US-09-949-016-1881	Sequence 1881, Ap	373	151.5	8.4	2003	1	US-08-469-569-21	Sequence 21, Appli
301	160	8.9	3944	4	US-09-949-016-1882	Sequence 1882, Ap	374	151.5	8.4	2003	1	US-08-249-322A-21	Sequence 21, Appli
302	160	8.9	3944	4	US-09-949-016-1883	Sequence 1883, Ap	375	151.5	8.4	2003	1	US-08-469-569A-21	Sequence 21, Appli
303	159	8.8	462	4	US-09-270-767-2319	Sequence 2319, Ap	376	151.5	8.4	2003	2	US-08-734-591A-21	Sequence 21, Appli
304	159	8.8	462	4	US-09-270-767-17601	Sequence 17601, A	377	151.5	8.4	2003	2	US-08-469-660-21	Sequence 21, Appli

378	151.5	8.4	2003	3	US-08-341-018-71	Sequence 71, Appl	451	141.5	7.8	1140	3	US-08-470-339-149	Sequence 149, App
379	151.5	8.4	2003	3	US-08-470-335-21	Sequence 21, Appl	452	141.5	7.8	1140	3	US-08-467-602-149	Sequence 149, App
380	151.5	8.4	2003	3	US-08-735-021-21	Sequence 21, Appl	453	141.5	7.8	1140	5	US-08-411-295F-48	Sequence 48, Appl
381	151.5	8.4	2003	3	US-08-734-664A-21	Sequence 21, Appl	454	141.5	7.8	1140	5	PCT-US94-05083C-145	Sequence 145, App
382	151.5	8.4	2003	3	US-08-470-339-21	Sequence 21, Appl	455	141.5	7.8	1140	5	PCT-US95-06846A-149	Sequence 149, App
383	151.5	8.4	2003	3	US-08-467-602-21	Sequence 21, Appl	456	141.5	7.8	1164	1	US-08-445-640-11	Sequence 11, Appl
384	151.5	8.4	2003	4	US-08-411-295F-64	Sequence 64, Appl	457	141.5	7.8	1164	3	US-08-170-558-11	Sequence 11, Appl
385	151.5	8.4	2003	5	PCT-US94-05083C-21	Sequence 21, Appl	458	141.5	7.8	1164	3	US-08-447-314-11	Sequence 11, Appl
386	151.5	8.4	2003	5	PCT-US95-06846A-21	Sequence 21, Appl	459	141.5	7.8	1164	3	US-08-445-461-11	Sequence 11, Appl
387	150.5	8.3	1364	4	US-09-924-103-3	Sequence 3, Appl	460	141.5	7.8	1164	4	US-09-223-490-11	Sequence 11, Appl
388	150.5	8.3	1287	4	US-09-023-655-1216	Sequence 1216, Ap	461	141.5	7.8	1193	1	US-08-036-555B-134	Sequence 134, App
389	150	8.3	1079	1	US-08-471-570-13	Sequence 13, Appl	462	141.5	7.8	1193	1	US-08-469-569-134	Sequence 134, App
390	150	8.3	1079	1	US-08-471-570-5	Sequence 5, Appl	463	141.5	7.8	1193	1	US-08-249-322A-134	Sequence 134, App
391	150	8.3	2676	1	US-08-471-570-7	Sequence 7, Appl	464	141.5	7.8	1193	2	US-08-469-660-134	Sequence 134, App
392	149.5	8.3	5690	2	US-08-447-464-2	Sequence 2, Appl	465	141.5	7.8	1193	5	PCT-US94-05083C-130	Sequence 130, App
393	149.5	8.3	5690	2	US-08-716-679-2	Sequence 2, Appl	466	141.5	7.8	1193	5	PCT-US95-06846A-134	Sequence 134, App
394	148.5	8.2	4078	4	US-09-016-434-1132	Sequence 1132, Ap	467	141.5	7.8	1194	4	US-08-411-295F-3	Sequence 3, Appl
395	148.5	8.2	6000	1	US-08-348-006B-6	Sequence 6, Appl	468	141	7.8	2079	4	US-09-949-016-3171	Sequence 3171, Ap
396	148.5	8.2	6000	2	US-08-800-825A-6	Sequence 6, Appl	469	141	7.8	2079	4	US-09-949-016-3172	Sequence 3172, Ap
397	148.5	8.2	6000	3	US-09-158-657-6	Sequence 6, Appl	470	141	7.8	2079	4	US-09-949-016-3173	Sequence 3173, Ap
398	148.5	8.2	6000	5	PCT-US94-10166-6	Sequence 6, Appl	471	141	7.8	2079	4	US-09-949-016-3174	Sequence 3174, Ap
399	148	8.2	2351	1	US-08-168-091A-1	Sequence 1, Appl	472	141	7.8	2079	4	US-09-949-016-3175	Sequence 3175, Ap
400	147.5	8.2	1347	4	US-09-638-648-6	Sequence 6, Appl	473	141	7.8	2079	4	US-09-949-016-3176	Sequence 3176, Ap
401	147.5	8.2	1348	4	US-09-638-649-6	Sequence 6, Appl	474	141	7.8	2079	4	US-09-949-016-3177	Sequence 3177, Ap
402	147	8.1	2430	4	US-09-620-312D-176	Sequence 176, App	475	141	7.8	2079	4	US-09-949-016-3178	Sequence 3178, Ap
403	145.5	8.1	1199	4	US-09-270-767-13050	Sequence 13050, A	476	141	7.8	2079	4	US-09-949-016-3179	Sequence 3179, Ap
404	145	8.0	726	3	US-09-254-465A-4	Sequence 4, Appl	477	141	7.8	2079	4	US-09-949-016-3180	Sequence 3180, Ap
405	145	8.0	726	4	US-09-953-499-4	Sequence 4, Appl	478	141	7.8	6172	4	US-08-774-528-89	Sequence 89, Appl
406	144	8.0	3992	4	US-09-944-807-9	Sequence 9, Appl	479	140.5	7.8	1659	4	US-09-969-532-7	Sequence 7, Appl
407	143.5	7.9	1103	2	US-08-602-725-33	Sequence 33, Appl	480	140.5	7.8	1692	4	US-09-969-532-5	Sequence 5, Appl
408	143.5	7.9	1896	3	US-09-413-554A-8	Sequence 8, Appl	481	140.5	7.8	1701	4	US-09-969-532-3	Sequence 3, Appl
409	143.5	7.9	3416	2	US-08-451-822A-15	Sequence 15, Appl	482	140.5	7.8	1734	4	US-09-969-532-1	Sequence 1, Appl
410	143.5	7.9	3416	3	US-08-323-430-15	Sequence 15, Appl	483	140.5	7.8	1767	4	US-08-866-510-11	Sequence 11, Appl
411	143	7.9	2313	1	US-08-232-538-5	Sequence 5, Appl	484	140.5	7.8	2661	4	US-09-969-532-15	Sequence 15, Appl
412	143	7.9	2313	1	US-09-427-353-1	Sequence 1, Appl	485	140.5	7.8	2694	4	US-09-969-532-11	Sequence 11, Appl
413	143	7.9	2651	2	US-08-786-164-5	Sequence 5, Appl	486	140.5	7.8	2703	4	US-09-969-532-9	Sequence 9, Appl
414	143	7.9	2651	4	US-09-953-318-19	Sequence 19, Appl	487	140.5	7.8	2736	4	US-09-969-532-2	Sequence 2, Appl
415	143	7.9	3394	4	US-09-953-318-100	Sequence 100, App	488	140.5	7.8	2742	1	US-08-286-105A-2	Sequence 2, Appl
416	142.5	7.9	1300	4	US-08-592-998C-8	Sequence 8, Appl	489	140.5	7.8	2742	2	US-08-441-104A-2	Sequence 2, Appl
417	142.5	7.9	1958	6	S169835-1	Patent No. S169835	490	140.5	7.8	2742	2	US-08-440-816A-2	Sequence 2, Appl
418	142.5	7.9	1958	6	S169835-1	Patent No. S169835	491	140.5	7.8	2742	3	US-09-417-381A-2	Sequence 2, Appl
419	142.5	7.9	2205	5	PCT-US93-00031-12	Sequence 12, Appl	492	140.5	7.8	2768	4	US-09-949-016-1697	Sequence 1697, Ap
420	142.5	7.9	2217	5	PCT-US93-00031-8	Sequence 8, Appl	493	140.5	7.8	3270	4	US-09-866-510-1	Sequence 1, Appl
421	142.5	7.9	3080	3	US-08-482-073-4	Sequence 4, Appl	494	140.5	7.8	3270	4	US-09-866-510-3	Sequence 3, Appl
422	142	7.9	992	1	US-08-481-130-24	Sequence 24, Appl	495	140.5	7.8	3270	4	US-09-866-510-5	Sequence 5, Appl
423	142	7.9	992	1	US-08-656-984A-24	Sequence 24, Appl	496	140.5	7.8	3270	4	US-09-866-510-7	Sequence 7, Appl
424	142	7.9	992	1	US-08-485-604-24	Sequence 24, Appl	497	140.5	7.8	3270	4	US-09-866-510-9	Sequence 9, Appl
425	142	7.9	992	2	US-08-487-595-24	Sequence 24, Appl	498	140.5	7.8	3270	4	US-09-866-510-9	Sequence 9, Appl
426	141.5	7.8	1108	1	US-08-036-555B-135	Sequence 135, App	499	140.5	7.8	3611	1	US-09-969-532-33	Sequence 33, Appl
427	141.5	7.8	1108	1	US-08-469-569-135	Sequence 135, App	500	140.5	7.8	3611	3	US-08-445-640-1	Sequence 1, Appl
428	141.5	7.8	1108	1	US-08-249-322A-135	Sequence 135, App	501	140.5	7.8	3611	3	US-08-170-558-1	Sequence 1, Appl
429	141.5	7.8	1108	1	US-08-469-526A-135	Sequence 135, App	502	140.5	7.8	3611	3	US-08-447-314-1	Sequence 1, Appl
430	141.5	7.8	1108	2	US-08-734-591A-135	Sequence 135, App	503	140.5	7.8	3611	4	US-08-445-461-1	Sequence 1, Appl
431	141.5	7.8	1108	2	US-08-469-660-135	Sequence 135, App	504	140.5	7.8	3611	4	US-09-223-490-1	Sequence 1, Appl
432	141.5	7.8	1108	3	US-08-341-018-5	Sequence 5, Appl	505	140.5	7.8	4054	1	US-08-180-195-35	Sequence 35, Appl
433	141.5	7.8	1108	3	US-08-470-335-135	Sequence 135, App	506	140.5	7.8	4054	2	US-08-477-329-35	Sequence 35, Appl
434	141.5	7.8	1108	3	US-08-735-021-135	Sequence 135, App	507	140.5	7.8	4054	2	US-08-475-458-35	Sequence 35, Appl
435	141.5	7.8	1108	3	US-08-734-664A-135	Sequence 135, App	508	140.5	7.8	4054	3	US-08-980-400-35	Sequence 35, Appl
436	141.5	7.8	1108	3	US-08-470-339-135	Sequence 135, App	509	140.5	7.8	4054	3	US-09-583-459A-35	Sequence 35, Appl
437	141.5	7.8	1108	3	US-08-467-602-135	Sequence 135, App	510	140.5	7.8	4054	3	US-09-583-210-35	Sequence 35, Appl
438	141.5	7.8	1108	4	US-08-411-295F-5	Sequence 5, Appl	511	140.5	7.8	4054	3	US-09-583-449A-35	Sequence 35, Appl
439	141.5	7.8	1108	5	PCT-US94-05083C-131	Sequence 131, App	512	140.5	7.8	4100	1	US-09-435-059-35	Sequence 35, Appl
440	141.5	7.8	1108	5	PCT-US95-06846A-135	Sequence 135, App	513	140.5	7.8	4100	1	US-08-168-917-3	Sequence 3, Appl
441	141.5	7.8	1140	1	US-08-036-555B-149	Sequence 149, App	514	140.5	7.8	4100	2	US-08-460-510-3	Sequence 3, Appl
442	141.5	7.8	1140	1	US-08-469-569-149	Sequence 149, App	515	140.5	7.8	4100	2	US-08-460-490-3	Sequence 3, Appl
443	141.5	7.8	1140	1	US-08-249-322A-149	Sequence 149, App	516	140.5	7.8	4100	5	PCT-US92-00730-3	Sequence 3, Appl
444	141.5	7.8	1140	1	US-08-469-526A-149	Sequence 149, App	517	140.5	7.8	6373	3	PCT-US92-00862-3	Sequence 3, Appl
445	141.5	7.8	1140	2	US-08-734-591A-149	Sequence 149, App	518	140.5	7.8	6373	3	US-08-462-728-1	Sequence 1, Appl
446	141.5	7.8	1140	2	US-08-469-660-149	Sequence 149, App	519	140.5	7.8	6373	4	US-08-461-917-1	Sequence 1, Appl
447	141.5	7.8	1140	3	US-08-341-018-55	Sequence 55, Appl	520	140.5	7.8	6373	4	US-08-464-436-1	Sequence 1, Appl
448	141.5	7.8	1140	3	US-08-470-335-149	Sequence 149, App	521	140.5	7.8	6375	1	US-08-464-436-1	Sequence 1, Appl
449	141.5	7.8	1140	3	US-08-735-021-149	Sequence 149, App	522	140.5	7.8	6375	1	US-08-168-917-5	Sequence 5, Appl
450	141.5	7.8	1140	3	US-08-734-664A-149	Sequence 149, App	523	140.5	7.8	6375	2	US-08-460-510-5	Sequence 5, Appl

524	140.5	7.8	6375	5	PCT-US92-00730-5	Sequence 5, Appli	597	134.5	7.4	1602	3	US-09-651-200-11	Sequence 11, Appl
525	140.5	7.8	6375	5	PCT-US92-00862-5	Sequence 5, Appli	598	134.5	7.4	1929	5	PCT-US93-00031-18	Sequence 18, Appl
526	140.5	7.8	6378	4	US-09-023-655-1194	Sequence 1194, Ap	599	134.5	7.4	1941	5	PCT-US93-00031-10	Sequence 10, Appl
527	140.5	7.8	6378	4	US-09-919-497-40	Sequence 40, Appl	600	134.5	7.4	1941	5	PCT-US93-00031-22	Sequence 22, Appl
528	140.5	7.8	6378	4	US-09-949-016-832	Sequence 832, App	601	134.5	7.4	2220	5	PCT-US93-00031-16	Sequence 16, Appl
529	140.5	7.8	6412	4	US-09-769-987-1	Sequence 1, Appli	602	134.5	7.4	2229	3	US-09-651-200-5	Sequence 5, Appli
530	140	7.8	6510	4	US-09-270-767-29243	Sequence 29243, A	603	134.5	7.4	2811	3	US-08-482-073-3	Sequence 3, Appli
c 531	140	7.8	753	4	US-09-270-767-11521	Sequence 11521, A	604	134.5	7.4	2813	2	US-08-344-155C-99	Sequence 99, Appl
532	140	7.8	5084	1	US-08-306-691B-21	Sequence 21, Appl	605	134.5	7.4	2813	3	US-09-009-490A-90	Sequence 90, Appl
533	140	7.8	5084	1	US-09-023-655-1335	Sequence 1335, Ap	606	134.5	7.4	3063	4	US-09-620-312D-844	Sequence 844, App
534	140	7.8	5084	5	PCT-US93-06251-25	Sequence 25, Appl	607	134	7.4	1573	6	5169835-5	Patent No. 5169835
535	140	7.8	8083	3	US-09-383-630-4	Sequence 4, Appli	608	134	7.4	1573	6	5169835-5	Patent No. 5169835
536	140	7.8	8083	3	US-09-383-630-5	Sequence 5, Appli	609	133.5	7.4	1467	4	US-09-499-846-11	Sequence 11, Appl
537	139.5	7.7	2110	4	US-09-907-794A-319	Sequence 319, App	610	133	7.4	952	4	US-09-684-708A-22	Sequence 22, Appl
538	139.5	7.7	2110	4	US-09-905-125A-319	Sequence 319, App	611	133	7.4	1004	4	US-09-684-708A-24	Sequence 24, Appl
539	139.5	7.7	2110	4	US-09-902-775A-319	Sequence 319, App	612	133	7.4	1858	2	US-08-359-705B-7	Sequence 7, Appli
540	139.5	7.7	2110	4	US-09-906-700-319	Sequence 319, App	613	133	7.4	1858	2	US-08-286-846A-7	Sequence 7, Appli
541	139.5	7.7	2110	4	US-09-903-603A-319	Sequence 319, App	614	133	7.4	1858	2	US-08-457-880A-7	Sequence 7, Appli
542	139.5	7.7	2110	4	US-09-904-920A-319	Sequence 319, App	615	133	7.4	1858	3	US-08-444-622A-7	Sequence 7, Appli
543	139.5	7.7	2110	4	US-09-909-064-319	Sequence 319, App	616	133	7.4	1858	3	US-08-942-562-7	Sequence 7, Appli
544	139.5	7.7	2110	4	US-09-905-381A-319	Sequence 319, App	617	133	7.4	1858	3	US-08-942-562-7	Sequence 7, Appli
545	139.5	7.7	2110	4	US-09-906-618-319	Sequence 319, App	618	133	7.4	2715	2	US-09-156-923-7	Sequence 7, Appli
546	139	7.7	989	1	US-08-282-951-5	Sequence 5, Appli	619	133	7.4	2715	2	US-08-359-705B-5	Sequence 5, Appli
547	139	7.7	1438	7	US-08-755-235-1	Sequence 1, Appli	620	133	7.4	2715	2	US-08-286-846A-5	Sequence 5, Appli
548	139	7.7	2477	1	US-08-429-742-1	Sequence 1, Appli	621	133	7.4	2715	3	US-08-457-880A-5	Sequence 5, Appli
549	139	7.7	25633	4	US-09-949-016-12084	Sequence 12084, A	622	133	7.4	2715	3	US-08-942-562-5	Sequence 5, Appli
550	139	7.7	25633	4	US-09-949-016-13721	Sequence 13721, A	623	133	7.4	2715	3	US-08-942-562-5	Sequence 5, Appli
551	138.5	7.7	1193	1	US-08-469-526A-134	Sequence 134, App	624	133	7.4	2903	4	US-09-949-016-5033	Sequence 5033, Ap
552	138.5	7.7	1193	2	US-08-734-591A-134	Sequence 134, App	625	133	7.4	2940	1	US-08-286-305A-8	Sequence 8, Appli
553	138.5	7.7	1193	3	US-08-341-018-3	Sequence 3, Appli	626	133	7.4	2940	2	US-08-441-104A-8	Sequence 8, Appli
554	138.5	7.7	1193	3	US-08-470-335-134	Sequence 134, App	627	133	7.4	2940	2	US-08-440-816A-8	Sequence 8, Appli
555	138.5	7.7	1193	3	US-08-735-021-134	Sequence 134, App	628	133	7.4	2940	3	US-09-417-381A-8	Sequence 8, Appli
556	138.5	7.7	1193	3	US-08-734-664A-134	Sequence 134, App	629	133	7.4	7476	4	US-09-949-016-17005	Sequence 17005, A
557	138.5	7.7	1193	3	US-08-470-339-134	Sequence 134, App	630	132.5	7.3	2009	3	US-08-468-856B-8	Sequence 8, Appli
558	138.5	7.7	1193	3	US-08-467-602-134	Sequence 134, App	631	132.5	7.3	2009	3	US-08-468-856A-8	Sequence 8, Appli
559	138.5	7.7	1545	4	US-09-949-016-5509	Sequence 5509, Ap	632	132	7.3	2166	3	US-09-175-928-1	Sequence 1, Appli
560	138.5	7.7	1710	4	US-09-723-368-3	Sequence 3, Appli	633	132	7.3	2434	3	US-09-272-496-1	Sequence 1, Appli
561	138.5	7.7	3199	4	US-09-628-188A-2	Sequence 2, Appli	634	132	7.3	2434	3	US-09-949-016-133	Sequence 133, App
562	137	7.6	1164	1	US-08-445-640-5	Sequence 5, Appli	635	132	7.3	2836	3	US-09-724-864-30	Sequence 30, Appl
563	137	7.6	1164	3	US-08-170-558-5	Sequence 5, Appli	636	131.5	7.3	1182	3	US-09-336-536-38	Sequence 38, Appl
564	137	7.6	1164	3	US-08-447-314-5	Sequence 5, Appli	637	131.5	7.3	1295	3	US-09-254-465A-8	Sequence 8, Appli
565	137	7.6	1164	3	US-08-445-461-5	Sequence 5, Appli	638	131.5	7.3	1295	4	US-09-907-794A-63	Sequence 63, Appl
566	137	7.6	1164	3	US-09-223-490-5	Sequence 5, Appli	639	131.5	7.3	1295	4	US-09-905-125A-63	Sequence 63, Appl
567	137	7.6	1591	3	US-08-468-856B-9	Sequence 9, Appli	640	131.5	7.3	1295	4	US-09-902-775A-63	Sequence 63, Appl
568	137	7.6	1591	3	US-08-468-859A-9	Sequence 9, Appli	641	131.5	7.3	1295	4	US-09-906-700-63	Sequence 63, Appl
c 569	137	7.6	2598	4	US-09-949-016-3414	Sequence 3414, Ap	642	131.5	7.3	1295	4	US-09-903-603A-63	Sequence 63, Appl
570	137	7.6	3111	3	US-08-891-845-1	Sequence 1, Appli	643	131.5	7.3	1295	4	US-09-904-920A-63	Sequence 63, Appl
571	137	7.6	3111	4	US-09-514-573-1	Sequence 1, Appli	644	131.5	7.3	1295	4	US-09-903-064-63	Sequence 63, Appl
572	136.5	7.6	1004	3	US-09-383-586-24	Sequence 24, Appli	645	131.5	7.3	1295	4	US-09-905-381A-63	Sequence 63, Appl
573	136.5	7.6	1004	4	US-09-823-038A-24	Sequence 24, Appli	646	131.5	7.3	1295	4	US-09-906-618-63	Sequence 63, Appl
574	136.5	7.6	2244	3	US-09-354-151-1	Sequence 1, Appli	647	131.5	7.3	1295	4	US-09-953-499-8	Sequence 8, Appli
575	136.5	7.6	2426	4	US-09-023-655-1156	Sequence 1156, Ap	648	131.5	7.3	1846	3	US-09-336-536-37	Sequence 37, Appl
576	136.5	7.6	2557	2	US-09-044-506A-1	Sequence 1, Appli	649	131	7.3	734	1	US-08-471-570-11	Sequence 11, Appl
577	136.5	7.6	2557	3	US-08-478-208-31	Sequence 31, Appli	650	131	7.3	1027	4	US-09-684-708A-26	Sequence 26, Appl
578	136.5	7.6	2557	3	US-08-478-208-31	Sequence 31, Appli	651	131	7.3	1423	4	US-09-823-038A-46	Sequence 46, Appl
579	136.5	7.6	2557	6	5264554-1	Sequence 72, Appli	652	131	7.3	1584	3	US-08-928-383B-1	Sequence 1, Appli
580	136.5	7.6	2557	6	5264554-1	Patent No. 5264554	653	131	7.3	1604	4	US-09-419-788-18	Sequence 18, Appl
581	136	7.5	1326	4	US-09-799-451-382	Sequence 382, App	654	131	7.3	1683	4	US-09-866-510-23	Sequence 23, Appl
582	136	7.5	1377	3	US-09-435-956A-2	Sequence 2, Appli	655	131	7.3	3086	4	US-09-684-708A-20	Sequence 20, Appl
583	136	7.5	1603	1	US-08-471-570-3	Sequence 3, Appli	656	131	7.3	3321	4	US-09-866-510-13	Sequence 13, Appl
584	136	7.5	1932	5	PCT-US93-00031-20	Sequence 20, Appli	657	131	7.3	3321	4	US-09-866-510-15	Sequence 15, Appl
585	136	7.5	2310	1	US-08-471-570-9	Sequence 9, Appli	658	131	7.3	3321	4	US-09-866-510-17	Sequence 17, Appl
586	135	7.5	1042	2	US-08-427-497B-6	Sequence 6, Appli	659	131	7.3	3321	4	US-09-866-510-19	Sequence 19, Appl
587	135	7.5	1494	4	US-09-499-846-5	Sequence 5, Appli	660	131	7.3	3321	4	US-09-866-510-21	Sequence 21, Appl
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589	135	7.5	1578	4	US-09-499-846-3	Sequence 3, Appli	662	131	7.3	4465	1	US-08-477-329-1	Sequence 1, Appli
590	135	7.5	1578	4	US-09-499-846-7	Sequence 7, Appli	663	131	7.3	4465	2	US-08-475-458-1	Sequence 1, Appli
591	135	7.5	2214	1	US-08-245-295-7	Sequence 7, Appli	664	131	7.3	4465	3	US-08-980-400-1	Sequence 1, Appli
592	135	7.5	2214	1	US-08-481-130-7	Sequence 7, Appli	665	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
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595	135	7.5	2214	1	US-08-487-595-7	Sequence 7, Appli	668	131	7.3	4465	3	US-09-433-059-1	Sequence 1, Appli
596	135	7.5	2768	4	US-09-774-528-426	Sequence 426, App	669	131	7.3	5427	1	US-08-168-917-1	Sequence 1, Appli

670	131	7.3	5427	2	US-08-460-510-1	Sequence 1, Appli	743	127.5	7.1	1554	4	US-09-949-016-3333	Sequence 3333, Ap
671	131	7.3	5427	2	US-08-460-490-1	Sequence 1, Appli	744	127.5	7.1	1554	4	US-09-949-016-3334	Sequence 3334, Ap
672	131	7.3	5427	3	US-08-462-728-3	Sequence 3, Appli	745	127.5	7.1	1554	4	US-09-949-016-3335	Sequence 3335, Ap
673	131	7.3	5427	3	US-08-461-917-3	Sequence 3, Appli	746	127.5	7.1	1652	1	US-08-036-555B-148	Sequence 148, App
674	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	747	127.5	7.1	1652	1	US-08-469-569-148	Sequence 148, App
675	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	748	127.5	7.1	1652	1	US-08-249-322A-148	Sequence 148, App
676	131	7.3	5427	5	PCT-US92-00730-1	Sequence 1, Appli	749	127.5	7.1	1652	1	US-08-469-526A-148	Sequence 148, App
677	131	7.3	5427	5	PCT-US92-00862-1	Sequence 1, Appli	750	127.5	7.1	1652	2	US-08-734-591A-148	Sequence 148, App
678	131	7.3	5570	4	US-09-023-655-1193	Sequence 193, Ap	751	127.5	7.1	1652	2	US-08-469-660-148	Sequence 148, App
679	130.5	7.2	1022	3	US-09-152-060-35	Sequence 35, Appli	752	127.5	7.1	1652	3	US-08-341-018-53	Sequence 53, Appli
680	130.5	7.2	1401	4	US-09-604-107A-7	Sequence 7, Appli	753	127.5	7.1	1652	3	US-08-470-335-148	Sequence 148, App
681	130.5	7.2	1452	4	US-09-949-016-5250	Sequence 5250, Ap	754	127.5	7.1	1652	3	US-08-735-021-148	Sequence 148, App
682	130.5	7.2	1452	4	US-09-949-016-5251	Sequence 5251, Ap	755	127.5	7.1	1652	3	US-08-734-664A-148	Sequence 148, App
683	130	7.2	743	4	US-08-411-295F-1	Sequence 1, Appli	756	127.5	7.1	1652	3	US-08-470-339-148	Sequence 148, App
684	130	7.2	744	1	US-08-036-555B-133	Sequence 133, App	757	127.5	7.1	1652	3	US-08-467-602-148	Sequence 148, App
685	130	7.2	744	1	US-08-469-569-133	Sequence 133, App	758	127.5	7.1	1652	4	US-08-411-295F-46	Sequence 46, Appli
686	130	7.2	744	1	US-08-249-322A-133	Sequence 133, App	759	127.5	7.1	1652	5	PCT-US94-05083C-144	Sequence 144, App
687	130	7.2	744	1	US-08-469-526A-133	Sequence 133, App	760	127.5	7.1	1652	5	PCT-US95-06846A-148	Sequence 148, App
688	130	7.2	744	2	US-08-734-591A-133	Sequence 133, App	761	127.5	7.1	1831	3	US-09-484-970B-84	Sequence 84, Appli
689	130	7.2	744	2	US-08-469-660-133	Sequence 133, App	762	127.5	7.1	32207	2	US-08-770-379-20	Sequence 20, Appli
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691	130	7.2	744	3	US-08-470-335-133	Sequence 133, App	764	127.5	7.1	32207	3	US-09-230-371A-20	Sequence 20, Appli
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693	130	7.2	744	3	US-08-734-664A-133	Sequence 133, App	766	127	7.0	1730	4	US-09-919-172-19	Sequence 19, Appli
694	130	7.2	744	3	US-08-470-339-133	Sequence 133, App	767	127	7.0	2430	4	US-09-949-016-5179	Sequence 5179, Ap
695	130	7.2	744	3	US-08-467-602-133	Sequence 133, App	768	127	7.0	2885	4	US-09-949-016-5773	Sequence 5773, Ap
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c 819	124	6.9	439	4	US-09-270-767-16840	Sequence 16840, A	892	121.5	6.7	948	4	US-09-910-174B-27	Sequence 27, Appl
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823	124	6.9	2010	2	US-08-330-161-12	Sequence 10, Appl	896	121.5	6.7	5207	4	US-10-274-978-1	Sequence 1, Appli
824	124	6.9	2010	2	US-08-456-241-12	Sequence 12, Appl	897	121.5	6.7	5207	4	US-10-697-263-1	Sequence 1, Appli
825	124	6.9	2010	2	US-08-440-401-10	Sequence 10, Appl	898	121.5	6.7	5207	4	US-10-697-263-1	Sequence 1, Appli
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832	124	6.9	2164	3	US-08-703-089-6	Sequence 6, Appli	c 905	120.5	6.7	609	3	US-08-833-488B-5	Sequence 5, Appli
833	124	6.9	2387	3	US-08-891-845-11	Sequence 11, Appl	c 906	120.5	6.7	609	3	US-08-833-488B-8	Sequence 8, Appli
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840	124	6.9	3501	1	US-07-906-357A-3	Sequence 3, Appli	913	120	6.6	3296	4	US-09-949-016-1456	Sequence 1456, Ap
841	124	6.9	3501	2	US-08-601-891-3	Sequence 3, Appli	914	120	6.6	4286	4	US-09-949-016-557	Sequence 557, App
842	124	6.9	3501	2	US-09-021-324-3	Sequence 3, Appli	915	120	6.6	4286	4	US-09-899-634C-1	Sequence 1, Appli
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846	124	6.9	3608	4	US-09-016-434-1408	Sequence 1408, App	c 919	119.5	6.6	759	3	US-08-833-488B-23	Sequence 23, Appl
847	124	6.9	3608	4	US-09-949-016-847	Sequence 847, App	920	119.5	6.6	915	4	US-09-419-788B-14	Sequence 14, Appl
848	124	6.9	3635	1	US-08-252-626A-1	Sequence 1, Appli	921	119.5	6.6	1295	1	US-08-245-295-6	Sequence 6, Appli
849	123	6.8	1693	6	5169835-3	Patent No. 5169835	922	119.5	6.6	1295	1	US-08-481-130-6	Sequence 6, Appli
850	123	6.8	1693	6	5169835-3	Patent No. 5169835	923	119.5	6.6	1295	1	US-08-656-984A-6	Sequence 6, Appli
851	123	6.8	1744	3	US-09-484-970B-83	Sequence 83, Appli	924	119.5	6.6	1295	1	US-08-485-604-6	Sequence 6, Appli
852	123	6.8	2165	2	US-08-263-911-8	Sequence 8, Appli	925	119.5	6.6	1295	2	US-08-487-595-6	Sequence 6, Appli
853	123	6.8	2181	3	US-09-254-465A-7	Sequence 7, Appli	926	119.5	6.6	1295	3	US-08-863-790-25	Sequence 25, Appl
854	123	6.8	2181	3	US-09-254-465A-11	Sequence 11, Appli	927	119.5	6.6	1295	3	US-08-296-749-25	Sequence 25, Appl
855	123	6.8	2181	4	US-09-953-499-7	Sequence 7, Appli	928	119.5	6.6	1518	3	US-09-240-915-2	Sequence 2, Appli
856	123	6.8	2181	4	US-09-953-499-11	Sequence 11, Appli	929	119.5	6.6	1518	3	US-09-591-435-2	Sequence 2, Appli
857	123	6.8	2463	1	US-08-339-578-1	Sequence 1, Appli	930	119.5	6.6	1582	4	US-09-419-788-25	Sequence 25, Appl
858	123	6.8	2537	3	US-09-173-151A-34	Sequence 34, Appli	931	119.5	6.6	1654	4	US-09-419-788-28	Sequence 28, Appl
859	123	6.8	5727	4	US-09-628-188A-1	Sequence 1, Appli	932	119.5	6.6	2360	4	US-09-023-655-1288	Sequence 1288, Ap
860	122.5	6.8	483	1	US-08-096-277-17	Sequence 17, Appl	933	119.5	6.6	2587	4	US-09-949-016-3321	Sequence 3321, Ap
861	122.5	6.8	483	2	US-08-550-815-17	Sequence 17, Appl	934	119.5	6.6	2587	4	US-09-949-016-3322	Sequence 3322, Ap
862	122.5	6.8	483	3	US-08-703-089-17	Sequence 17, Appl	935	119.5	6.6	2587	4	US-09-949-016-3323	Sequence 3323, Ap
863	122.5	6.8	1387	2	US-08-973-424-2	Sequence 2, Appli	936	119.5	6.6	2587	4	US-09-949-016-3324	Sequence 3324, Ap
864	122.5	6.8	1813	4	US-09-907-794A-38	Sequence 38, Appli	937	119.5	6.6	2587	4	US-09-949-016-3325	Sequence 3325, Ap
865	122.5	6.8	1813	4	US-09-905-125A-38	Sequence 38, Appl	938	119.5	6.6	2587	4	US-09-949-016-3326	Sequence 3326, Ap
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868	122.5	6.8	1813	4	US-09-903-603A-38	Sequence 38, Appl	941	119	6.6	1098	4	US-09-899-634C-3	Sequence 3, Appli
869	122.5	6.8	1813	4	US-09-904-920A-38	Sequence 38, Appl	942	119	6.6	2387	4	US-09-949-016-2268	Sequence 2268, Ap
870	122.5	6.8	1813	4	US-09-909-064-38	Sequence 38, Appl	943	119	6.6	2387	4	US-09-313-942-27	Sequence 27, Appl
871	122.5	6.8	1813	4	US-09-905-381A-38	Sequence 38, Appl	944	119	6.6	3733	4	US-09-949-016-2188	Sequence 2188, Ap
872	122.5	6.8	1813	4	US-09-906-618-38	Sequence 38, Appl	945	118.5	6.6	1077	4	US-09-419-788-27	Sequence 27, Appl
873	122	6.8	536	4	US-09-569-611C-2	Sequence 2, Appli	946	118.5	6.6	2165	2	US-08-263-911-6	Sequence 6, Appli
874	122	6.8	858	4	US-09-270-767-13041	Sequence 13041, A	947	118.5	6.6	8865	4	US-09-949-016-4238	Sequence 4238, Ap
875	122	6.8	991	3	US-08-833-488B-19	Sequence 19, Appl	948	118.5	6.6	8906	2	US-08-826-267-1	Sequence 1, Appli
c 876	122	6.8	991	3	US-08-833-488B-21	Sequence 21, Appl	949	117.5	6.5	576	4	US-09-270-767-2049	Sequence 2049, Ap
877	122	6.8	1476	3	US-08-753-007A-7	Sequence 7, Appli	950	117.5	6.5	576	4	US-09-270-767-17331	Sequence 17331, A
878	122	6.8	1476	3	US-09-398-496-7	Sequence 7, Appli	951	117.5	6.5	617	3	US-08-833-488B-13	Sequence 13, Appl
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881	122	6.8	2105	4	US-09-949-016-3204	Sequence 3204, Ap	954	117.5	6.5	1008	1	US-07-904-073-1	Sequence 1, Appli
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883	122	6.8	2268	3	US-08-753-007A-31	Sequence 31, Appl	956	117.5	6.5	1770	3	US-08-924-376-1	Sequence 1, Appli
884	122	6.8	2268	3	US-09-398-496-31	Sequence 31, Appl	957	117.5	6.5	1770	3	US-08-685-212-1	Sequence 1, Appli
885	122	6.8	2390	4	US-09-774-528-334	Sequence 334, App	958	117.5	6.5	1770	3	US-08-466-932A-1	Sequence 1, Appli
886	122	6.8	3575	4	US-09-023-655-1395	Sequence 1395, Ap	959	117.5	6.5	1770	5	PCT-US94-02414-1	Sequence 1, Appli
887	122	6.8	18472	4	US-09-949-016-12891	Sequence 12891, A	960	117.5	6.5	1770	5	PCT-US96-08899-1	Sequence 1, Appli
888	122	6.8	18478	4	US-09-949-016-15925	Sequence 15925, A	961	117.5	6.5	3011	1	US-07-821-716-1	Sequence 1, Appli

962	117.5	6.5	3011	4	US-08-406-824A-5	Sequence 5, Appli	1035	115	6.4	820	4	US-09-270-767-1214	Sequence 1214, Ap
963	117.5	6.5	4079	4	US-09-016-434-1219	Sequence 1219, Ap	1036	115	6.4	820	4	US-09-270-767-16496	Patent No. 5223394
964	117.5	6.5	4907	4	US-09-949-016-2701	Sequence 1201, Ap	1037	115	6.4	1078	6	5223394-10	Patent No. 5223394
965	117.5	6.5	4910	4	US-09-021-655-1125	Sequence 1225, Ap	1038	115	6.4	1078	6	5223394-10	Sequence 9, Appli
966	117.5	6.5	4910	4	US-09-814-915A-75	Sequence 75, Appl	1039	115	6.4	1346	3	US-07-935-695-9	Sequence 9, Appli
967	117.5	6.5	4910	4	US-09-949-016-129	Sequence 129, App	1040	115	6.4	1346	3	US-08-477-460B-1	Sequence 1, Appli
968	117	6.5	551	4	US-09-023-655-786	Sequence 786, App	1041	115	6.4	1796	3	US-08-379-516-1	Sequence 1, Appli
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972	117	6.5	1607	3	US-09-398-496-3	Sequence 3, Appli	1045	115	6.4	1796	3	US-08-484-681-1	Sequence 1, Appli
973	117	6.5	2295	3	US-09-131-648-4	Sequence 4, Appli	1046	115	6.4	1796	3	US-09-766-995-1	Sequence 1, Appli
974	117	6.5	2295	3	US-09-949-016-1143	Sequence 1143, Ap	1047	115	6.4	1796	4	PCT-US93-07422-1	Sequence 1, Appli
975	117	6.5	2461	4	US-09-620-312D-350	Sequence 350, App	1048	115	6.4	1796	5	US-08-896-537A-1	Sequence 1, Appli
976	117	6.5	2467	3	US-08-753-007A-1	Sequence 1, Appli	1049	115	6.4	2027	4	US-09-799-451-425	Sequence 425, App
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985	117	6.5	2639	4	US-09-909-064-68	Sequence 68, Appl	1058	114.5	6.3	1781	1	US-08-485-604-4	Sequence 4, Appli
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987	117	6.5	2639	4	US-09-906-618-68	Sequence 68, Appl	1060	114.5	6.3	1781	1	US-08-487-113D-2	Sequence 2, Appli
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995	116.5	6.5	918	4	US-09-419-788-13	Sequence 13, Appl	1068	114.5	6.3	1781	3	US-08-475-680-2	Sequence 2, Appli
996	116.5	6.5	924	2	US-08-332-562A-82	Sequence 82, Appl	1069	114.5	6.3	1781	3	US-08-296-749-2	Sequence 2, Appli
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999	116.5	6.5	2372	4	US-09-023-655-1076	Sequence 1076, Ap	1072	114.5	6.3	25321	4	US-09-949-016-14039	Sequence 14039, A
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1002	116	6.4	1323	3	US-09-651-200-9	Sequence 9, Appli	1075	113.5	6.3	797	1	US-08-323-445A-3	Sequence 3, Appli
1003	116	6.4	2636	1	US-08-554-612C-12	Sequence 12, Appl	1076	113.5	6.3	797	1	US-08-515-903A-3	Sequence 3, Appli
1004	116	6.4	2888	1	US-09-651-200-3	Sequence 3, Appli	1077	113.5	6.3	797	5	PCT-US95-12840-3	Sequence 4, Appli
1005	116	6.4	2898	1	US-08-554-612C-51	Sequence 51, Appl	1078	113.5	6.3	921	3	US-08-996-338-4	Sequence 4, Appli
1006	116	6.4	2909	1	US-08-554-612C-10	Sequence 10, Appl	1079	113.5	6.3	921	4	US-09-556-972-4	Sequence 4, Appli
1007	116	6.4	2909	1	US-08-554-612C-11	Sequence 11, Appl	1080	113.5	6.3	975	4	US-08-996-338-11	Sequence 11, Appl
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1011	115.5	6.4	687	3	US-08-833-488B-30	Sequence 30, Appl	1084	113.5	6.3	1557	4	US-09-556-972-2	Sequence 2, Appli
1012	115.5	6.4	755	1	US-08-323-445A-5	Sequence 5, Appli	1085	113.5	6.3	1739	4	US-09-016-434-1268	Sequence 1268, Ap
1013	115.5	6.4	755	1	US-08-515-903A-5	Sequence 5, Appli	1086	113.5	6.3	1817	1	US-08-473-981A-5	Sequence 5, Appli
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1016	115.5	6.4	1693	2	US-08-487-113D-118	Sequence 118, App	1089	113.5	6.3	2830	3	US-09-110-618-3	Sequence 3, Appli
1017	115.5	6.4	1693	2	US-08-720-420A-118	Sequence 118, App	1090	113.5	6.3	2830	3	US-09-578-178-3	Sequence 3, Appli
1018	115.5	6.4	2675	1	US-08-070-165F-5	Sequence 5, Appli	1091	113.5	6.3	2830	4	US-09-577-806-3	Sequence 3, Appli
1019	115.5	6.4	2675	2	US-08-885-418-5	Sequence 5, Appli	1092	113.5	6.3	2830	4	US-09-621-502-7	Sequence 7, Appli
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1028	115	6.4	344	4	US-09-614-124B-1321	Sequence 1321, Ap	c1101	113	6.3	536	4	US-09-658-824-1461	Sequence 1461, Ap
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1110	112.5	6.2	1557	1	US-08-656-984A-26	Sequence 26, Appl	1183	110	6.1	1742	3	US-09-517-605-7	Sequence 7, Appl
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1117	112	6.2	2309	3	US-09-075-215A-16	Sequence 16, Appl	1190	109.5	6.1	1452	3	US-09-039-982A-36	Sequence 36, Appl
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c1119	111.5	6.2	989	3	US-09-361-434-23	Sequence 23, Appl	1192	109.5	6.1	1452	3	US-09-039-762A-36	Sequence 36, Appl
1120	111.5	6.2	989	3	US-09-635-025-21	Sequence 21, Appl	1193	109.5	6.1	1452	3	US-09-042-492D-36	Sequence 36, Appl
c1121	111.5	6.2	989	3	US-09-635-025-23	Sequence 23, Appl	1194	109.5	6.1	1452	3	US-08-913-612A-36	Sequence 36, Appl
1122	111.5	6.2	1359	4	US-08-961-309-69	Sequence 69, Appl	1195	109.5	6.1	1452	4	US-10-266-463A-36	Sequence 36, Appl
1123	111.5	6.2	1377	4	US-09-773-877B-25	Sequence 25, Appl	1196	109.5	6.1	1518	3	US-09-240-915-1	Sequence 1, Appl
1124	111.5	6.2	1704	3	US-09-032-337-38	Sequence 38, Appl	1197	109.5	6.1	1518	3	US-09-591-435-1	Sequence 1, Appl
1125	111.5	6.2	1907	4	US-09-949-016-1692	Sequence 1692, Ap	1198	109.5	6.1	1599	2	US-08-689-870-1	Sequence 1, Appl
1126	111.5	6.2	1928	4	US-09-723-368-1	Sequence 1, Appl	1199	109.5	6.1	1599	2	US-08-689-870-1	Sequence 1, Appl
1127	111.5	6.2	1928	4	US-09-949-016-407	Sequence 407, App	1200	109.5	6.1	1611	3	US-09-039-982A-35	Sequence 35, Appl
1128	111.5	6.2	3120	1	US-08-222-618-22	Sequence 22, Appl	1201	109.5	6.1	1611	3	US-09-039-641-35	Sequence 35, Appl
1129	111.5	6.2	3120	3	US-08-446-648-22	Sequence 22, Appl	1202	109.5	6.1	1611	3	US-09-039-762A-35	Sequence 35, Appl
1130	111.5	6.2	3120	4	US-09-982-610-22	Sequence 22, Appl	1203	109.5	6.1	1611	3	US-09-042-492D-35	Sequence 35, Appl
1131	111.5	6.2	3120	5	PC-T-US95-04288-22	Sequence 22, Appl	1204	109.5	6.1	1611	3	US-08-913-612A-35	Sequence 35, Appl
1132	111.5	6.2	4989	3	US-09-560-633-3	Sequence 3, Appl	1205	109.5	6.1	1611	4	US-10-266-463A-35	Sequence 35, Appl
1133	111	6.1	966	3	US-09-361-434-19	Sequence 19, Appl	1206	109.5	6.1	1656	3	US-08-318-038D-16	Sequence 2, Appl
c1134	111	6.1	966	3	US-09-361-434-20	Sequence 20, Appl	1207	109.5	6.1	1656	3	US-08-318-038D-16	Sequence 2, Appl
1135	111	6.1	966	3	US-09-635-025-19	Sequence 19, Appl	1208	109.5	6.1	1656	3	US-08-227-496C-20	Sequence 20, Appl
c1136	111	6.1	966	3	US-09-635-025-20	Sequence 20, Appl	1209	109.5	6.1	1656	3	US-08-435-568A-2	Sequence 2, Appl
1137	111	6.1	1264	4	US-09-579-845-5	Sequence 5, Appl	1210	109.5	6.1	1784	1	US-08-554-612C-13	Sequence 13, Appl
1138	111	6.1	1286	4	US-09-949-016-3587	Sequence 3587, Ap	1211	109.5	6.1	1846	1	US-08-483-389-117	Sequence 117, App
1139	111	6.1	1357	1	US-08-091-519-1	Sequence 1, Appl	1212	109.5	6.1	2986	3	US-09-062-416-1	Sequence 1, Appl
1140	111	6.1	1357	1	US-08-442-043A-1	Sequence 1, Appl	1213	109.5	6.1	3003	4	US-09-023-655-1115	Sequence 1115, Ap
1141	111	6.1	1357	4	US-09-461-908-1	Sequence 1, Appl	1214	109.5	6.1	3016	2	US-08-344-155C-97	Sequence 97, Appl
1142	111	6.1	1357	4	US-08-441-893A-1	Sequence 1, Appl	1215	109.5	6.1	3017	3	US-09-009-490A-86	Sequence 86, Appl
1143	111	6.1	1357	4	US-08-406-824A-7	Sequence 7, Appl	1216	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1144	111	6.1	1357	4	US-09-921-667-7	Sequence 7, Appl	1217	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1145	111	6.1	1357	5	PC-T-US91-03478-1	Sequence 6, Appl	1218	109	6.0	2142	4	US-09-774-528-100	Sequence 100, App
1146	111	6.1	1458	4	US-08-030-175-6	Sequence 6, Appl	1219	109	6.0	2163	4	US-09-774-528-99	Sequence 99, Appl
1147	111	6.1	1458	4	US-08-030-175-7	Sequence 7, Appl	1220	109	6.0	3734	4	US-09-579-692B-7	Sequence 7, Appl
1148	110.5	6.1	534	4	US-09-702-705-1325	Sequence 1325, Ap	1221	108.5	6.0	1255	3	US-09-412-554A-7	Sequence 7, Appl
1149	110.5	6.1	534	4	US-09-736-457-1325	Sequence 1325, Ap	1222	108.5	6.0	1320	2	US-08-125-462-3	Sequence 3, Appl
1150	110.5	6.1	534	4	US-09-614-124B-1325	Sequence 1325, Ap	1223	108.5	6.0	1320	2	US-08-891-848-3	Sequence 3, Appl
1151	110.5	6.1	534	4	US-09-671-325-1325	Sequence 1325, Ap	1224	108.5	6.0	2818	4	US-09-620-312D-92	Sequence 92, Appl
1152	110.5	6.1	534	4	US-09-658-824-1325	Sequence 1325, Ap	1225	108.5	6.0	2820	4	US-09-799-451-370	Sequence 370, App
1153	110.5	6.1	2614	2	US-08-795-868-15	Sequence 15, Appl	1226	108.5	6.0	4900	1	US-08-245-295-5	Sequence 5, Appl
1154	110.5	6.1	2614	3	US-09-303-069-15	Sequence 15, Appl	1227	108.5	6.0	4900	1	US-08-481-130-5	Sequence 5, Appl
1155	110.5	6.1	2614	3	US-09-134-250-15	Sequence 15, Appl	1228	108.5	6.0	4900	1	US-08-656-984A-5	Sequence 5, Appl
1156	110.5	6.1	2906	4	US-09-907-794A-291	Sequence 291, App	1229	108.5	6.0	4900	1	US-08-485-604-5	Sequence 5, Appl
1157	110.5	6.1	2906	4	US-09-905-125A-291	Sequence 291, App	1230	108.5	6.0	4900	2	US-08-487-595-5	Sequence 5, Appl
1158	110.5	6.1	2906	4	US-09-902-775A-291	Sequence 291, App	1231	108.5	6.0	4900	3	US-08-863-790-26	Sequence 26, Appl
1159	110.5	6.1	2906	4	US-09-906-700-291	Sequence 291, App	1232	108.5	6.0	4900	3	US-08-296-749-26	Sequence 26, Appl
1160	110.5	6.1	2906	4	US-09-903-603A-291	Sequence 291, App	1233	108.5	6.0	5077	1	US-08-245-295-8	Sequence 8, Appl
1161	110.5	6.1	2906	4	US-09-904-920A-291	Sequence 291, App	1234	108.5	6.0	5077	1	US-08-481-130-8	Sequence 8, Appl
1162	110.5	6.1	2906	4	US-09-909-064-291	Sequence 291, App	1235	108.5	6.0	5077	1	US-08-656-984A-8	Sequence 8, Appl
1163	110.5	6.1	2906	4	US-09-905-381A-291	Sequence 291, App	1236	108.5	6.0	5077	1	US-08-485-604-8	Sequence 8, Appl
1164	110.5	6.1	2926	4	US-09-906-618-291	Sequence 291, App	1237	108.5	6.0	5077	2	US-08-487-595-8	Sequence 8, Appl
1165	110.5	6.1	2926	2	US-08-724-394A-13	Sequence 13, Appl	1238	108	6.0	836	3	US-08-463-903-1	Sequence 1, Appl
1166	110.5	6.1	2970	4	US-09-566-921-105	Sequence 105, App	1239	108	6.0	836	3	US-07-935-695-1	Sequence 1, Appl
1167	110.5	6.1	71700	4	US-09-949-016-16418	Sequence 16418, A	1240	108	6.0	856	3	US-08-463-903-16	Sequence 16, Appl
1168	110	6.1	738	2	US-08-224-591-13	Sequence 13, Appl	1241	108	6.0	856	3	US-07-935-695-16	Sequence 16, Appl
1169	110	6.1	738	2	US-08-392-338A-22	Sequence 22, Appl	1242	108	6.0	1642	4	US-10-000-489-77	Sequence 77, Appl
1170	110	6.1	738	2	US-08-926-789-13	Sequence 13, Appl	1243	108	6.0	1645	2	US-08-724-394A-14	Sequence 14, Appl
1171	110	6.1	738	3	US-09-166-750-22	Sequence 22, Appl	1244	108	6.0	4626	4	US-09-566-921-4	Sequence 4, Appl
1172	110	6.1	738	3	US-09-166-093-22	Sequence 22, Appl	1245	108	6.0	2154	4	US-09-949-016-16374	Sequence 16374, A
1173	110	6.1	738	3	US-09-172-019-22	Sequence 22, Appl	1246	107.5	6.0	597	2	US-08-768-964-11	Sequence 11, Appl
1174	110	6.1	738	3	US-09-166-094-22	Sequence 22, Appl	c1247	107.5	6.0	597	3	US-08-768-964-16	Sequence 16, Appl
1175	110	6.1	738	4	US-09-443-213-22	Sequence 22, Appl	1248	107.5	6.0	597	3	US-09-005-299-11	Sequence 11, Appl
1176	110	6.1	738	5	PC-T-US93-11138-13	Sequence 13, Appl	c1249	107.5	6.0	597	3	US-09-005-299-16	Sequence 16, Appl
1177	110	6.1	1213	6	5223418-1	Patent No. 5223418	1250	107.5	6.0	597	3	US-09-515-431-11	Sequence 11, Appl
1178	110	6.1	1213	6	5223418-1	Patent No. 5223418	c1251	107.5	6.0	597	3	US-09-515-431-16	Sequence 16, Appl
1179	110	6.1	1352	3	US-08-463-903-11	Sequence 11, Appl	1252	107.5	6.0	789	2	US-08-768-964-4	Sequence 4, Appl
1180	110	6.1	1352	3	US-07-935-695-11	Sequence 11, Appl	c1253	107.5	6.0	789	2	US-08-768-964-5	Sequence 5, Appl

1254	107.5	6.0	789	3	US-09-005-299-4	Sequence 4, Appli	1327	103.5	5.7	409	4	US-09-702-705-1328	Sequence 1328, Ap
c1255	107.5	6.0	789	3	US-09-005-299-5	Sequence 5, Appli	1328	103.5	5.7	409	4	US-09-736-457-1328	Sequence 1328, Ap
1256	107.5	6.0	789	3	US-09-515-431-4	Sequence 4, Appli	1329	103.5	5.7	409	4	US-09-614-124B-1328	Sequence 1328, Ap
c1257	107.5	6.0	789	3	US-09-515-431-5	Sequence 5, Appli	1330	103.5	5.7	409	4	US-09-671-325-1328	Sequence 1328, Ap
1258	107.5	6.0	803	1	US-08-323-445A-7	Sequence 7, Appli	1331	103.5	5.7	409	4	US-09-658-824-1328	Sequence 14, Appl
1259	107.5	6.0	803	1	US-08-515-903A-7	Sequence 7, Appli	1332	103.5	5.7	522	2	US-08-768-964-14	Sequence 15, Appl
1260	107.5	6.0	803	5	PCT-US95-12840-7	Sequence 7, Appli	c1333	103.5	5.7	522	2	US-08-768-964-15	Sequence 14, Appl
1261	107.5	6.0	1069	2	US-08-768-964-1	Sequence 1, Appli	1334	103.5	5.7	522	3	US-09-005-299-14	Sequence 15, Appl
c1262	107.5	6.0	1069	2	US-08-768-964-3	Sequence 3, Appli	c1335	103.5	5.7	522	3	US-09-005-299-15	Sequence 14, Appl
1263	107.5	6.0	1069	3	US-09-005-299-1	Sequence 1, Appli	1336	103.5	5.7	522	3	US-09-515-431-14	Sequence 15, Appl
c1264	107.5	6.0	1069	3	US-09-005-299-3	Sequence 3, Appli	c1337	103.5	5.7	522	3	US-09-515-431-15	Sequence 6, Appli
1265	107.5	6.0	1069	3	US-09-515-431-1	Sequence 1, Appli	1338	103.5	5.7	714	2	US-08-768-964-6	Sequence 8, Appli
c1266	107.5	6.0	1069	3	US-09-515-431-3	Sequence 3, Appli	c1339	103.5	5.7	714	2	US-08-768-964-8	Sequence 6, Appli
c1267	107.5	6.0	63183	4	US-09-949-016-13047	Sequence 13047, A	1340	103.5	5.7	714	3	US-09-005-299-6	Sequence 8, Appli
c1268	107.5	6.0	63183	4	US-09-949-016-13048	Sequence 13048, A	c1341	103.5	5.7	714	3	US-09-005-299-8	Sequence 6, Appli
1269	107	5.9	752	6	S455030-12	Patent No. S455030	1342	103.5	5.7	714	3	US-09-515-431-6	Sequence 8, Appli
1270	107	5.9	752	6	S455030-12	Patent No. S455030	c1343	103.5	5.7	714	3	US-09-515-431-8	Sequence 20, Appli
1271	107	5.9	1149	3	US-08-477-460B-5	Sequence 5, Appli	1344	103.5	5.7	819	4	US-09-910-174B-20	Sequence 20, Appl
1272	107	5.9	1149	3	US-08-379-516-5	Sequence 5, Appli	1345	103.5	5.7	819	4	US-09-620-461-20	Sequence 20, Appl
1273	107	5.9	1149	3	US-09-329-916-5	Sequence 5, Appli	1346	103.5	5.7	1223	4	US-09-949-016-2283	Sequence 309, App
1274	107	5.9	1149	3	US-08-485-372A-5	Sequence 5, Appli	1347	103.5	5.7	2200	4	US-09-774-528-309	Sequence 1, Appli
1275	107	5.9	1149	3	US-09-409-006A-5	Sequence 5, Appli	1348	103.5	5.7	2229	4	US-09-910-174B-1	Sequence 1, Appli
1276	107	5.9	1149	3	US-08-484-681-5	Sequence 5, Appli	1349	103.5	5.7	2229	4	US-09-620-461-1	Sequence 3, Appli
1277	107	5.9	1149	5	PCT-US93-07422-5	Sequence 5, Appli	1350	103.5	5.7	2831	2	US-08-808-982-3	Sequence 3, Appli
1278	107	5.9	1149	5	PCT-US93-07422-5	Sequence 5, Appli	1351	103.5	5.7	2831	3	US-09-306-902A-3	Sequence 3, Appli
1279	107	5.9	1561	3	US-09-656-952-18	Sequence 18, Appl	1352	103.5	5.7	7783	4	US-09-495-880A-3	Sequence 3, Appli
1280	107	5.9	1591	3	US-09-656-952-17	Sequence 17, Appl	1353	103.5	5.7	19272	4	US-09-949-016-13462	Sequence 13462, A
1281	107	5.9	1592	3	US-09-656-952-1	Sequence 1, Appli	c1354	103.5	5.7	20662	4	US-09-949-016-15156	Sequence 15156, A
1282	106.5	5.9	819	2	US-08-400-115-3	Sequence 3, Appli	1355	103	5.7	538	3	US-09-221-298-3	Sequence 3, Appli
1283	106.5	5.9	877	3	US-08-463-903-14	Sequence 14, Appl	1356	103	5.7	538	3	US-09-401-064-3	Sequence 3, Appli
1284	106.5	5.9	877	3	US-07-935-695-14	Sequence 14, Appl	1357	103	5.7	723	4	US-09-791-540-5	Sequence 30, Appl
1285	106	5.9	744	2	US-08-392-338A-12	Sequence 12, Appl	1358	103	5.7	744	4	US-09-910-174B-30	Sequence 63, Appl
1286	106	5.9	744	3	US-09-166-750-12	Sequence 12, Appl	1359	103	5.7	1020	3	US-08-961-309-63	Sequence 7, Appli
1287	106	5.9	744	3	US-09-166-093-12	Sequence 12, Appl	1360	103	5.7	1273	3	US-08-466-368-1	Sequence 1, Appli
1288	106	5.9	744	3	US-09-172-019-12	Sequence 12, Appl	1361	103	5.7	1273	3	US-08-328-500-1	Sequence 1, Appli
1289	106	5.9	744	3	US-09-166-094-12	Sequence 12, Appl	1362	103	5.7	2691	3	US-09-651-200-1	Sequence 1, Appli
1290	106	5.9	744	4	US-09-443-213-12	Sequence 12, Appl	1363	103	5.7	4092	2	US-08-469-532D-106	Sequence 106, App
1291	106	5.9	1361	3	US-08-463-903-21	Sequence 21, Appl	1364	103	5.7	5714	4	US-09-620-312D-393	Sequence 393, App
1292	106	5.9	1361	3	US-07-935-695-21	Sequence 21, Appl	1365	103	5.7	5714	4	US-08-756-387B-12	Sequence 12, Appl
1293	106	5.9	23218	4	US-09-949-016-11987	Sequence 11987, A	1366	102.5	5.7	516	2	US-08-756-387B-13	Sequence 12, Appl
1294	106	5.9	23219	4	US-09-949-016-13396	Sequence 13396, A	1367	102.5	5.7	516	3	US-09-285-873-12	Sequence 12, Appl
1295	105.5	5.8	1029	3	US-09-032-337-40	Sequence 40, Appl	1368	102.5	5.7	516	3	US-09-944-277A-12	Sequence 12, Appl
1296	105.5	5.8	1359	3	US-08-227-496C-17	Sequence 17, Appl	1369	102.5	5.7	591	2	US-08-756-387B-10	Sequence 10, Appl
1297	105.5	5.8	1515	3	US-09-240-915-4	Sequence 4, Appli	1370	102.5	5.7	591	3	US-08-788-954-1	Sequence 1, Appli
1298	105.5	5.8	1515	3	US-09-591-435-4	Sequence 4, Appli	1371	102.5	5.7	591	3	US-09-285-873-10	Sequence 10, Appl
1299	105	5.8	1051	4	US-09-749-528-85	Sequence 85, Appl	1372	102.5	5.7	591	2	US-09-944-277A-10	Sequence 10, Appl
1300	105	5.8	1618	4	US-09-949-016-1390	Sequence 1390, Ap	1373	102.5	5.7	699	2	US-08-756-387B-7	Sequence 7, Appli
1301	105	5.8	1638	4	US-09-949-016-250	Sequence 250, App	1374	102.5	5.7	699	3	US-09-285-873-7	Sequence 7, Appli
1302	105	5.8	3645	4	US-08-999-689A-3	Sequence 3, Appli	1375	102.5	5.7	699	4	US-09-944-277A-7	Sequence 7, Appli
1303	104.5	5.8	413	3	US-09-254-465A-27	Sequence 27, Appl	1376	102.5	5.7	773	3	US-08-897-956A-6	Sequence 6, Appli
1304	104.5	5.8	413	4	US-09-953-499-27	Sequence 27, Appl	1377	102.5	5.7	773	3	US-08-756-387B-4	Sequence 4, Appli
1305	104.5	5.8	1065	3	US-08-875-811-40	Sequence 40, Appl	c1378	102.5	5.7	774	2	US-08-756-387B-5	Sequence 5, Appli
1306	104.5	5.8	1428	3	US-08-812-946A-3	Sequence 3, Appli	1379	102.5	5.7	774	3	US-09-285-873-4	Sequence 4, Appli
1307	104.5	5.8	1450	2	US-08-724-394A-16	Sequence 16, Appl	c1380	102.5	5.7	774	3	US-09-285-873-5	Sequence 5, Appli
1308	104	5.8	713	2	US-08-238-037-3	Sequence 3, Appli	1381	102.5	5.7	774	4	US-09-944-277A-4	Sequence 4, Appli
1309	104	5.8	1174	1	US-07-869-933-10	Sequence 10, Appl	c1382	102.5	5.7	774	4	US-09-944-277A-5	Sequence 5, Appli
1310	104	5.8	1174	3	US-09-103-663-10	Sequence 10, Appl	1383	102.5	5.7	1065	3	US-08-875-811-48	Sequence 48, Appl
1311	104	5.8	1198	2	US-08-756-387B-3	Sequence 3, Appli	1384	102.5	5.7	1161	3	US-08-205-657A-24	Sequence 24, Appl
c1312	104	5.8	1198	2	US-08-756-387B-1	Sequence 1, Appli	1385	102.5	5.7	1161	3	US-08-702-525-24	Sequence 24, Appl
1313	104	5.8	1198	3	US-09-285-873-1	Sequence 1, Appli	1386	102.5	5.7	1161	4	US-09-837-867A-24	Sequence 24, Appl
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1315	104	5.8	1198	4	US-09-944-277A-1	Sequence 1, Appli	1388	102.5	5.7	2955	3	US-08-897-956A-4	Sequence 4, Appli
c1316	104	5.8	1198	4	US-09-944-277A-3	Sequence 3, Appli	1389	102.5	5.7	6151	5	PCT-US91-02954-12	Sequence 12, Appl
1317	104	5.8	1350	1	US-08-157-101A-9	Sequence 9, Appli	1390	102.5	5.7	78157	4	US-09-949-016-16466	Sequence 16466, A
1318	104	5.8	1377	5	PCT-US91-02954-2	Sequence 2, Appli	1391	102.5	5.7	78157	4	US-09-949-016-16467	Sequence 16467, A
1319	104	5.8	1444	4	US-09-773-877B-23	Sequence 23, Appli	1392	102	5.6	1415	5	PCT-US92-08090-4	Sequence 4, Appli
1320	104	5.8	1503	3	US-09-254-465A-5	Sequence 5, Appli	1393	102	5.6	1421	5	PCT-US92-08090-3	Sequence 3, Appli
1321	104	5.8	1503	4	US-09-953-499-5	Sequence 5, Appli	1394	102	5.6	1448	5	PCT-US92-08090-2	Sequence 2, Appli
1322	104	5.8	1576	1	US-08-157-101A-6	Sequence 6, Appli	1395	102	5.6	1882	4	US-09-566-921-46	Sequence 46, Appl
1323	104	5.8	1614	4	US-09-016-434-1151	Sequence 1151, Ap	1396	102	5.6	2465	5	PCT-US92-08090-1	Sequence 1, Appli
1324	104	5.8	6727	2	US-08-125-462-2	Sequence 2, Appli	1397	101.5	5.6	751	3	US-09-039-982A-34	Sequence 34, Appl
1325	104	5.8	6727	2	US-08-891-848-2	Sequence 2, Appli	1398	101.5	5.6	751	3	US-09-039-641-34	Sequence 34, Appl
1326	103.5	5.7	359	4	US-09-270-767-27274	Sequence 27274, A	1399	101.5	5.6	751	3	US-09-039-762A-34	Sequence 34, Appl

1400	101.5	5.6	751	3	US-09-042-492D-34	Sequence 34, Appl	1473	100	5.5	921	2	US-08-184-009-202	Sequence 202, App
1401	101.5	5.6	751	3	US-08-913-612A-34	Sequence 34, Appl	1474	100	5.5	921	2	US-08-458-356-202	Sequence 202, App
1402	101.5	5.6	751	4	US-10-266-463A-34	Sequence 34, Appl	1475	100	5.5	921	3	US-08-460-736-202	Sequence 202, App
1403	101.5	5.6	765	2	US-08-667-939A-14	Sequence 14, Appl	1476	100	5.5	921	4	US-09-535-370-202	Sequence 202, App
1404	101.5	5.6	765	3	US-08-433-123-14	Sequence 14, Appl	1477	100	5.5	921	4	US-09-663-667-202	Sequence 202, App
1405	101.5	5.6	972	3	US-08-848-760B-11	Sequence 11, Appl	1478	100	5.5	1389	2	US-08-417-495-2	Sequence 2, Appl
1406	101.5	5.6	972	4	US-09-828-028-11	Sequence 11, Appl	1479	100	5.5	1389	2	US-08-284-391B-2	Sequence 2, Appl
1407	101.5	5.6	1002	3	US-09-039-982A-33	Sequence 33, Appl	1480	100	5.5	1389	3	US-09-218-950-2	Sequence 2, Appl
1408	101.5	5.6	1002	3	US-09-039-641-33	Sequence 33, Appl	1481	100	5.5	1389	4	US-08-394-388A-2	Sequence 2, Appl
1409	101.5	5.6	1002	3	US-09-039-762A-33	Sequence 33, Appl	1482	100	5.5	1389	5	PCT-US92-01785-2	Sequence 2, Appl
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1417	101.5	5.6	1120	2	US-08-101-624-1	Sequence 1, Appl	1490	100	5.5	1716	2	US-08-147-772-3	Sequence 3, Appl
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1419	101.5	5.6	1120	3	US-08-280-757B-1	Sequence 1, Appl	1492	100	5.5	1716	2	US-08-101-624-24	Sequence 24, Appl
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1425	101.5	5.6	1120	4	US-09-837-867A-22	Sequence 22, Appl	1498	100	5.5	1716	3	US-08-702-525-16	Sequence 16, Appl
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1430	101.5	5.6	1304	3	US-09-218-950-28	Sequence 28, Appl							
1431	101.5	5.6	1304	4	US-08-394-388A-28	Sequence 28, Appl							
1432	101.5	5.6	1424	3	US-09-326-186B-226	Sequence 226, App							
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1441	101.5	5.6	2793	3	US-09-134-250-13	Sequence 13, Appl							
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1443	101	5.6	528	4	US-09-270-767-28193	Sequence 28193, A							
1444	101	5.6	837	3	US-09-570-367C-22	Sequence 22, Appl							
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1446	101	5.6	837	4	US-09-934-634-22	Sequence 22, Appl							
1447	101	5.6	1311	4	US-09-252-931A-10188	Sequence 10188, A							
1448	101	5.6	1416	1	US-08-236-311-2	Sequence 2, Appl							
1449	101	5.6	1416	3	US-08-457-918-2	Sequence 2, Appl							
1450	101	5.6	1416	4	US-10-157-408-2	Sequence 2, Appl							
1451	101	5.6	1742	3	US-08-466-368-3	Sequence 3, Appl							
1452	101	5.6	1742	4	US-08-470-998-1	Sequence 1, Appl							
1453	101	5.6	1742	4	US-08-328-500-8	Sequence 8, Appl							
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1460	100.5	5.6	818	3	US-09-420-592A-3	Sequence 3, Appl							
1461	100.5	5.6	818	4	US-09-983-442-3	Sequence 3, Appl							
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1463	100.5	5.6	826	4	US-09-270-767-1015	Sequence 1015, Ap							
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1467	100.5	5.6	2482	3	US-09-329-916-3	Sequence 3, Appl							
1468	100.5	5.6	2482	3	US-08-485-372A-3	Sequence 3, Appl							
1469	100.5	5.6	2482	3	US-09-409-006A-3	Sequence 3, Appl							
1470	100.5	5.6	2482	3	US-08-484-681-3	Sequence 3, Appl							
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US-09-700-397-1

Sequence 1, Application US/09700397

Patent No. 6664383

GENERAL INFORMATION:

FILE REFERENCE: Q61459

CURRENT APPLICATION NUMBER: US/09/700,397

CURRENT FILING DATE: 2001-01-05

PRIOR FILING DATE: JP 10-131815

PRIOR APPLICATION NUMBER: PCT/JP99/02485

PRIOR FILING DATE: 1998-05-14

PRIOR APPLICATION NUMBER: PCT/JP99/02485

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

TYPE: DNA

LENGTH: 1032

ORGANISM: Homo sapiens

US-09-700-397-1

Alignment Scores:

Pred. No.: 1,43e-221 Length: 1032

Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

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Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

Db 1 ATGAAACCACTCCAGCCAAATAATGCAATTCATCTCTGGGCAATCTTCACGGGGCTG 60

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40

Db 61 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

ALIGNMENTS

RESULT 1

US-09-700-397-1

Sequence 1, Application US/09700397

Patent No. 6664383

GENERAL INFORMATION:

FILE REFERENCE: Q61459

CURRENT APPLICATION NUMBER: US/09/700,397

CURRENT FILING DATE: 2001-01-05

PRIOR FILING DATE: JP 10-131815

PRIOR APPLICATION NUMBER: PCT/JP99/02485

PRIOR FILING DATE: 1998-05-14

PRIOR APPLICATION NUMBER: PCT/JP99/02485

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

TYPE: DNA

LENGTH: 1032

ORGANISM: Homo sapiens

US-09-700-397-1

Alignment Scores:

Pred. No.: 1,43e-221 Length: 1032

Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-700-397-1 (1-1032)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

Db 1 ATGAAACCACTCCAGCCAAATAATGCAATTCATCTCTGGGCAATCTTCACGGGGCTG 60

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40

Db 61 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

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Db 121 GCTATGACACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATATTGAC 180
Qy 61 AsnArgValThrArgValAlaTrrPLeuAsnArgSerThrLeuTyrAlaGlyAsnAsp 80
Db 181 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
Qy 81 LysTrpCysLeuAspProArgValValLeuSerAsnThrGlnThrGlnTyrSerile 100
Db 241 AAGTGGTGCCCTGGATCCTCGCGTGGTCTCTTGAGCAACACCCCAACGCGATCAGCATC 300
Qy 101 GluileGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 301 GAGATCCAGACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGTGCAGCAGAC 360
Qy 121 AsnHisProLysThrSerArgValHisLeuileValGlnValSerProLysIleValGlu 140
Db 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGATAG 420
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Qy 161 GlyArgProGluProThrValThrTrrPArgHisIleSerProLysAlaValGlyPheVal 180
Db 481 GGTAGACCAGAGCCTACCGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTGTG 540
Qy 181 SerGluAspGluTyrLeuGluileGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 541 AGTGAAGACGAATACTCTGGAATTCAGGGCATCACCGGAGCAGTCAAGGGGACTACGAG 600
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValArgValIleValThrValAsn 220
Db 601 TGCAGTGCTCTCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAGGTCAACGTGAAC 660
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCCTCAGCAGAAATTCAGTGGTACAAGATGACAAA 780
Qy 261 ArgLeuileGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 781 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAGTGGAAACACAGCCTTTCTCTCAAACTC 840
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaLaserAsnLys 300
Db 841 ATCTTCTTCAATGTCTCTGACATGACATATGGGAATACACTTGGCTGGCCCTCCAAACAAG 900
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 901 CTGGGCCACCAATGCCAGCATCATGTATTATTTGGTCCAGGCGCGCTCAGGCGAGTGAAGC 960
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrrPLeuLeuProLeuLeuValIleHisLeu 340
Db 961 AACGGCAGCTCGAGGAGGGAGGCTGCGTCTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTG 1020
Qy 341 LeuLeuLysPhe 344
Db 1021 CTCTCAAAATTT 1032
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RESULT 2

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US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
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; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
; NAME/KEY: sig_peptide
; LOCATION: (130)..(213)
; NAME/KEY: mat_peptide
; LOCATION: (214)..()
US-09-700-397-2
Alignment Scores:
Pred. NO.: 3,35e-221 Length: 1693
Score: 1805.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-017-084A-523 (1-344) x US-09-700-397-2 (1-1693)
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrrPAlaIlePheThrGlyLeu 20
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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 190 GCTGCTGTGTCTCTTCCAGGAGTGCCTGGCGCAGCGAGATGCCACCTTCCCCAAA 249
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 250 GCTATGGACAAACGTGACGGTCCGGCAGGGGAGAGCCGCCCTCAGGTGCATATTGAC 309
Qy 61 AsnArgValThrArgValAlaTrrPLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 310 AACCGGTTCACCGGGTGGCTGGCTAAACCGCAGCACCCTCTCTATGCTGGGAATGAC 369
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerile 100
Db 370 AAGTGGTGCCCTGGATCCTCGCGTGGTCTCTTGAGCAACACCCAAACGCGATCAGCATC 429
Qy 101 GluileGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 430 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGTGCAGCAGAC 489
Qy 121 AsnHisProLysThrSerArgValHisLeuileValGlnValSerProLysIleValGlu 140
Db 490 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGATAG 549
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 550 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 609
Qy 161 GlyArgProGluProThrValThrTrrPArgHisIleSerProLysAlaValGlyPheVal 180
Db 610 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTGTG 669
Qy 181 SerGluAspGluTyrLeuGluileGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 670 AGTGAAGACGNAATCTTGGAAATTCAGGGCATCACCGGGAGAGTCAAGGGGACTACGAG 729
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValIleValThrValAsn 220
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Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleAspLeu 260

Db 850 CTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAACAAGGATGACAAA 909

Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

Db 910 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCTCTCAAAACTC 969

Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300

Db 970 ATCTTCTCAATGTCTCTGAACATGACTATGGAACACTACATTGGTGGCCTCCAAACAG 1029

Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1030 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1089

Qy 321 ArgGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340

Db 1090 AACGGCAGCTCAGGAGGGCGGCTGCGTCTGGCTGCTCTTCTTGTCTTGCACCTG 1149

Qy 341 LeuLeuLysPhe 344

Db 1150 CTCTCAAAATTT 1161

RESULT 3

US-09-700-397-5

; Sequence 5, Application US/09700397

; Patent No. 6664383

; GENERAL INFORMATION:

; APPLICANT: Ono Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of

; FILE REFERENCE: 061459

; CURRENT APPLICATION NUMBER: US/09/700,397

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: JP 10-131815

; PRIOR FILING DATE: 1998-05-14

; PRIOR APPLICATION NUMBER: PCT/JP99/02485

; PRIOR FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-700-397-5

Alignment Scores:

Pred. No.: 1.41e-200 Length: 939

Score: 1642.00 Matches: 313

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 90.92% Indels: 0

DB: 4 Gaps: 0

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Db 1 CGCAGCGGAGATGCCACCTTCCCAAGCTATGGCAACGTCGACCGTTCGGCAGGGGGAG 60

Qy 52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArg 71

Db 61 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCGGGTGGCTGGCTAAACCGC 120

Qy 72 SerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArgValLeuLeu 91

Db 121 AGCACCACCTCTATGCTGGGAATGACAAAGTGGTGGCTTGGATCTCTCGCGTGTCTTCTG 180

Qy 92 SerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGly 111

Db 181 AGCAACACCCAAACGACGTACAGCATCGAGATCCAGAACGTTGGATGTGTATGACGAGGC 240

Qy 112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisIleu 131

Db 241 CCTTACACCTCTCGGTGCAGACACACCAACCAACCAAGACCTCTAGGGTCCACCTCAT 300

Qy 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151

Db 301 GTGCAGGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAGGGAAAC 360

Qy 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171

Db 361 AATATTAGCTTCACTGCTAGCAACTGGTAGACCAGAGCCTACGGTTACTTTGGAGACAC 420

Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191

Db 421 ATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTTGGAAATTTCCAGGGCATC 480

Qy 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211

Db 481 ACCCGGAGCAGTCAGGGGACTTACAGTGCAGTGCCTCCAATGACGTGGCCGCCGCCGTG 540

Qy 212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231

Db 541 GTACGGAGAGTAAGGTCACTGTAACATATCCACCACATATTCAGAAAGCCCAAGGGTACA 600

Qy 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251

Db 601 GGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660

Qy 252 GluPheGlnTyrTyrLysAspLysArgLeuIleGluGlyLysLysVal 271

Db 661 GAATTCAGTGTGACAGGATGACAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTG 720

Qy 272 GluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGly 291

Db 721 GAAACAGACACTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGG 780

Qy 292 AsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311

Db 781 AACTACACTTCGTGGCTCCCAACAGCTGGGCCACACCAATGCCAGCATCATGTATTT 840

Qy 312 GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrp 331

Db 841 GGTCCAGGCGCGCTCAGCGAGGTGAGCAACGGCAGCTCAGGAGGGCAGGCTGCGTCTGG 900

Qy 332 LeuLeuProLeuLeuValLeuHisLeuLeuLysPhe 344

Db 901 CTGCTGCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 939

RESULT 4

US-09-976-594-403

; Sequence 403, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 403

; LENGTH: 1195

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

Alignment Scores:
Pred. No.: 3.83e-109 Length: 1195
Score: 931.50 Matches: 180
Percent Similarity: 73.85% Conservative: 60
Best Local Similarity: 55.38% Mismatches: 80
Query Match: 51.58% Indels: 5
DB: 4 Gaps: 4

US-10-017-084A-523 (1-344) x US-09-976-594-403 (1-1195)

Qy 20 LeuAlaLeuLeuLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 49 CTGAGATTGCTCTGCTCTTCCACAGAGTGGCTGTTCGACGGTGGAT-----TTT 102
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 103 AACCGAGCGACGACACATCACCGTAGGCGAGGGGACACAGCCATCTCAGTGGCTT 162
Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly 78
Db 163 CTAGAAGACAAGAACTCAAGGTGGCTGGTTGAACCGTTCTGGCATCATTTTGTGGA 222
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 98
Db 223 CATGACAAAGTGGTCTCTGGAGCCCGGGTGGAGTGGAGAAACGCCATTTCTTGGATAC 282
Qy 99 SerIleGluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGln 118
Db 283 AGCTCCCAATCCAGAGGTGGATGCTATGATGAGGGTTCTACACTTGTCTAGTTCAG 342
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 343 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTACAAAGTCCCAACCAAGATC 402
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
Db 403 TCCAAATATCTCTCGAGTGTCACTGTGAATGAGGCGACCAACGTCGTCTGTCATG 462
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 463 GCCAATGCCCTCTGAACCTGTATACCTGGAGACACCTTACCACTGGAAGGAA 522
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 523 TTTGAAGGAGAAGAATAATCTGGAGATCTTGGCATCACAGGAGCAGTCAGGCAAA 582
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaProValValArgArgValIysValThr 218
Db 583 TATGAGTCAAGCTGCCAAGAGGTCTCCCTGGCGGATGTCAACAAAGTCAAGGTCACT 642
Qy 219 ValAsnTyProProTyIleSerGluAlaIysGlyThrGlyValProValGlyGlnLys 238
Db 643 GTGAATATCTCTCCACTATCACAGATCCAGAGCATGAAGCCACACAGGACGAA 702
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyIysAsp 258
Db 703 GCTTCACTCAAAATGTAGGCGCTCGGCAGTGGCTGCACCTGACTTTTGAAGTGGTACGGGAT 762
Qy 259 AspLysArgLeuIleGluGlyIleGlyValIysValGluAsnArgProPheLeuSer 278
Db 763 GACACTAGG---ATAAATAGTGCCCAATGGCTTTGAGATTAAAGCAGCAGGAGGGCCAGTCT 819
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyArgIleAsnTyThrCysValAlaSer 298
Db 820 TCCCTGAGGTGCACCAACGTCACTGAGGAGCACTACGGCACTACCTGTGTGGCTGCC 879
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 880 AACAGCTGGGGGTCAACCAATGCCAGCTAGTCTCTTTTTCAGACCTGGGTGGTGAGAGGA 939

Qy 319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
Db 940 ATA---AATGATCATCATGCTGCGCGTACCCTGCTGCTGGCAGCATCTCTGCTC 996
Qy 339 HisLeuLeuLeuLys 343
Db 997 TGCCTTCTCAGCAA 1011

RESULT 5

US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Fimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1014
; OTHER INFORMATION:
; US-08-414-657D-5

Alignment Scores:
Pred. No.: 1.27e-108 Length: 1014
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 2 Gaps: 4

US-10-017-084A-523 (1-344) x US-08-414-657D-5 (1-1014)

Qy 20 LeuAlaLeuLeuLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 49 CTGAGACTGCTCTGCTCTTCCACAGGACTGCCCGTTCGACGGTGGAT-----TTT 102

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QY 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
   ::::::::::::::::::::
Db 103 AACCGAGGACGACGACAAATCAGCTGAGGAGGAGGACACGCGCATCTCAGGTGTG 162
QY 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGly 78
   ::::::::::::::::::::
Db 163 GTAGAAGACAAAGTCTGAAAGTGGCTGTGTTGAACCGCTCTGGCATCATCTTCGCTGA 222
QY 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
   ::::::::::::::::::::
Db 223 CACGACAGTGTCTCTGACCTCGGTTGAGTGGAGAAACGCCATGCTCTGGAATAC 282
QY 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
   ::::::::::::::::::::
Db 283 AGCCTCCGAATCCAGAAGTGTATGATGATGAAGGATCTCACATGCTCAGTTGAG 342
QY 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
   ::::::::::::::::::::
Db 343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTGATTGTACAAAGTTCCACCAAGATC 402
QY 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
   ::::::::::::::::::::
Db 403 TCCAACTCTCTCGGATGCTACTGTGATGAGGAGCAATGTAACTCTGTCTGATG 462
QY 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
   ::::::::::::::::::::
Db 463 GCCAATGGCGCCCTGAACTGTATCTACCTGAGACACCTTACACCACTTGGGAAGAA 522
QY 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
   ::::::::::::::::::::
Db 523 TTTGAAGGAGAAAGAAATATCTGAGATCTTGAAGATCTTGAAGGAGCAAGTCCAGGCAA 582
QY 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgValValValThr 218
   ::::::::::::::::::::
Db 583 TATGATGCAAGCTGCCACAGAGTCTCTCCGGGATGTCAACAAAGTCAAGTCACT 642
QY 219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
   ::::::::::::::::::::
Db 643 GTGAAGTATCCACCCACCATCACAGTCTAAGAGCAATGAAGCCACACACGAGCAAA 702
QY 239 GlyThrLeuGlnCysGluAsnAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
   ::::::::::::::::::::
Db 703 GCTTCCCTCAATGTGAAGCTCTCAGCGGTGCTGACCTGACTTTGAGTGTGACCGGAT 762
QY 259 AspLysArgLeuIleGluGlyLysGlyValLysValLysValGluAsnArgProPheLeuSer 278
   ::::::::::::::::::::
Db 763 GACACGAG---ATAACAGTCAACAGCGCTTGAGATTGAAGACGACTGAGGGCCAGTCC 819
QY 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
   ::::::::::::::::::::
Db 820 TCCCTGAGCGTGACCAAGCTACTGAGGAACACTAGCGCAACTATACCTGTGTGCTGCC 879
QY 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
   ::::::::::::::::::::
Db 880 AACAAAGTGGGGTCAACCAATGCCAGCTAGTCTTTTCAGACCCGGGGTGGTGAGAGA 939
QY 319 ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeu 338
   ::::::::::::::::::::
Db 940 ATC---AACGGATTCATGCTGCGCTGACCTGACCTGTGCTCTGGCAGCGTCCCTGTTTC 996
QY 339 HisLeuLeuLys 343
   ::::::::::::::
Db 997 TGCCTTCTCAGCAAA 1011
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RESULT 6

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US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
```

```
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
CITY: 997 Lenox Drive, Building 3, Suite 210
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1014
OTHER INFORMATION:
US-09-135-080-7
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Alignment Scores:
Pred. No.: 1,27e-108 Length: 1014
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 3 Gaps: 4
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US-10-017-084A-523 (1-344) x US-09-135-080-7 (1-1014)

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QY 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
   ::::::::::::::::::::
Db 49 CTGAGACTGCTCTGCTCTTCTTCCACAGGACTGCGCGTTCGCGCGTGGAT-----TTT 102
QY 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
   ::::::::::::::::::::
Db 103 AACCGAGGACGACGACAAATCAGCTGAGGAGGAGGACACGCGCATCTCTCAGGTGTG 162
QY 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGly 78
   ::::::::::::::::::::
Db 163 GTAGAAGACAAAGTCTGAAAGTGGCTGTGTTGAACCGCTCTGGCATCATCTTCGCTGA 222
QY 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
   ::::::::::::::::::::
Db 223 CACGACAGTGTCTCTGAGCCTCGGTTGAGTGGAGAAACGCCATGCTCTGGAATAC 282
QY 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
   ::::::::::::::::::::
Db 283 AGCCTCCGAATCCAGAAGTGTATGATGAAGGATCTCTCACATGCTCAGTTGAG 342
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Db 638 TATGAGTGAAGGCTGCCAAGAGTCTCTCCCGCGGATGTCAAAACAAGTCAAGTCACT 697
Qy 219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 698 GTGAACATATCAACCCACCATCACAGTGTAGAGCAATGAAGCCACACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp 258
Db 758 GCTTCCCTCAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGGTACCGGAT 817
Qy 259 AspLysArgLeuGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACACAGG---ATAAACAGTGCACCAACCGCCTTGAGTTAAGAGCACTGAGGCGCAGTCC 874
Qy 279 LysLeuLeuPhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 875 TCCCTGAGGTGACCAACGTCACCTAGGACACTACGGCACTACTACTGTGTGCTGCC 934
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 935 AACAGCTCGGGTCAACCAATGCCAGCTAGTCTCTTTTTCAGACCCGGGTGGTGAGAGA 994
Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValThrLeuLeuProLeuLeuValLeu 338
Db 995 ATC---AACGGATCCATCAGTCTGCGCGTACCACCTGTGTGCTGCTGCGCAGCTCCCTGTT 1051
Qy 339 HisLeuLeuLeuLys 343
Db 1052 TGCCTTCTCAGCAAA 1066

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RESULT 8

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US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56....1069
; OTHER INFORMATION:
US-09-135-080-3

Alignment Scores:
Pred. No.: 1,79e-108 Length: 1238
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 3 Gaps: 4

US-10-017-084a-523 (1-344) x US-09-135-080-3 (1-1238)
Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 104 CTGAGACTGCTCTGCTTCTTCCACAGGACTGCGCGTTCGCAGCGTGGAT-----TTT 157
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 158 AACCGAGCGCACGCAACATCACCGTGAGGCGGGGACACGGCCATCCTCAGGTGTGTG 217
Qy 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGly 78
Db 218 GTAGAAGCAAGAAGCTCGAAGTGGCTGGTTGAACCGCTCTGGCATCATCTCCCTGGA 277
Qy 79 AsnAspLysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
Db 278 CACGACAAGTGGTCTCTGACCCCTCGGCTGGAGAAACGCAATGCTCTGGAATAC 337
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 338 AGCCTCCGAATCCAGAAGGTGGATGCTATGATGAAGGATCCTACACATGCTCAGTTCA 397
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTTGACAGTTCCACCAAGATC 457
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
Db 458 TCCAACTCTCTCGGATGTCACGTGAATGAGGCGAGCAATGTAACCTGTGCTGCATG 517
Qy 159 AlaThrGlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGly 178
Db 518 GCCAATGGCGCCCTGAAACCTGTTATACCTGGAGACACCTTACACCACTTGAAGAGAA 577
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 578 TTGAGGAGAGAGAGAAATATCTGAGATCTAGGATCACCAGGGAACAGTCAGGCAAA 637
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
Db 638 TATGAGTGAAGGCTGCCAAGAGTCTCTCCCGCGGATGTCAAACAAGTCAAGTCACT 697
Qy 219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 698 GTGAACATATCAACCCACCATCACAGTGTAGAGCAATGAAGCCACACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp 258
Db 758 GCTTCCCTCAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGGTACCGGAT 817
Qy 259 AspLysArgLeuGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACACAGG---ATAAACAGTGCACCAACCGCCTTGAGTTAAGAGCACTGAGGCGCAGTCC 874
Qy 279 LysLeuLeuPhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298

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Db 875 TCCCTGACGGTGACCAAGTCTACTGAGGAACACTAGGCAACTATACCTGTGGCTGCC 934
 Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
 Db 935 AACAAAGCTCGCGGTGACCAATGCCAAGTCCAGCCTAGTCTCTTTTCAGACCGGGTGGAGAGGA 994
 Qy 319 ValSerLeuGlyHisThrSerArgAlaGlyCysValTrpLeuLeuProLeuValValLeu 338
 Db 995 ATC---AACGGATCATCATGCTGCGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 1051
 Qy 339 HisLeuLeuLeuLys 343
 Db 1052 TGCCTTCTCAGCANA 1066

RESULT 9
 US-08-414-657D-1
 ; Sequence 1, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 977 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 2..976
 ; OTHER INFORMATION:
 ; US-08-414-657D-1

Alignment Scores:
 Pred. No.: 2,89e-108 Length: 977
 Score: 923.50 Matches: 177
 Percent Similarity: 74.06% Conservative: 60
 Best Local Similarity: 55.31% Mismatches: 78
 Query Match: 51.14% Indels: 5
 DB: 2 Gaps: 4

US-10-017-084A-523 (1-344) x US-08-414-657D-1 (1-977)
 Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
 Db 29 CTGAGATTGCTCTGCCCTTCTCCACAGCACTGCTGTTCGACGGTGGAT-----TTT 82
 Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
 Db 83 AACCGAGCGGACGACCAATCATCCGTGAGGAGGAGGAGGACACAGCATCTCTCAGGTGGT 142
 Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly 78
 Db 143 CTAGAAGACAAGAACTCAAAGTGGCTGTGAACCGTTCTGGCATCAATTTTGTCTGA 202
 Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 98
 Db 203 CATGACAAGTGGTCTCTGGACCCACGGGTGAGCTGGAGAAACCGCCATTTCTCGAATAC 262
 Qy 99 SerIleGluIleGlnAsnValAspValTyAspGluGlyProTyThrCysSerValGln 118
 Db 263 AGCTCCGAATCCAGAAGTGGATGCTATGATGAGGGTTCCTACACTTGTCTCAGTTTCA 322
 Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
 Db 323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAAAGTCCCAACCAAGATC 382
 Qy 139 ValGluIleSerSerAspIleSerIleAsnGluIleAsnIleSerLeuThrCysIle 158
 Db 383 TCCAATATCTCTCGGATGTCACGTGAATGAGGCGACACAGTACTCTGGTCTGCAATG 442
 Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
 Db 443 GCCAATGGCGTCTCTGAACCTGTTATCACCTGGAGACACCTTACACCAACGGAAGGAA 502
 Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
 Db 503 TTTCAAGGAGAGAAGAATATCTGGAGATCTCTGGCATCTCCAGGAGGACGCTCAGGCAAA 562
 Qy 199 TyrGluCysSerAlaSerAsnAspValAlaProValValArgValValValValThr 218
 Db 563 TATGAGTGCAAGCTGCCAAGAGTCTCTCTCGGGATGTCAAACAAAGTCAAGTCACT 622
 Qy 219 ValAsnTyProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
 Db 623 GTGAATATCTCTCCACTATCACAGATCCAAAGAGCAATGAAGCCACACAGGACGACAA 682
 Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp 258
 Db 683 GCTTCACTCAAATGTGAGGCGCTCGGAGTGCCTGACCTGTGAGTGGTACCGGAT 742
 Qy 259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
 Db 743 GACACTAGG---ATAAATAGTGCATGGCTTGAGATTAGAGACACGAGGGCCAGTCT 799
 Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyTrpGlyAsnTyThrCysValAlaSer 298
 Db 800 TCCCTGACGGTGACCAAGCTCACTGAGGAGCCTACGCACTACACCTGTGTGGTGGC 859
 Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
 Db 860 AACAAAGCTGGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGGTGAAGAGA 919
 Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValValLeu 338
 Db 920 ATA---AATGATCCATCAGTCTGCGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 976

RESULT 10
 US-09-135-080-1
 ; Sequence 1, Application US/09135080
 ; Patent No. 6423827
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat R.
 ; APPLICANT: Pimenta, Aurea

US-08-414-657D-8

Alignment Scores:

Pred. No.: 3,59e-106 Length: 945
Score: 907.00 Matches: 170
Percent Similarity: 75.50% Conservative: 58
Best Local Similarity: 56.29% Mismatches: 70
Query Match: 50.22% Indels: 4
DB: 2 Gaps: 3

US-10-017-084A-523 (1-344) x US-08-414-657D-8 (1-945)

QY 20 LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
DB 49 CTGAGCTGCTCTGCTCTCTCCACAGCAGCTGCGCTGCGAGCGTGGAT-----TTT 102
QY 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
DB 103 AACCGAGCGGACGACATACCTGAGCGAGCGGGGACACGGCCATCTCTAGGTGTGTG 162
QY 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
DB 163 GTAGAGACAGAACTCGAAGTGGCTGTGTGAACCGCTCTGGCATCATCTCTCGTGA 222
QY 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
DB 223 CACGACAAAGTGTCTCTGACCTCGGGTTGAGCTGGAGAAACGCCCATGCTCTGGAATAC 282
QY 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
DB 283 AGCTCCGAATCCAGAGGTGATGTCTATGATGAAGGATCTCATACATGCTCAAGTTGAG 342
QY 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
DB 343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGTGTACAGTTCCACCAAGATC 402
QY 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
DB 403 TCCAACTCTCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAAACCTGTGTCATG 462
QY 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
DB 463 GCCTAAGGGCGCCCTGAACCTGTTATCACTCGAGACACCTTACACCACTTGAAGAGAA 522
QY 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
DB 523 TTTGAGGAGAGAGATATCTGAGATCTTAGGCATCACCAGGAGACAGTCAGCGCAA 582
QY 199 TyrGluCysSerAlaSerAsnAspValAlaLaProValValArgValLysValThr 218
DB 583 TATGAGTCAGAGCTGCCAACGAGGTCTCTCCGGGATGTCAAAACAAAGTCAAGTCACT 642
QY 219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
DB 643 GTGAATATCCACCCACCATCACAGTCTTAAGAGCAATGAAGCCACACAGGAGCAAA 702
QY 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
DB 703 GCTTCCCTCAATGTGAAGCCTCAGCGTGCCTGACCTGACTTTGAGTGTACCGGAT 762
QY 259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
DB 763 GACACCAAGG---ATAAACAGTGCACAAACGGCCTTGAGATTAGACAGCATGAGGGCCAGTCC 819
QY 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
DB 820 TCCCTGACGGGTGACCAACGCTCTAGGGAACACTACGGCAACTATACCTGTGTGCTGCC 879
QY 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGlu 318
DB 880 AACAGTCTGGCGTCACCCATCCAGCCTTAGTCTTTTCAGACCCCGGGTGTGTGAGAGA 939
QY 319 ValSer 320

DB 940 ATCAAC 945

RESULT 13

US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...912
; OTHER INFORMATION:
US-08-414-657D-6
Alignment Scores:
Pred. No.: 1,48e-105 Length: 912
Score: 902.00 Matches: 171
Percent Similarity: 74.68% Conservative: 59
Best Local Similarity: 55.52% Mismatches: 74
Query Match: 49.94% Indels: 4
DB: 2 Gaps: 3
US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)

QY 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
DB 1 GTTCCACCGTGGAT-----TTTAAACCGAGCGACGCAACATCACCGTGAAGCGGGG 54
QY 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
DB 55 GACACAGCCATCTCTCAGTGTGCTTCTAGAGACAGAACTCAAGGTGCGCTGTGTGAC 114
QY 71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValLeu 90

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Db 115 CGTCTGCATCATTTTGGCATACAGTGTCTCTGGACCCACGGGTGAGCTG 174
Qy 91 LeuSerAenThrGlnThrGlnTyrSerIleGluLeuGlnAenValAspValTyrAspGlu 110
Db 175 GAGAAACGCCATTCTCTGGATATACAGCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234
Qy 111 GlyProTyrThrCysSerValGlnThrAspAenHisProLysThrSerArgValHisLeu 130
Db 235 GGTTCCTACATCTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTGTG 294
Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
Db 295 ATCGTACAGTCCACCAAGATCTCCAAATATCTCTCGGATGTCACGTGTAATGAGGCG 354
Qy 151 AsnAenIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
Db 355 AGCAACGTGACTCTGGTCTGCATGCCAATATGAGTGCAGGCTGCCAAGGTGTATCACCTGGAGA 414
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
Db 415 CACCTTACCAACTGGGAAGGAATTGGAAGAGAAAGAAATATCTGGAGATCTCTGGC 474
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCACCAGGAGCAGTCAAGCAATATGAGTGCAGGCTGCCAAGGCTCTCTCGGCG 534
Qy 211 ValValArgArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGly 230
Db 535 GATGTCAAACAGTCAAGGTCACTGTGAATATCTCTCCACTATCACAGAATCCAAAGAGC 594
Qy 231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
Db 595 AATGAAGCCACACAGGACGACAGCTTCATCAATGTGAGGCTCGGAGTGCCTGCA 654
Qy 251 AlaGluPheGlnThrTyrLysAspAspLysArgLeuIleGluGlyLysGlyValLys 270
Db 655 CTGACTTGTAGTGTACCGGATGACACTAGG---ATAAATAGTGCCTGAGTCTGAG 711
Qy 271 ValGluAenArgProPheLeuSerLysLeuIlePhePheAenValSerGluHisAspTyr 290
Db 712 ATTAAGACGCGGAGGCGCAGTCTCTCCCTGACGGTGACCAACGTCACTGAGGAGCACATAC 771
Qy 291 GlyAenTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
Db 772 GGCACACTACCTGTGTGGCTGCCAACAAAGCTGGGGGTCCACAAATGCCAGGCTAGTCTCT 831
Qy 311 PheGlyProGlyAlaValSerGluValSerAenGlyThrSerArgArgAlaGlyCysVal 330
Db 832 TTCAGACTGGTGGTGGTGGAGGAGATA---AATGGATCCATCAGTCTGGCCGTACCACCTG 888
Qy 331 TrpLeuLeuProLeuLeuValLeu 338
Db 889 TGGTCTGCTGGCAGCATCTCTGCTC 912
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RESULT 14

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US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
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; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
; US-08-414-657D-9
;
; Alignment Scores:
; Pred. No.: 1,31e-103 Length: 861
; Score: 886.50 Matches: 164
; Percent Similarity: 76.21% Conservative: 57
; Best Local Similarity: 56.55% Mismatches: 66
; Query Match: 49.09% Indels: 3
; DB: 2 Gaps: 2
;
; US-10-017-084A-523 (1-344) x US-08-414-657D-9 (1-861)
;
; Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAenValThrValArgGlnGly 50
; Db 1 GTTCCGACGTGGAT-----TTTAACGGAGCGACGGACAAACATCACCTGAGGCGAGGG 54
;
; Qy 51 GluSerAlaThrLeuArgCysThrIleAspAenArgValThrArgValAlaTrpLeuAen 70
; Db 55 GACACAGCCATCTCTCAGTGGTCTTAGAAGACAAAGAACTCAAAGTGGCTGGTGTGAAC 114
;
; Qy 71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
; Db 115 CGTTCTGGCATCATTTTGTCTGGACATGACAAAGTGGTCTCTGGACCCCAAGGTTGAGCTG 174
;
; Qy 91 LeuSerAenThrGlnThrGlnTyrSerIleGluIleGlnAenValAspValTyrAspGlu 110
; Db 175 GAGAAACGCCATTCTCTGGAAATACAGCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234
;
; Qy 111 GlyProTyrThrCysSerValGlnThrAspAenHisProLysThrSerArgValHisLeu 130
; Db 235 GGTTCCTACATCTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTGTG 294
;
; Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
; Db 295 ATCGTACAAAGTCCCAAGACCTCCCAAGATCTCTCTCGGATGTCACGTGTAATGAGGCG 354
;
; Qy 151 AsnAenIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
; Db 355 AGCAACGTGACTCTGGTCTGCTGATGCCCAATATGAGTGCCTGAACTGTATCACCTGGAGA 414
;
; Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
; Db 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db 415 CACCTTACCAACTGGAGGGAATTGGAAGAGAGAGAAATATCTCGAGATCTTGGC 474
Qy 191 IleThrArgGluInSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCCACGAGGAGCAGTCAGGCAAAATATGATGCAAAAGCTGCCAACGAGGTCTCTCGGG 534
Qy 211 ValValArgArgValLysValThrValAlaAntyrProProTyrIleSerGluAlaLysGly 230
Db 535 GATGTCAAAACAGTCAAGGTCACTGTGAACATATCTCCCACTATCACAGAATCCAAGAGC 594
Qy 231 ThrGlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
Db 595 AATGAGCCACACAGGAGCAGACCTTCCCTCAATGTGAAGCTCAGCGGTGCTGCA 654
Qy 251 AlaGluPheGlnTyrIleAspLysArgLeuLeuGluGlyLysGlyValLys 270
Db 655 CCTGACTTGTAGTGTACCGGATGACACTAGG---ATAAATAGTGCCTGCTTGG 711
Qy 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
Db 712 ATTAAGAGCAGGAGGCGGCGAGTCTTCCCTGACCGGTGACCAACGTCACTGAGGAGCACTAC 771
Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
Db 772 GGCACACTACACTGTGTGGCTGCCAACAGCTGGGGGTCAACCAATGCCAGCCTAGTCTT 831

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; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
US-08-414-657D-10
Alignment Scores:
Pred. No.: 1,77e-103 Length: 861
Score: 885.50 Matches: 164
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.03% Indels: 3
DB: 2 Gaps: 2
US-10-017-084A-523 (1-344) x US-08-414-657D-10 (1-861)
Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
Db 1 GTTCGACGCTGGAT-----TTTAACCGAGGCGACGACACATCACCGTGAGCGAGGG 54
Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaAlaThrLeuAsn 70
Db 55 GACCGGCGATCTCTCGGTGTGTGTGAAGACAAAGAACTCGAAAGTGGCCCTGGTTGAAC 114
Qy 71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArgValValLeu 90
Db 115 CGCTCTGGCATCATCTTCGCTGGACACGACAAAGTGTCTCTGGACCCCTCGGGTTGAGCTG 174
Qy 91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValThrArgGlu 110
Db 175 GAGAAACGCCATGCTCTCGAATATACAGCCTCCGAATCCAGAAGGTGGATGTCTTATGATGAA 234
Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
Db 235 GGATCTACATGCTCAGTTCAGACACAGACATGAGCCCAAGACCTCTCAGTTTACTTCTG 294
Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
Db 295 ATGTGTACAGTTCCACCAAGATCTCCAACATCTCTCGGATGTCTCACTGTGAATGAGGCG 354
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
Db 355 AGCAATGTAAACCTGTCTGATGCCCAATGGCGCCCTGGAACCTGTATTACCTGGAGA 414
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
Db 415 CACCTTACACCACTTGGAGAGAAATTTGAAGAGAGAGAAATATCTCGAGATCTCTAGC 474
Qy 191 IleThrArgGluInSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCCACGAGGAAACAGTCAGGCAAAATATGATGCAAGGCTGCCAACGAGGTCTCTCGGG 534
Qy 211 ValValArgArgValLysValThrValAlaAntyrProProTyrIleSerGluAlaLysGly 230
Db 535 GATGTCAAAACAGTCAAGGTCACTGTGAACATATCCACCCACCATCACAGAGTCTAAGAGC 594
Qy 231 ThrGlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
Db 595 AATGAGCCACACAGGAGCAGACCTTCCCTCAATGTGAAGCTCAGCGGTGCTGCA 654
Qy 251 AlaGluPheGlnTyrIleAspLysArgLeuLeuGluGlyLysGlyValLys 270
Db 655 CCTGACTTGTAGTGTACCGGATGACACACAGG---ATAAACAGTGCCTGAGTCTTGG 711
Qy 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
Db 712 ATTAAGAGCAGTGGGCGGCGAGTCTCTCCCTGACCGGTGACCAACGTCACTGAGGAGCACTAC 771
Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Qy 311 PheGlyProGlyAlaValSerGluValSer 320
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Db 832 TTCAGACCCGGTCGGTGAGAGGAATCAAC 861

Search completed: June 16, 2005, 15:42:35
Job time : 253 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 16, 2005, 06:58:07 ; Search time 2109 Seconds
(without alignments)
1012.516 Million cell updates/sec

Perfect score: 1806
Sequence: 1 MKTIQPKMNSISWAIFGL.....RRACVWLLPLVLVHLLKP 344

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Pgapop 6.0 , Pgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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-DB=Published Applications NA -QFMT=faeTap -SUFITX=rnpb-MINMATCH=0.1
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-TRANS=human40.cdi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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53	1806	100.0	1679	14	US-10-066-269-103	Sequence 103, App
65	1806	100.0	1679	14	US-10-167-749-522	Sequence 522, App
227	1806	100.0	1679	15	US-10-223-085-55	Sequence 55, Appl
233	1806	100.0	1679	15	US-10-219-065-125	Sequence 125, App
263	1806	100.0	1679	15	US-10-223-084-55	Sequence 55, Appl
264	1806	100.0	1679	15	US-10-223-088-55	Sequence 55, Appl
270	1806	100.0	1679	15	US-10-223-090-55	Sequence 55, Appl
272	1806	100.0	1679	15	US-10-223-087-55	Sequence 55, Appl
275	1806	100.0	1679	15	US-10-223-089-55	Sequence 55, Appl
488	1806	100.0	1679	16	US-10-223-081-55	Sequence 55, Appl
557	1806	100.0	1679	16	US-10-223-082-55	Sequence 55, Appl
559	1806	100.0	1679	17	US-10-170-481A-522	Sequence 522, App
619	1806	100.0	1679	17	US-10-162-521A-522	Sequence 522, App
627	1806	100.0	1679	17	US-10-305-654-55	Sequence 55, Appl
642	1806	100.0	1679	18	US-10-081-056-55	Sequence 55, Appl
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663	1806	100.0	1679	21	US-10-805-667-522	Sequence 522, App
664	1806	100.0	1679	21	US-10-897-359-522	Sequence 522, App
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1013	757	41.9	1136	17	US-10-015-115-25	Sequence 25, Appl	1086	246.5	13.6	3360	21	US-10-843-641A-2446	Sequence 2446, Appl
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1018	690	38.2	437	10	US-09-918-595-2450	Sequence 2450, Appl	1091	240	13.3	12667	21	US-10-852-335A-44	Sequence 44, Appl
1019	681.5	37.7	1056	18	US-10-332-947-24	Sequence 24, Appl	1092	238	13.2	6829	15	US-10-084-817-189	Sequence 189, Appl
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1045	274	15.2	6801	15	US-10-274-583-3	Sequence 3, Appl	1118	232	12.8	8270	16	US-10-032-189-55	Sequence 55, Appl
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1139	229.5	12.7	7329	18	US-10-435-751-165	Sequence 165, App
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1145	229.5	12.7	7570	18	US-10-435-751-195	Sequence 195, App
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1148	229.5	12.7	7602	18	US-10-435-751-171	Sequence 171, App
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1152	229.5	12.7	7650	18	US-10-435-751-164	Sequence 164, App
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1154	229.5	12.7	7650	18	US-10-435-751-176	Sequence 176, App
1155	229.5	12.7	7650	18	US-10-435-751-182	Sequence 182, App
1156	229.5	12.7	7650	18	US-10-435-751-188	Sequence 188, App
1157	229.5	12.7	7650	18	US-10-435-751-194	Sequence 194, App
1158	229.5	12.7	7651	18	US-10-435-751-207	Sequence 207, App
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1168	224.5	12.4	7491	18	US-10-435-751-151	Sequence 151, App
1169	224.5	12.4	7491	18	US-10-435-751-153	Sequence 153, App
1170	224.5	12.4	7642	20	US-10-723-860-2584	Sequence 2584, Ap
1171	224.5	12.4	7642	20	US-10-723-860-6725	Sequence 6725, Ap
1172	224.5	12.4	38299	19	US-10-741-601-5755	Sequence 5755, Ap
1173	224	12.4	2436	17	US-10-133-937-80	Sequence 80, Appl
1174	224	12.4	2436	17	US-10-159-563-80	Sequence 80, Appl
1177	224	12.4	3662	9	US-09-905-291A-289	Sequence 289, App
1245	224	12.4	3662	16	US-10-299-976-289	Sequence 289, App
1246	224	12.4	3662	16	US-10-299-937-289	Sequence 289, App
1247	224	12.4	3662	17	US-10-298-931-289	Sequence 289, App
1248	224	12.4	3662	17	US-10-448-923-289	Sequence 289, App
1249	224	12.4	3662	17	US-10-449-656-289	Sequence 289, App
1250	224	12.4	3662	17	US-10-448-713-289	Sequence 289, App
1251	224	12.4	3662	17	US-10-425-447-289	Sequence 289, App
1252	224	12.4	3662	19	US-10-215-371-289	Sequence 289, App
1253	224	12.4	3662	19	US-10-771-187-289	Sequence 289, App
1254	224	12.4	3662	21	US-10-963-467-289	Sequence 289, App
1255	224	12.4	3662	21	US-10-978-255-289	Sequence 289, App
1258	224	12.4	4053	9	US-09-905-291A-293	Sequence 293, App

Search completed: June 16, 2005, 12:57:30
Job time : 2173 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 16, 2005, 10:29:07 ; Search time 3857 Seconds
(without alignments)
3394.895 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMNSISWAIFGL.....RRAGCVLLPLVLHLLKF 344

Scoring table:

BLASUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cn2_1/USPTO spoal/US10017084/runat_14062005_151229_18855/app query.fasta_1.519
-DB=EST -QWTF=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blasmus62 -TRANS=human40.coi -LIST=1500
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10017084 @CN 1 1 3437 @runat_14062005_151229_18855 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSRLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gest1:*
9: gb_gest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	1780	98.6	1808	3	AK045973 Mus muscu
2	1780	98.6	1808	3	AK046377 Mus muscu
3	1506	83.4	874	9	AY406347 Homo sapi
4	1488	82.4	874	9	AY406349 Mus muscu
5	1324	73.3	773	9	AY406348 Pan trogl
6	1321	73.1	1450	7	CO635648 Contig266
7	1254	69.4	765	6	CD354474 UI-M-GMO-
8	1199.5	66.4	856	5	BU155617 AGENCOURT
9	1167	64.6	1039	2	BE798585 601581610

10	1117.5	61.9	748	7	CN362539	17004705
11	1112	61.6	890	6	CD327172	AGENCOURT
12	1094.5	60.6	759	7	CF737474	UI-M-HD0-
13	1062.5	58.8	1027	1	AL533026	AL533026
14	1062.5	58.8	2512	3	CR602526	full-length
15	1047	58.0	740	5	BU368328	603789424
16	1042	57.7	840	5	BU320256	603851118
17	1005.5	55.7	849	4	BI755360	603024964
18	982.5	54.4	865	4	BI666583	603291469
19	973	53.9	601	6	CB582386	AMGNNUC:N
20	952	52.7	600	7	CR548212	DKFZP459M
21	932.5	51.6	1017	9	AY406971	Homo sapi
22	929	51.4	793	5	BU365385	603786031
23	926.5	51.3	1017	9	AY406973	Mus muscu
24	926	51.3	545	2	BE263639	601192064
25	925.5	51.2	979	4	BG261691	602373361
26	920	50.9	737	7	CN533076	UI-M-HD0-
27	916.5	50.7	2768	3	AK030681	Mus muscu
28	912	50.5	732	4	BI551784	603197479
29	910	50.4	553	2	BE864555	UI-M-BH1-
30	908.5	50.3	1015	9	AY406972	Pan trogl
31	907	50.2	524	2	BE014142	125737 MA
32	902.5	50.0	859	6	CD325278	AGENCOURT
33	894	49.5	636	7	CR540711	DKFZP459F
34	894	49.5	2467	3	AK044845	Mus muscu
35	890	48.8	784	1	BI549918	603194765
36	881	48.8	768	1	AU080629	AU080629
37	875	48.4	754	4	BI550038	603192502
38	869	48.1	580	4	BI548566	603189502
39	868	48.1	680	7	CR751151	DKFZP459F
40	862.5	47.8	661	4	BM009450	603629962
41	862.5	47.8	953	4	BM423716	AGENCOURT
42	858.5	47.5	1033	4	BM807426	AGENCOURT
43	855.5	47.4	1083	4	BM809227	AGENCOURT
44	843.5	46.7	2330	3	BC080168	Xenopus l
45	830	46.0	739	5	BU277649	603866829
46	814.5	45.1	728	6	CD353574	UI-M-GMO-
47	814.5	45.1	1138	4	BM556708	AGENCOURT
48	814	45.1	804	7	CN232247	WLB048A12
49	811.5	44.9	557	4	BM256660	520043 MA
50	805	44.6	2096	3	AK035218	Mus muscu
51	801	44.4	705	4	BG704152	602687364
52	799	44.2	1953	3	AK030503	Mus muscu
53	795	44.0	660	6	BY723873	BY723873
54	793.5	43.9	759	7	CN094277	EC2BBA9CA
55	791.5	43.8	764	5	BM945665	UI-M-EMO-
56	781.5	43.3	780	7	CK313831	SB02038B2
57	774.5	42.9	724	7	CK312152	SB02011A1
58	772.5	42.8	849	6	CA472810	AGENCOURT
59	771.5	42.7	533	4	BI341675	369186 MA
60	770	42.6	671	2	BB644996	BB644996
61	767.5	42.5	582	5	BP194945	BP194945
62	763	42.2	437	6	CB724811	EST0732 R
63	761.5	42.2	858	6	CD325821	AGENCOURT
64	761	42.1	663	4	BM724307	UI-B-EOL-
65	759	42.0	2534	3	AK039193	Mus muscu
66	748	41.4	690	7	CN233126	WLB057E10
67	743	41.1	613	7	CR540607	DKFZP459A
68	742	41.1	827	6	CA306798	UI-H-PT1-
69	730	40.4	633	4	BG706987	602672194
70	727	40.3	677	5	BQ444788	UI-M-ERO-
71	726.5	40.2	1304	5	BM911516	AGENCOURT
72	709	39.3	815	5	BU230452	603320607
73	707.5	39.2	819	5	BU750937	CH3#036 G
74	707.5	39.2	823	5	BU750936	CH3#036 G
75	706	39.1	754	4	BI598759	603245538
76	705	39.0	934	7	CN015939	AGENCOURT
77	703.5	39.0	778	3	CN078143	EC2BBA14C
78	697	38.6	683	2	BB640070	BB640070
79	697	38.6	3166	3	AK042854	Mus muscu
80	695	38.5	470	7	CR537991	DKFZP459N
81	688	38.1	695	7	CD228731	RJB060E12
82	688	38.1	754	7	CO043662	UI-M-ERO-

83	687.5	38.1	2798	3	AK028345	Mus muscu	156	498	27.6	611	6	CA355517	CA355517 627428 NC
84	685.5	38.0	602	2	BB611718	BB611718	157	498	27.6	914	5	EX843874	EX843874 BX843874
85	682	37.8	870	5	BU515609	AGENCOURT	158	497	27.5	768	5	EX868437	EX868437 BX868437
86	672	37.2	534	4	BM686717	UI-E-CQO-	c 159	492.5	27.3	753	1	AI589824	tm74909.x
87	671	37.2	603	5	BU390882	BU390882 603807132	160	490	27.1	599	7	CN229507	RJB072D02
88	671	37.2	846	1	AU051132	AU051132 600511332	161	488.5	27.0	835	5	EX881962	EX881962 BX881962
89	670.5	37.1	660	7	CR543317	CR543317 DKF2p459N	162	486	26.9	290	7	F05894	HSC0PH101.n
90	666.5	36.9	796	7	CO399311	AGENCOURT	c 163	485	26.9	578	2	BE121132	UI-R-CAO-
91	666	36.9	764	4	BT752729	603028343	164	484	26.8	456	6	CD803885	UI-M-GVO-
92	665	36.8	563	6	CB296974	12B22045	165	483	26.7	347	7	CN094278	EC2BBA9CA
93	661	36.6	548	2	BE015245	127482 MA	166	483	26.7	755	5	EX913106	EX913106 BX913106
94	654	36.2	880	6	CD303536	CD303536 AGENCOURT	167	480.5	26.6	664	7	CN362538	170006001
95	651	36.0	704	7	CN228803	RJB061B04	168	480	26.6	795	1	AU080106	AU080106 AU080106
96	644.5	35.7	640	7	CR545244	CR545244 DKF2p459F	169	478	26.5	566	7	CF977262	2-84-B04.
97	637.5	35.3	496	5	BE201259	BP201259 BP201259F	170	477	26.4	478	5	BY245406	BY245406 BY245406
98	632.5	35.0	621	5	BM466102	BM466102 AGENCOURT	171	476	26.4	661	6	CA452139	UI-M-F20-
99	632.5	35.0	1148	4	BM466102	BM466102 AGENCOURT	172	475.5	26.3	392	2	BE651010	UI-M-BH3-
100	632	35.0	688	2	BB646531	BB646531	173	475	26.3	646	6	CA334396	NISC 1808
101	629	34.8	674	6	CD767791	AGENCOURT	174	474.5	26.3	953	5	BU116264	603139651
102	619.5	34.3	786	7	CO811192	AGENCOURT	175	473	26.2	284	7	CR543721	DKF2p459H
103	616	34.1	867	6	CD300857	AGENCOURT	176	468.5	25.9	703	7	CF530869	UI-M-GHO-
104	614.5	34.0	511	5	EX493152	EX493152 DKF2p781G	c 177	468.5	25.9	772	7	CK776016	967158 MA
105	613	33.9	513	5	EX279850	EX279850	178	468	25.9	936	5	BQ227365	AGENCOURT
106	612.5	33.9	858	7	CO914076	CO914076 AGENCOURT	179	467.5	25.9	617	6	BY730405	BY730405 BY730405
107	607.5	33.6	492	2	AW967001	EST379075	180	467	25.9	390	4	BM719375	UI-E-EJ1-
108	607	33.6	587	7	CN088583	EC2BBA30B	181	467	25.9	390	4	BM719375	UI-E-EJ1-
109	604.5	33.5	639	7	CV030684	9878 Full	182	467	25.9	390	5	BM931279	UI-E-EJ1-
110	603	33.4	656	7	CK619540	mk25d06.y	c 183	467	25.9	394	4	BM684112	UI-E-EJ1-
111	591	32.7	522	4	BU553032	603193672	c 184	467	25.9	608	5	BQ188988	UI-E-EJ1-
112	591	32.7	678	5	BU624639	UI-H-FG1-	c 185	467	25.9	394	5	BM684852	UI-E-EJ1-
113	590	32.7	672	6	CA444805	UI-H-DH1-	c 186	467	25.9	394	5	BQ184395	UI-E-EJ1-
114	590	32.7	926	6	CD325412	AGENCOURT	c 187	467	25.9	394	7	CK108095	UI-E-EJ1-
115	589	32.6	677	6	CD217649	PgrIn.Pk0	c 188	467	25.9	403	4	BM684212	UI-E-EJ1-
116	589	32.6	697	5	BQ021243	UI-H-DH1-	c 189	467	25.9	700	5	BQ189788	UI-E-EJ1-
117	577	31.9	652	7	BN078144	EC2BBA14C	190	467	25.9	734	5	BU323269	UI-E-EJ1-
118	575	31.8	567	2	BF078551	228917 MA	191	467	25.9	884	5	BU323269	603405983
119	569.5	31.5	1084	6	CD255729	AGENCOURT	192	466.5	25.8	564	7	CO602836	DG8-24911
120	569	31.5	611	7	CN075612	CN075612 EC2BBA10C	c 193	463.5	25.7	666	5	BM951674	UI-N-EGO-
121	567	31.4	655	4	BU548049	BU548049 603196558	194	463	25.6	795	7	CO395735	AGENCOURT
122	565.5	31.3	528	2	BB856778	BB856778	c 195	461	25.5	572	2	BF407747	UI-R-BU2-
123	564.5	31.3	896	5	BQ890272	AGENCOURT	c 196	460	25.5	282	7	R75391	MD0B0556R MO
124	564	31.2	708	7	CN083621	EC2BBA22D	197	459	25.4	858	2	BF676478	602086277
125	561.5	31.1	519	7	CV038761	198 000 B	198	459	25.4	858	2	BF676478	602086277
126	561	31.1	726	5	BU912600	BU912600	199	457.5	25.3	718	6	CB460692	720592 MA
127	560.5	31.0	719	7	CK465166	CK465166 936244 MA	c 200	455	25.2	456	1	AI369684	QY71903.x
128	559.5	31.0	572	6	CR265380	1004285 H	201	453.5	25.1	651	6	BY726997	BY726997
129	559	31.0	2296	3	CR592222	full1-1eng	c 202	448	24.8	257	2	AW327110	20640 WAR
130	558	30.9	656	6	CA307492	UI-H-FT1-	c 203	448	24.8	909	5	BU132565	603120307
131	554.5	30.7	625	2	BB643056	BB643056	c 204	445.5	24.7	637	6	CB528708	UI-H-FT2-
132	553	30.6	636	7	CK843444	UI-R-BU2-	c 205	444	24.6	894	6	CB199088	AGENCOURT
133	552.5	30.6	670	7	CN083622	CN083622 EC2BBA22D	206	443.5	24.6	791	7	CK308721	SB02047A2
134	548	30.3	862	7	CK397022	AGENCOURT	207	441.5	24.4	497	7	CV035959	4134532 B
135	545	30.2	590	7	CR545391	CR545391 DKF2p459M	208	441	24.4	801	5	BU357013	603475462
136	544	30.1	663	2	BB633037	BB633037	c 209	440.5	24.4	700	7	CN458398	UI-N-HNO-
137	543.5	30.1	640	7	CO351229	DR AOV FL	210	440	24.4	445	5	BY269882	BY269882
138	543.5	30.1	647	7	CV030870	10123 Full	211	433.5	24.0	584	5	BP257486	BP257486 BP257486
139	541.5	30.0	415	7	R18841	Y922G06.r1	212	432.5	23.9	892	5	BP462753	BP462753
140	536	29.7	497	2	BB854833	BB854833	c 213	432	23.9	457	5	BY249728	BY249728
141	535.5	29.7	906	5	BU186468	BU186468 AGENCOURT	c 214	427.5	23.7	580	7	CN089827	EC2BBA32B
142	532.5	29.5	825	5	BP166655	BP166655 BP166655	c 215	426	23.6	544	6	CA439326	UI-E-DWO-
143	531.5	29.4	867	7	CO543317	LYEST116	c 216	426	23.6	544	6	CA439326	UI-H-DT1-
144	529	29.3	329	7	F06205	F06205 HSC10F041.n	217	416.5	23.4	481	5	BY256150	BY256150
145	525	29.1	593	7	CK845949	CK845949 968393 MA	218	416	23.1	496	7	CK693129	2F101-P00
146	523.5	29.0	923	1	ALU583491	ALU583491	c 219	413	22.9	494	1	AA548396	nj14604.8
147	518	28.7	565	2	BB663866	BB663866 147903 MA	220	411.5	22.8	617	4	BU622933	BU622933
148	512.5	28.4	535	9	AY409767	Homo sapi	221	407.5	22.6	778	7	CK315507	CK315507 SB02026A1
149	511	28.3	764	6	CA350929	CA350929 621861 NC	222	407.5	22.6	788	4	BI767217	BI767217 QV0257906
150	510	28.2	579	2	BB644523	BB644523	223	402	22.3	277	4	BI011319	QV2-EN009
151	509.5	28.2	773	4	BG208674	BG208674 RST28306	224	401.5	22.2	600	6	CA526928	CA526928 8023-83 M
152	508.5	28.2	535	9	AY409769	AY409769 Mus muscu	225	396.5	22.0	862	5	BP462754	BP462754
153	508	28.1	739	7	CK679857	CK679857 2F101-P00	c 226	394	21.8	598	1	AI815935	AI815935 au45902.x
154	507	28.1	659	2	AW149545	xf39c10.x	c 227	390.5	21.6	771	7	CN528825	UI-M-HQO-
155	506.5	28.0	703	5	BU117309	603138889	c 228	390	21.6	465	1	AI934791	wp89e04.x

156	498	27.6	611	6	CA355517	CA355517 627428 NC
157	498	27.6	914	5	EX843874	EX843874 BX843874
158	497	27.5	768	5	EX868437	EX868437 BX868437
c 159	492.5	27.3	753	1	AI589824	tm74909.x
160	490	27.1	599	7	CN229507	RJB072D02
161	488.5	27.0	835	5	EX881962	EX881962 BX881962
162	486	26.9	290	7	F05894	HSC0PH101.n
c 163	485	26.9	578	2	BE121132	UI-R-CAO-
164	484	26.8	456	6	CD803885	UI-M-GVO-
165	483	26.7	347	7	CN094278	EC2BBA9CA
166	483	26.7	755	5	EX913106	EX913106 BX913106
167	480.5	26.6	664	7	CN362538	170006001
168	480	26.6	795	1	AU080106	AU080106 AU080106
169	478	26.5	566	7	CF977262	2-84-B04.
170	477	26.4	478	5	BY245406	BY245406 BY245406
171	476	26.4	661	6	CA452139	UI-M-F20-
172	475.5	26.3	392	2	BE651010	UI-M-BH3-
173	475	26.3	646	6	CA334396	NISC 1808
174	474.5	26.3	953	5	BU116264	603139651
175	473	26.2	284	7	CR543721	DKF2p459H
176	468.5	25.9	703	7	CF530869	UI-M-GHO-
c 177	468.5	25.9	772	7	CK776016	967158 MA
178	468	25.9	936	5	BQ227365	AGENCOURT
179	467.5	25.9	617	6	BY730405	BY730405 BY730405
180	467	25.9	390	4	BM719375	UI-E-EJ1-
181	467	25.9	390	4	BM719375	UI-E-EJ1-
182	467	25.9	390	5	BM931279	UI-E-EJ1-
c 183	467	25.9	394	4	BM684112	UI-E-EJ1-
c 184	467	25.9	394	5	BM684852	UI-E-EJ1-
c 185	467	25.9	394	5	BQ184395	UI-E-EJ1-
c 186	467	25.9	394	5	BQ184512	UI-E-EJ1-
c 187	467	25.9	394	7	CK300895	UI-E-EJ1-
c 188	467	25.9	403	4	BM684212	UI-E-EJ1-
189	467	25.9	700	5	BQ188988	UI-E-EJ1-
190	467	25.9	734	5	BQ187606	UI-E-EJ1-

229	389.5	21.6	878	5	BP165624	BP165624	302	296.5	16.4	417	6	CA884109	CA884109	B0107H12-
230	389	21.5	450	5	BY263302	BY263302	303	295	16.3	994	6	CD325921	CD325921	AGENCOURT
c 231	388	21.5	294	7	W15256	zc16h07.81	c 304	294.5	16.3	451	1	AA933871	AA933871	OL91d04.8
232	388	21.5	357	5	BY303236	BY303236	305	293	16.2	220	7	H16176	ym21g09.r1	BY21g09.r1
233	385	21.3	673	7	CR736885	CR736885	306	293	16.2	665	9	EX243020	Danilo.rer	EX243020
234	384.5	21.3	444	1	AA682970	ae89a04.s	307	293	16.2	761	6	CD755145	AGENCOURT	CD755145
235	380.5	21.1	775	4	B1199955	602761121	308	291.5	16.1	899	5	BY134624	603119839	BY134624
236	379.5	21.0	660	5	BM337636	BM337636	309	291	16.1	402	5	BY289266	BY289266	BY289266
237	377.5	20.9	853	5	BP164129	BP164129	c 310	290.5	16.1	733	7	CO619752	DG9-1d13	CO619752
238	376.5	20.8	535	9	AY409768	Pan.trog1	c 311	290	16.1	585	7	CO628980	DG9-3m14	CO628980
c 239	376	20.8	470	1	A1580850	ta33e06.x	c 312	289.5	16.0	726	5	BU395513	603404749	BU395513
240	373.5	20.7	478	6	CA885050	B0115E08.x	313	288.5	16.0	411	5	BY288341	BY288341	BY288341
c 241	372	20.6	511	1	A1415689	mc70a03.x	314	288	15.9	422	4	BI390270	PSpic.pk0	BI390270
c 242	371.5	20.6	723	9	AG035406	AG035406	c 315	285	15.8	691	7	CK661190	LP20417.5	CK661190
243	370	20.5	863	6	CA475514	AGENCOURT	c 316	285	15.8	693	7	CK657729	LP24251.5	CK657729
244	365.5	20.2	809	2	BF304194	BF304194	317	283	15.7	386	6	CB806970	AMGNNUC.N	CB806970
245	364	20.2	268	1	AA296886	EST112650	318	283	15.7	488	5	EX477962	DKF2p686N	EX477962
246	363.5	20.1	801	5	EX852740	EX852740	319	282.5	15.6	2193	9	AY411859	Mus.muscu	AY411859
c 247	363	20.1	519	1	AA826266	od03e04.s	320	282.5	15.6	2709	3	AK082621	Mus.muscu	AK082621
248	362	20.0	229	1	AA450172	zx42d09.r	321	282.5	15.6	2713	3	AK051197	Mus.muscu	AK051197
249	358	19.8	855	5	BP158085	BP158085	c 322	278.5	15.4	473	5	BY261511	BY261511	BY261511
250	357.5	19.8	483	7	CR536826	DKF2p459J	323	278	15.4	2190	9	AY411858	Pan.trog1	AY411858
c 251	355.5	19.7	368	2	BP350775	QV0-HT036	324	276	15.3	2190	9	AY411857	Homo.sapi	AY411857
252	355	19.7	348	7	RS5964	y98e11.r1	325	275	15.2	583	6	CA353359	624860.NC	CA353359
253	355	19.7	431	5	BY276402	BY276402	c 326	273.5	15.1	314	7	CM075611	EC2BBA10C	CM075611
254	353	19.5	711	5	BU363662	603790080	c 327	271.5	15.0	316	1	A1884993	w188c02.x	A1884993
255	352.5	19.5	729	2	BB585976	BB585976	c 328	269.5	14.9	452	1	A1262821	qk35h10.x	A1262821
256	351	19.4	429	5	BY272572	BY272572	329	269.5	14.9	656	2	BB617916	BB617916	BB617916
257	350	19.4	504	5	BY281785	BY281785	c 330	268	14.8	402	2	AW522667	UI-R-B00-	AW522667
258	348.5	19.3	868	5	BQ672092	AGENCOURT	331	268	14.8	3089	3	BC062942	Mus.muscu	BC062942
259	342.5	19.0	960	5	BQ933325	AGENCOURT	332	267.5	14.8	392	5	BY267956	BY267956	BY267956
c 260	341	18.9	525	1	AL919221	AL919221	333	265.5	14.7	421	5	BY275639	BY275639	BY275639
261	339.5	18.8	825	5	BP464677	BP464677	334	263	14.6	2397	3	AK033973	Mus.muscu	AK033973
262	338.5	18.7	514	4	BG814603	daf69d01.	335	263	14.6	2509	3	AK046800	Mus.muscu	AK046800
263	338.5	18.7	807	5	BP168056	BP168056	336	263	14.6	3880	3	AK043760	Mus.muscu	AK043760
264	331.5	18.4	801	7	CK303983	CK303983	337	263	14.6	3892	3	AK038842	Mus.muscu	AK038842
265	331	18.3	594	5	B0400899	B0400899	338	260	14.4	412	5	BY274659	BY274659	BY274659
266	330	18.3	410	5	BY276506	BY276506	339	257.5	14.3	401	5	BY266910	BY266910	BY266910
267	329	18.2	651	6	CB557691	AMGNNUC.N	340	257.5	14.3	3315	3	HS0805302	Homo.sapi	AL834270
c 268	327.5	18.1	458	7	CO667956	CO667956	341	257	14.2	1080	5	BM916998	BY266910	BM916998
269	323.5	17.9	562	5	BU381982	603582664	342	256	14.2	336	5	BY134531	AGENCOURT	BY134531
270	320.5	17.7	470	5	BX954423	DKF2p781K	343	254.5	14.1	763	1	A1427225	mc70a03.y	A1427225
271	320.5	17.7	613	7	CF892168	AO106B07	344	253	14.0	456	6	BY249027	BY249027	BY249027
272	320	17.7	579	7	CM089828	EC2BBA32B	345	253	14.0	760	6	CD636199	56030958J	CD636199
c 273	318.5	17.6	446	7	CO352257	DR.AOV.SU	346	253	14.0	929	5	EX409828	EX409828	EX409828
c 274	315	17.4	422	1	A1288864	gm24f12.x	347	251.5	13.9	700	6	CD636207	56031034J	CD636207
c 275	314	17.4	845	4	BM042630	603615963	348	251.5	13.9	815	1	AU079716	AU079716	AU079716
c 276	312.5	17.3	641	2	AW379374	CM2-HT024	c 349	251	13.9	332	2	B8826737	QV1-EN004	B8826737
277	312	17.3	514	1	A1285235	qk59h04.x	350	251	13.9	374	2	B8826640	QV1-EN004	B8826640
278	311	17.2	378	2	BF601149	266043.MA	351	251	13.9	734	7	CF735216	UI-M-HB0-	CF735216
279	311	17.2	489	6	CB726015	AMGNNUC.N	352	250	13.8	751	7	CF746910	UI-M-HB0-	CF746910
280	310.5	17.2	527	5	BY243052	BY243052	353	250	13.8	797	7	CF746875	UI-M-HB0-	CF746875
c 281	310.5	17.2	552	4	BI337752	361275.MA	354	248.5	13.8	649	6	CD636249	56038485J	CD636249
c 282	310.5	17.2	789	7	CR531801	CR531801	355	248.5	13.8	783	6	CD636239	56038369J	CD636239
c 283	310	17.2	359	2	B8156390	QV0-HT036	356	248.5	13.8	785	6	CD636241	56038385J	CD636241
c 284	310	17.2	415	5	BY263876	BY263876	357	246.5	13.6	5626	3	CR749495	Homo.sapi	CR749495
c 285	310	17.2	461	2	BF463934	UI-M-CG0P	358	246	13.6	385	5	BY275013	BY275013	BY275013
c 286	308	17.1	694	7	CK699353	CK699353	c 359	246	13.6	737	4	BM679797	UI-R-EJ0-	BM679797
287	307.5	17.0	705	7	CH108877	EC2CAA32D	360	246	13.6	780	5	BU555185	AGENCOURT	BU555185
288	307	17.0	178	6	CB118055	K-EST0164	361	246	13.6	3198	9	AY416712	Homo.sapi	AY416712
289	306.5	17.0	730	5	BX610460	BX610460	362	245.5	13.6	724	6	CD636193	56030942J	CD636193
c 290	306.5	17.0	770	7	CR526028	CR526028	363	245.5	13.6	751	3	CD636243	56038393J	CD636243
c 291	304	16.8	528	2	AW490008	UI-M-BH3-	364	244.5	13.5	1871	3	BC029119	Homo.sapi	BC029119
292	303.5	16.8	790	5	BP141505	BP141505	365	243.5	13.5	649	6	CD636211	56031058J	CD636211
293	302.5	16.7	394	9	AY400233	Homo.sapi	366	243.5	13.5	190	6	CD636247	56038477J	CD636247
294	302.5	16.7	394	9	AY400234	Pan.trog1	367	243.5	13.5	1946	3	BC028193	Homo.sapi	BC028193
295	300.5	16.6	481	5	BY247646	BY247646	c 368	242.5	13.4	354	2	B8826697	QV1-EN004	B8826697
296	300	16.6	377	7	CF977263	2-98-A10.	369	242	13.4	668	6	CD636194	56030944H	CD636194
297	300	16.6	646	5	BM346790	BM346790	370	241.5	13.4	632	6	CD636203	56030974J	CD636203
298	298	16.5	372	6	BY768835	BY768835	c 371	241	13.3	733	9	BX190380	Danilo.rer	BX190380
299	298	16.5	386	5	BY263646	BY263646	372	240.5	13.3	629	6	CD636245	56038469J	CD636245
c 300	297	16.4	708	7	CK661144	LP20336.5	373	239.5	13.3	656	2	B8645027	BB645027	B8645027
301	296.5	16.4	382	9	AY400235	Mus.muscu	374	238.5	13.2	374	5	BY294857	BY294857	BY294857

c 375	238.5	13.2	377	2	BF358688	QV1-ET000	448	213	11.8	669	6	CB246171	UI-M-F00-
376	238.5	13.2	758	6	CD636251	56038493J	c 449	213	11.8	737	5	BX915880	BX915880
377	237.5	13.2	3133	9	AY416714	Mus muscu	450	213	11.8	761	5	BU355132	603475958
378	237.5	13.2	3179	3	AK028527	Mus muscu	451	213	11.8	1288	3	CR728377	Tetraodon
379	237.5	13.2	3948	3	AK036116	Mus muscu	452	213	11.8	1304	3	CR644432	Tetraodon
380	236.5	13.1	646	4	BI393264	pgpin.pk0	453	213	11.8	3219	3	AK041230	Mus muscu
381	236	13.1	529	6	CD284927	G39161.77	454	213	11.8	3518	3	BC036088	Homo sapi
c 382	235	13.0	479	2	AW524531	UI-R-B00-	455	212	11.7	1253	3	CR636279	Tetraodon
383	235	13.0	711	7	CO669353	DG33-50b1	456	212	11.7	1270	3	CR637013	Tetraodon
c 384	233	12.9	582	7	CO626674	DG9-278a2	457	211.5	11.7	710	6	CA349374	619770 NC
385	232	12.8	747	7	CF743366	UI-M-GV0-	458	211.5	11.7	768	6	CD636212	56031066H
386	232	12.8	758	6	CB525885	UI-M-FY0-	459	211.5	11.7	3342	9	AY403616	Mus muscu
387	231.5	12.8	3057	9	AY417678	Homo sapi	460	211.5	11.7	4015	3	AK028770	Mus muscu
388	231.5	12.8	4327	3	BC039255	Homo sapi	461	211.5	11.7	4429	3	AK028889	Mus muscu
389	231	12.8	3392	3	BC036338	Homo sapi	462	211	11.7	687	4	BI827613	603073581
390	231	12.8	3480	9	AY418997	Homo sapi	c 463	211	11.7	723	5	BX923781	BX923781
391	230	12.7	339	2	BE826667	QV1-EN004	464	211	11.7	1623	3	AK038917	Mus muscu
392	230	12.7	872	5	BU411493	602954338	465	211	11.7	4113	3	AK053077	Mus muscu
393	229.5	12.7	705	6	CD636208	56031050H	466	210	11.6	640	9	CC573801	CH240_450
c 394	229	12.7	782	8	A2731274	RPCI-24-1	467	209.5	11.6	588	6	CD636204	56030983H
395	228.5	12.7	442	7	CN081576	EC2BBA19C	468	209	11.6	870	4	BI911385	603183295
396	228.5	12.7	897	7	CN161781	951102 MA	469	209	11.6	3037	3	AK052440	Mus muscu
397	228.5	12.7	2530	3	AK018522	Mus muscu	470	208.5	11.5	492	4	BI359722	384371 MA
398	228	12.6	194	4	BI337742	361263 MA	471	208.5	11.5	562	5	BX952176	DKF2p781K
399	228	12.6	816	5	BU385923	603858616	472	208.5	11.5	694	7	CF125589	UI-HF-E10
c 400	228	12.6	3468	3	AK052972	Mus muscu	473	208	11.5	700	2	BB652926	BB652926
401	227	12.6	3988	3	BC034594	Mus muscu	c 474	208	11.5	712	6	CD620699	56100889J
402	227	12.6	4131	3	AK078536	Mus muscu	475	208	11.5	990	9	AY418721	Mus muscu
403	226.5	12.5	550	2	BE012499	121990 MA	476	207.5	11.5	1290	3	CR649578	Tetraodon
404	226.5	12.5	763	4	BG519515	602577790	477	207.5	11.5	2104	3	AK033487	Mus muscu
c 405	226	12.5	368	7	CN086072	EC2BBA26C	478	207.5	11.5	4441	3	AK081990	Mus muscu
406	224.5	12.4	3050	9	AY417680	Mus muscu	479	207	11.5	842	6	CA317300	UI-M-FW0-
407	224	12.4	652	7	CV462964	CS_hyp_49	480	206.5	11.4	685	4	BJ000543	BJ000543
408	224	12.4	4187	3	AK053044	Mus muscu	c 481	206.5	11.4	779	6	CA511514	UI-R-FJ0-
409	223	12.3	336	4	BG199531	RST18822	c 482	206.5	11.4	904	6	CE756103	CB756103
c 410	223	12.3	433	1	AL921475	AL921475	c 483	206	11.4	778	6	CD620690	56100785H
411	223	12.3	494	4	BI515616	BB160019B	484	206	11.4	1516	3	CR727897	Tetraodon
412	223	12.3	544	4	BI515616	BB160019B	485	205.5	11.4	783	7	CF540537	UI-M-GV0-
413	223	12.3	3540	9	AY418995	Homo sapi	486	205.5	11.4	2017	7	AK042488	Mus muscu
414	222	12.3	723	5	BU704037	UI-M-F00-	487	205	11.4	729	7	CN533735	UI-M-H00-
c 415	222	12.3	932	5	BX409829	BX409829	488	205	11.4	990	9	AY418719	Homo sapi
416	221.5	12.3	1118	3	AK013775	Mus muscu	c 489	205	11.4	1228	3	CR648907	Tetraodon
417	220.5	12.2	1372	3	AK053839	Mus muscu	c 490	204.5	11.3	701	5	BX669319	BX669319
c 418	220.5	12.2	2126	3	AK011391	Mus muscu	491	204.5	11.3	893	5	BU523040	AGENCOURT
c 419	220	12.2	754	6	CA448116	UI-H-ED1-	492	204.5	11.3	1237	3	CR641398	Tetraodon
c 420	220	12.2	770	2	AW117456	AW117456	c 493	204	11.3	843	5	BX854499	BX854499
421	220	12.2	2664	3	AK043379	Mus muscu	c 494	203.5	11.3	613	6	CD636184	56020447H
422	219.5	12.2	3345	9	AY403614	Homo sapi	c 495	203.5	11.3	3642	3	AK084609	Mus muscu
423	219	12.1	821	5	BU389844	603511165	c 496	203	11.2	334	1	AI422503	tf1le04.x
424	218.5	12.1	916	5	BO672140	AGENCOURT	497	202.5	11.2	651	7	CK831552	4055165 B
425	218	12.1	712	5	BU212380	AGENCOURT	498	202.5	11.2	687	5	BP461989	BP461989
426	218	12.1	2874	3	AK036262	Mus muscu	499	202	11.2	810	5	BU338342	603514255
c 427	217.5	12.0	586	4	BM696801	UI-B-DW0-	c 500	202	11.2	846	5	BO423040	AGENCOURT
428	217.5	12.0	866	5	BO923836	AGENCOURT	c 501	202	11.2	867	7	CN163166	952638 MA
c 429	217	12.0	780	5	BX917601	BX917601	c 502	202	11.2	3123	3	AK049284	Mus muscu
430	216.5	12.0	375	5	BY292584	BY292584	c 503	201.5	11.2	467	4	BI134406	UI-M-BH3-
431	216.5	12.0	473	7	CO280999	EK155707.	c 504	201.5	11.2	701	7	CO422929	GGE2HT102
432	215.5	11.9	657	2	BE618284	BE618284	505	201.5	11.2	1304	3	CR639237	Tetraodon
433	215.5	11.9	1311	3	CR731011	Tetraodon	506	201.5	11.2	1548	3	CR728005	Tetraodon
434	214.5	11.9	734	6	CB448011	702065 MA	507	201	11.1	865	7	CK401822	AUF_1fint
435	214.5	11.9	742	7	CO395507	AGENCOURT	508	201	11.1	1788	9	AY411536	Mus muscu
436	214	11.8	711	1	AU004083	AU004083	509	200.5	11.1	525	6	CB720159	AMGNNUC:N
437	214	11.8	724	7	CO561566	AGENCOURT	510	200.5	11.1	541	6	CD803660	UI-M-GV0-
438	214	11.8	813	4	BE651587	603298063	511	200.5	11.1	935	5	BO893857	BO893857
439	214	11.8	1280	3	CR648110	Tetraodon	512	200	11.1	530	6	CD636197	56030950J
440	214	11.8	2464	3	AK043507	Mus muscu	c 513	200	11.1	703	7	CV434528	CS_hyp_36
441	214	11.8	2535	3	BC012380	Homo sapi	c 514	200	11.1	1062	5	BX343871	BX343871
442	214	11.8	2553	3	BC046975	Mus muscu	515	199.5	11.0	783	7	CN055172	Salamande
443	213.5	11.8	701	5	BW223428	BW223428	c 516	199.5	11.0	1025	7	CR754135	CR754135
444	213.5	11.8	1306	3	CR605082	full-leng	c 517	199.5	11.0	1074	7	CR754275	CR754275
445	213.5	11.8	1315	3	CR733537	Tetraodon	518	199.5	11.0	1267	3	CR634286	Tetraodon
446	213	11.8	558	7	CR875240	SGP136467	c 519	199	11.0	816	1	AU117395	AU117395
447	213	11.8	593	5	BX499713	DKF2p779M	520	199	11.0	954	1	AL551492	AL551492

521	199	11.0	2236	3	BC030834	BC030834 Homo sapi	594	190.5	10.5	779	5	BU419715	BU419715 603953627
522	199	11.0	2705	3	AK090377 Mus muscu	AK090377 Mus muscu	595	190.5	10.5	797	7	QK311806	QK311806 SB02010A1
523	199	11.0	4068	9	AY406427 Mus muscu	AY406427 Mus muscu	596	190.5	10.5	924	5	BQ882851	BQ882851 AGENCOURT
524	198.5	11.0	618	6	CD636200	CD636200 56030966H	597	190.5	10.5	1499	3	CR636336	CR636336 Tetraodon
525	198.5	11.0	732	7	CN358175	CN358175 170005328	598	190	10.5	514	5	EX111689	EX111689 Bx111689
526	198.5	11.0	796	6	CD620697	CD620697 56100881J	599	190	10.5	769	5	EX857871	EX857871 Bx857871
527	198.5	11.0	4919	3	BC040674	BC040674 Homo sapi	c 600	190	10.5	1463	8	CC288776	CC288776 CH261-170
528	198	11.0	625	4	BQ032692	BQ032692 BQ032692	601	189.5	10.5	714	7	CN460823	CN460823 UI-M-HB0-
529	198	11.0	728	7	CF728819	CF728819 UI-M-HB0-	602	189.5	10.5	748	5	BU058289	BU058289 UI-M-F00-
530	198	11.0	838	7	CK028945	CK028945 AGENCOURT	603	189.5	10.5	946	4	B1549835	B1549835 603194572
531	198	11.0	1104	7	CR755975	CR755975 CR755975	604	189.5	10.5	2211	9	AY418471	AY418471 Pan trogl
532	197.5	10.9	534	7	CR950627	CR950627 Ha rx0.36	605	189.5	10.5	3057	9	AY417679	AY417679 Pan trogl
533	197.5	10.9	766	6	CA326802	CA326802 UI-M-FY0-	606	189	10.5	609	6	CA381472	CA381472 660987 NC
534	197.5	10.9	795	7	CN532710	CN532710 UI-M-H00-	607	189	10.5	683	2	BB318882	BB318882 BB318882
535	197.5	10.9	1145	7	CR754709	CR754709 CR754709	608	189	10.5	706	6	CA324144	CA324144 UI-M-FY0-
536	197	10.9	433	4	BG515406	BG515406 dae04h10.	609	189	10.5	710	7	CK638303	CK638303 UI-M-H00-
537	197	10.9	474	2	BB682022	BB682022 BB682022	610	189	10.5	938	5	BK708988	BK708988 BX708988
538	197	10.9	631	4	BM426245	BM426245 dgfn2n.pk0	611	188.5	10.4	603	1	AL679324	AL679324 AL679324
539	197	10.9	781	6	CD620693	CD620693 56100781J	612	188.5	10.4	663	5	BU708530	BU708530 UI-M-F10-
540	196.5	10.9	582	5	BP355301	BP355301 BP355301	613	188.5	10.4	720	3	CR644200	CR644200 Tetraodon
541	196.5	10.9	686	6	CA372777	CA372777 646750 NC	614	188.5	10.4	773	6	CD348004	CD348004 UI-M-FY0-
542	196.5	10.9	812	5	BQ180027	BQ180027 UI-M-EW0-	615	188.5	10.4	839	4	B1851286	B1851286 603377864
543	196.5	10.9	923	5	BU140452	BU140452 603135370	616	188.5	10.4	922	4	BM802337	BM802337 AGENCOURT
544	196.5	10.9	1272	3	CR731454	CR731454 Tetraodon	617	188.5	10.4	4185	3	AK083540	AK083540 Mus muscu
545	196.5	10.9	3647	3	BC046957	BC046957 Mus muscu	618	188	10.4	313	2	AW430704	AW430704 70599 MAR
546	196	10.9	895	7	CN761982	CN761982 ID0AAA3BG	619	188	10.4	558	6	CB448500	CB448500 702638 MA
547	196	10.9	925	4	BG419088	BG419088 602446318	620	188	10.4	722	7	CN530508	CN530508 UI-M-H00-
548	196	10.9	987	6	CD507156	CD507156 CDA83-C12	621	188	10.4	833	6	CD636250	CD636250 56038493H
549	196	10.9	4068	9	AY406425	AY406425 Homo sapi	622	188	10.4	1121	7	CR755403	CR755403 CR755403
550	195.5	10.8	576	1	AL699151	AL699151 DKP2p686E	623	187.5	10.4	582	5	BP355339	BP355339 BP355339
551	195.5	10.8	632	7	CO432230	CO432230 UI-M-HX0-	624	187.5	10.4	652	8	BH269030	BH269030 CH230-66P
552	195.5	10.8	675	7	CN060015	CN060015 Salamande	625	187.5	10.4	655	1	A1980307	A1980307 pat.pk002
553	195.5	10.8	787	6	CD802924	CD802924 UI-M-GV0-	626	187.5	10.4	759	7	CN430206	CN430206 170005315
554	195.5	10.8	857	6	CD520168	CD520168 UI-M-G10-	627	187.5	10.4	784	7	CK478969	CK478969 AGENCOURT
555	195.5	10.8	1261	3	CR640626	CR640626 Tetraodon	628	187	10.4	497	5	BX515241	BX515241 BX515241
556	195.5	10.8	1263	3	CR647139	CR647139 Tetraodon	629	187	10.4	616	7	CN532902	CN532902 UI-M-H00-
557	195	10.8	617	5	BQ555199	BQ555199 H4032G01-	630	187	10.4	766	2	BE213159	BE213159 IPbrrn02000
558	195	10.8	666	7	CN832582	CN832582 AGENCOURT	c 631	187	10.4	837	3	CF345598	CF345598 AGENCOURT
559	194.5	10.8	455	7	CO337067	CO337067 EN13754.5	632	187	10.4	3531	3	AK035110	AK035110 Mus muscu
560	194.5	10.8	652	7	CR689464	CR689464 2F101-P00	633	187	10.4	3821	3	AK085461	AK085461 Mus muscu
561	194.5	10.8	730	6	CA357629	CA357629 630022 NC	634	186.5	10.3	664	4	BJ732469	BJ732469 BJ732469
562	194.5	10.8	763	6	CB519582	CB519582 UI-M-GH0-	635	186.5	10.3	835	7	CK847657	CK847657 970316 MA
563	194.5	10.8	852	7	CR422792	CR422792 CR422792	636	186.5	10.3	923	5	BU326524	BU326524 603489483
564	194	10.7	523	4	B1512632	B1512632 BBI60009B	637	186.5	10.3	1230	3	CR641410	CR641410 Tetraodon
565	194	10.7	896	6	CD514588	CD514588 AGENCOURT	638	186	10.3	644	6	CB518611	CB518611 UI-M-GH0-
566	194	10.7	3424	3	AK044694	AK044694 Mus muscu	639	186	10.3	648	5	BM935487	BM935487 UI-M-BH3-
567	193.5	10.7	837	6	CD352315	CD352315 UI-M-G10-	640	186	10.3	727	7	CO431177	CO431177 UI-M-HX0-
568	193.5	10.7	4178	3	AK087693	AK087693 Mus muscu	641	186	10.3	752	7	CF741342	CF741342 UI-M-GH0-
569	193	10.7	226	1	AA776056	AA776056 ae79a07.s	642	186	10.3	788	7	CF737289	CF737289 UI-M-HD0-
570	193	10.7	710	7	CN225540	CN225540 WLA073F11	643	186	10.3	791	7	CO557024	CO557024 AGENCOURT
571	193	10.7	808	5	BU746846	BU746846 CH3H007.D	644	186	10.3	883	7	CN985580	CN985580 58560.126
572	192.5	10.7	614	6	CD636183	CD636183 56020347J	645	186	10.3	1146	7	CR755551	CR755551 CR755551
573	192.5	10.7	944	5	BO681009	BO681009 AGENCOURT	646	186	10.3	1791	9	AY411534	AY411534 Homo sapi
574	192.5	10.7	945	9	CN804AD2	AL281711 Tetraodon	647	185.5	10.3	636	5	BU363294	BU363294 603585989
575	192.5	10.7	1259	3	CR636055	CR636055 Tetraodon	648	185.5	10.3	761	6	CA384559	CA384559 665213 NC
576	192.5	10.7	2283	9	AY418472	AY418472 Mus muscu	649	185.5	10.3	987	2	BF579256	BF579256 602093426
577	192.5	10.7	4329	3	AK040765	AK040765 Mus muscu	650	185.5	10.3	1215	9	AY421473	AY421473 Homo sapi
578	192	10.6	534	7	CR556169	CR556169 DKP2p459D	651	185.5	10.3	2299	9	AY418470	AY418470 Homo sapi
579	192	10.6	730	7	CO505029	CO505029 GGEZEB103	652	185	10.2	736	1	AA439246	AA439246 LD13756.5
580	192	10.6	839	6	CD578410	CD578410 UI-M-FY0-	653	185	10.2	951	5	BQ680360	BQ680360 AGENCOURT
581	192	10.6	877	5	BU322077	BU322077 603850177	654	185	10.2	990	9	AY418720	AY418720 Pan trogl
582	192	10.6	2132	3	BC045734	BC045734 Homo sapi	655	185	10.2	3638	3	AK045373	AK045373 Mus muscu
583	192	10.6	4068	9	AY406426	AY406426 Pan trogl	656	184.5	10.2	644	5	BQ561052	BQ561052 H4068A05-
584	191.5	10.6	581	8	BH269028	BH269028 CH230-66P	657	184.5	10.2	700	4	BM623297	BM623297 170006874
585	191.5	10.6	702	7	CN359049	CN359049 170004245	658	184.5	10.2	1497	3	AK053039	AK053039 Mus muscu
586	191.5	10.6	779	8	BH292378	BH292378 CH230-44D	659	184	10.2	565	4	BG732685	BG732685 333483 MA
587	191.5	10.6	1291	3	CR641448	CR641448 Tetraodon	660	184	10.2	669	4	BM624477	BM624477 170006874
588	191.5	10.6	3157	9	AY403615	AY403615 Pan trogl	661	184	10.2	662	7	CF745309	CF745309 UI-M-GV0-
589	191	10.6	613	4	BM487940	BM487940 pgm2n.pk0	662	184	10.2	791	7	CO572836	CO572836 imageqc 5
590	191	10.6	754	7	CF530715	CF530715 UI-M-FY0-	663	184	10.2	670	7	CO572836	CO572836 AGENCOURT
591	191	10.6	1055	4	BM551034	BM551034 AGENCOURT	c 664	184	10.2	838	6	CD636246	CD636246 56038477H
592	190.5	10.5	643	6	CA385573	CA385573 666709 NC	665	184	10.2	865	5	BX725298	BX725298 AGENCOURT
593	190.5	10.5	649	7	CO505951	CO505951 GGEZEB103	666	184	10.2	940	7	CK871065	CK871065 AGENCOURT

667	184	10.2	970	5	BUI07306	BUI07306	602954168	c	740	178	9.9	653	7	CF180026	CF180026	815076 MA
668	183.5	10.2	558	4	B1067163	B1067163	pgfin.pk0		741	178	9.9	738	5	BU448181	BU448181	603764925
669	183.5	10.2	774	6	CB247631	CB247631	UI-M-FY0-		742	178	9.9	871	7	CF551909	CF551909	AGENCYCOURT
670	183.5	10.2	863	6	CD514529	CD514529	AGENCYCOURT		743	178	9.9	883	7	BF792657	BF792657	602253836
671	183.5	10.2	904	5	BUI44883	BUI44883	603229681		744	178	9.9	893	9	CNS02MXY	AL204631	Tetraodon
672	183.5	10.2	974	5	BUI559792	BUI559792	AGENCYCOURT		745	178	9.9	1285	3	AK010350	AK010350	Mus muscu
673	183.5	10.2	1064	5	BX343872	BX343872	AGENCYCOURT		746	178	9.9	3903	3	AK076423	AK076423	Mus muscu
674	183	10.1	550	2	AW653843	AW653843	102720 MA		747	178	9.9	4544	3	AK052489	AK052489	Mus muscu
675	183	10.1	609	1	AL673319	AL673319	AGENCYCOURT		748	177.5	9.8	548	5	BQ636532	BQ636532	hd11a05.Y
676	183	10.1	671	5	BQ344752	BQ344752	603407056	c	749	177.5	9.8	593	5	EX676568	EX676568	EX676568
677	183	10.1	865	6	CA327194	CA327194	UI-M-FY0-		750	177.5	9.8	714	2	BF575974	BF575974	602132952
678	183	10.1	914	5	BUI84213	BUI84213	AGENCYCOURT		751	177.5	9.8	726	4	BJ708729	BJ708729	BJ708729
679	183	10.1	1064	5	BQ055710	BQ055710	AGENCYCOURT		752	177.5	9.8	734	2	BF529510	BF529510	602043274
680	182.5	10.1	627	7	CF534081	CF534081	UI-M-GH0-		753	177.5	9.8	951	5	BQ919823	BQ919823	AGENCYCOURT
681	182.5	10.1	717	7	CF534534	CF534534	UI-M-GH0-		754	177.5	9.8	1088	5	BQ062993	BQ062993	AGENCYCOURT
682	182.5	10.1	743	6	CD636180	CD636180	60005276H		755	177.5	9.8	1516	9	AY408377	AY408377	Mus muscu
683	182.5	10.1	799	6	CD620695	CD620695	56100873J		756	177.5	9.8	371	7	CO196400	CO196400	EK004112.
684	182.5	10.1	862	1	AA698836	AA698836	HL05774.5		757	177	9.8	757	6	CB953709	CB953709	AGENCYCOURT
685	182.5	10.1	1086	5	BQ071438	BQ071438	AGENCYCOURT		758	177	9.8	760	4	BI559288	BI559288	603241144
686	182	10.1	496	4	BF995884	BF995884	OVI-GN020		759	177	9.8	760	4	BI559288	BI559288	603241144
687	182	10.1	867	6	CB519811	CB519811	UI-M-GH0-		760	177	9.8	908	6	CD796854	CD796854	EST668215
688	182	10.1	900	5	BX350637	BX350637	AGENCYCOURT		761	177	9.8	909	5	BQ435144	BQ435144	AGENCYCOURT
689	182	10.1	922	5	BQ948697	BQ948697	AGENCYCOURT		762	177	9.8	2942	3	AK031495	AK031495	Mus muscu
690	182	10.1	2197	3	CR614873	CR614873	full-1eng		763	177	9.8	3865	3	AF077041	AF077041	Homo sapi
691	181.5	10.0	563	6	CA370225	CA370225	650349 NC	c	764	176.5	9.8	587	4	BM153637	BM153637	TCPAP2E11
692	181.5	10.0	629	7	CF723085	CF723085	UI-M-GV0-		765	176.5	9.8	607	5	BU948358	BU948358	io50a10.Y
693	181.5	10.0	676	2	BE731113	BE731113	601566230		766	176.5	9.8	652	6	CA376364	CA376364	654703 NC
694	181.5	10.0	731	4	BJ712564	BJ712564	BOVGen.10		767	176.5	9.8	671	7	CK003726	CK003726	AGENCYCOURT
695	181.5	10.0	740	7	CO881919	CO881919	Mus muscu		768	176.5	9.8	679	4	CR538523	CR538523	DKF2p459F
696	181.5	10.0	2906	3	AK051027	AK051027	601053.3		769	176.5	9.8	706	4	BI914768	BI914768	603184148
697	181	10.0	400	7	CO339200	CO339200	EP01053.1		770	176.5	9.8	787	6	CD636242	CD636242	56038393H
698	181	10.0	580	7	CK889202	CK889202	SGP161216	c	771	176.5	9.8	801	4	BI553374	BI553374	603193319
699	181	10.0	624	2	AV988998	AV988998	AGENCYCOURT		772	176.5	9.8	816	5	BQ881760	BQ881760	AGENCYCOURT
700	181	10.0	975	5	BX335437	BX335437	Mus muscu		773	176.5	9.8	898	5	BQ951309	BQ951309	AGENCYCOURT
701	181	10.0	4168	3	BC060216	BC060216	Mus muscu		774	176.5	9.8	1163	9	AY421474	AY421474	Pan trogl
702	181	10.0	4962	3	HS0804543	AL833232	Homo sapi		775	176.5	9.8	2334	9	AY408375	AY408375	Homo sapi
703	180.5	10.0	588	4	BJ031875	BJ031875	AGENCYCOURT		776	176.5	9.8	524	7	CN304965	CN304965	170005325
704	180.5	10.0	713	5	BU311407	BU311407	603543724		777	176	9.7	702	5	BX299781	BX299781	BX299781
705	180.5	10.0	802	1	AUI24625	AUI24625	AGENCYCOURT		778	176	9.7	727	6	CA346240	CA346240	677090 NC
706	180	10.0	290	2	BF362977	BF362977	CM4-NN008		779	176	9.7	744	7	CK693733	CK693733	2F101-P00
707	180	10.0	364	1	A1940007	A1940007	QVO-CT001		780	176	9.7	820	6	CD758447	CD758447	AGENCYCOURT
708	180	10.0	434	1	A1279142	A1279142	qml8e02.x		781	176	9.7	857	7	CK192396	CK192396	EST781711
709	180	10.0	442	5	BL112198	BL112198	AGENCYCOURT		782	176	9.7	2178	3	AK018613	AK018613	Mus muscu
710	180	10.0	468	2	BF110673	BF110673	7n55h10.x		783	176	9.7	2369	3	BC034042	BC034042	Homo sapi
711	180	10.0	502	1	A1796834	A1796834	we22h06.x		784	176	9.7	2894	3	AK033581	AK033581	Mus muscu
712	180	10.0	523	2	BE550993	BE550993	7b67a03.x	c	785	176	9.7	608	5	BQ582107	BQ582107	ill2h03.Y
713	180	10.0	583	6	CB586460	CB586460	AMGNNUC:N		786	175.5	9.7	631	5	BX709958	BX709958	BX709958
714	180	10.0	671	7	CF366096	CF366096	AV959095		787	175.5	9.7	675	6	CB722950	CB722950	UI-M-GH0-
715	180	10.0	681	2	CF366096	CF366096	836780 MA		788	175.5	9.7	675	6	CD625574	CD625574	55147942H
716	180	10.0	713	7	CN442065	CN442065	BE04028A1		789	175.5	9.7	702	7	CK781415	CK781415	UI-M-GV0-
717	180	10.0	776	7	CK780892	CK780892	UI-M-HQ0-		790	175.5	9.7	758	7	CK475728	CK475728	AGENCYCOURT
718	180	10.0	796	5	BX348968	BX348968	EX348968		791	175.5	9.7	831	6	CD636244	CD636244	AGENCYCOURT
719	180	10.0	858	6	CB196421	CB196421	AGENCYCOURT	c	792	175.5	9.7	847	7	CK475175	CK475175	AGENCYCOURT
720	180	10.0	866	7	CK872817	CK872817	AGENCYCOURT		793	175.5	9.7	952	5	BUS56507	BUS56507	AGENCYCOURT
721	180	10.0	1135	7	CK027809	CK027809	AGENCYCOURT		794	175.5	9.7	2271	9	AY418467	AY418467	Homo sapi
722	179.5	9.9	452	7	CO289807	CO289807	EK072116.		795	175.5	9.7	2334	9	AY408376	AY408376	Pan trogl
723	179.5	9.9	747	7	CF948722	CF948722	UI-M-HQ0-		796	175.5	9.7	234	1	AV349585	AV349585	AV349585
724	179	9.9	594	4	BU489405	BU489405	BJ489405		797	175	9.7	234	1	AV349585	AV349585	AV349585
725	179	9.9	645	4	BM488779	BM488779	pgm2n.pk0	c	798	175	9.7	303	1	AI422504	AI422504	tf11e05.x
726	179	9.9	794	7	CF533313	CF533313	UI-M-FY0-	c	799	175	9.7	526	4	BI045435	BI045435	MR3-FN020
727	179	9.9	811	6	CD636248	CD636248	56038485H		800	175	9.7	606	6	CB273099	CB273099	mai166h01.
728	179	9.9	939	7	CK865923	CK865923	AGENCYCOURT		801	175	9.7	631	4	BI553967	BI553967	603193844
729	179	9.9	2453	3	AK033574	AK033574	Mus muscu		802	175	9.7	651	7	CK679637	CK679637	2F101-P00
730	179	9.9	3939	3	AK036698	AK036698	Mus muscu		803	175	9.7	660	5	BM986302	BM986302	EST531210
731	178.5	9.9	710	6	CA378084	CA378084	656807 NC		804	175	9.7	714	6	CB527370	CB527370	UI-M-FY0-
732	178.5	9.9	772	7	CO430864	CO430864	UI-M-HQ0-		805	175	9.7	752	5	BU203628	BU203628	603103394
733	178.5	9.9	825	6	CD636240	CD636240	56038385H	c	806	175	9.7	770	7	CK780689	CK780689	UI-M-HQ0-
734	178.5	9.9	883	5	BQ955157	BQ955157	AGENCYCOURT		807	175	9.7	888	7	CN075890	CN075890	EC2BBA11A
735	178.5	9.9	894	5	BQ642447	BQ642447	AGENCYCOURT		808	174.5	9.7	550	7	CR544600	CR544600	DKF2p459F
736	178.5	9.9	910	5	BQ895192	BQ895192	AGENCYCOURT		809	174.5	9.7	582	5	BP316461	BP316461	BP316461
737	178.5	9.9	912	5	BU154175	BU154175	AGENCYCOURT		810	174.5	9.7	752	1	BU070206	BU070206	UI-M-FR0-
738	178.5	9.9	967	1	AL538691	AL538691	AGENCYCOURT		811	174.5	9.7	775	1	AU006387	AU006387	AU006387
739	178	9.9	208	1	AU281844	AU281844	AGENCYCOURT		812	174.5	9.7	836	2	BE747501	BE747501	601573016

813	174.5	9.7	847	7	CF374272	AGENCOURT	886	170.5	9.4	585	5	BP377151	BP377151
814	174.5	9.7	875	5	BX403262	BX403262	887	170.5	9.4	588	6	CB585172	CB585172
815	174	9.6	885	5	CN209637	4115576 B	888	170.5	9.4	600	4	BG806560	2032-50 M
816	174	9.6	581	1	BP217876	BP217876	889	170.5	9.4	600	5	BU920372	6053-62
817	174	9.6	625	1	AUL134398	AUL134398	890	170.5	9.4	614	6	CD351134	UI-M-FY0-
818	174	9.6	669	5	BX670963	BX670963	891	170.5	9.4	746	6	CD636196	56030950H
819	174	9.6	736	8	AZ989621	2M0273104	892	170.5	9.4	778	2	BF305263	601892727
820	174	9.6	940	7	CK865164	AGENCOURT	893	170.5	9.4	816	7	CF220046	AGENCOURT
821	174	9.6	2756	3	AK038385	Mus muscu	894	170.5	9.4	892	5	BU135652	603124302
822	174	9.6	3075	3	AK034142	Mus muscu	895	170.5	9.4	893	7	CN507252	AGENCOURT
823	174	9.6	4152	3	AK079332	Mus muscu	896	170.5	9.4	999	4	BM561628	AGENCOURT
824	173.5	9.6	569	6	CB616002	AMGNNUC:N	897	170	9.4	561	7	CN991327	67958 125
825	173.5	9.6	629	7	CF364674	834668 MA	898	170	9.4	723	9	CG784243	723C-GT-
826	173.5	9.6	634	6	CB577096	AMGNNUC:N	899	170	9.4	748	6	CD620698	56100889H
827	173.5	9.6	888	7	CK424119	AUF Ipsco	900	170	9.4	776	7	CN171251	AGENCOURT
828	173.5	9.6	2240	9	AY418469	AY418469	901	170	9.4	825	7	CF222141	AGENCOURT
829	173	9.6	527	1	AA741334	ob30f08_s	902	170	9.4	827	7	CF445411	CR445411
830	173	9.6	619	6	CD636182	56020347H	903	170	9.4	836	7	CF147692	AGENCOURT
831	173	9.6	642	4	BM310781	1948d12.Y	904	170	9.4	856	7	CF237672	AGENCOURT
832	173	9.6	765	7	CN535749	UI-M-HS0-	905	169.5	9.4	499	2	BF151777	uz20c07.Y
833	173	9.6	812	7	CO426708	UI-M-HU0-	906	169.5	9.4	563	7	CF534807	UI-M-GH0-
834	173	9.6	935	7	CK870930	AGENCOURT	907	169.5	9.4	581	5	BP195803	BP195803
835	173	9.6	1088	7	CK030075	AGENCOURT	908	169.5	9.4	662	2	BB665541	BB665541
836	173	9.6	2976	3	HSN801624	Homo sapi	909	169.5	9.4	708	6	CB423451	596888 MA
837	172.5	9.6	452	7	CN359001	170005322	910	169.5	9.4	752	7	CF729863	UI-M-HE0-
838	172.5	9.6	643	7	CF895017	AF0142H05-	911	169.5	9.4	755	4	BJ723979	BJ723979
839	172.5	9.6	646	4	BM576695	170006871	912	169.5	9.4	759	7	CK871118	AGENCOURT
840	172.5	9.6	685	7	CR790517	DKF2p459K	913	169.5	9.4	760	6	CA513275	UI-R-FJ0-
841	172.5	9.6	761	6	CD636201	56030966J	914	169.5	9.4	803	1	AUL131954	AUL131954
842	172.5	9.6	782	7	CK807818	AGENCOURT	915	169.5	9.4	804	7	CK869114	AGENCOURT
843	172.5	9.6	808	5	EX771524	EX771524	916	169.5	9.4	832	9	BX238729	Danilo rer
844	172.5	9.6	814	6	CD758575	AGENCOURT	917	169.5	9.4	834	9	CN157026	944474 MA
845	172.5	9.6	842	7	CK597432	AGENCOURT	918	169.5	9.4	1097	7	CK232248	ILLUMIGN
846	172.5	9.6	889	7	CF375649	AGENCOURT	919	169.5	9.4	1106	1	AL561703	AL561703
847	172.5	9.6	892	1	AU079295	AGENCOURT	920	169.5	9.4	3230	3	AK011916	Mus muscu
848	172.5	9.6	930	5	BQ950644	AGENCOURT	921	169	9.4	547	7	CK656925	3017HPEX2
849	172.5	9.6	933	7	CK867774	AGENCOURT	922	169	9.4	582	5	BP194396	BP194396
850	172.5	9.6	2784	3	AK052040	Mus muscu	923	169	9.4	595	1	AI722009	AI722009
851	172	9.5	616	1	AI924653	wn57h07.X	924	169	9.4	604	2	AW025115	wu71h04.X
852	172	9.5	728	7	CK593285	UI-M-HU0-	925	169	9.4	658	4	BJ011427	BJ011427
853	172	9.5	800	4	BG293215	602390177	926	169	9.4	702	5	BM098413	BM098413
854	172	9.5	802	7	CK777862	965008 MA	927	169	9.4	740	7	CF744590	UI-M-GV0-
855	172	9.5	811	5	EX761240	EX761240	928	169	9.4	767	6	CA345552	676226 NC
856	172	9.5	818	7	CN977731	28379 125	929	169	9.4	799	7	CR409324	CR409324
857	172	9.5	840	1	AL524519	AL524519	930	169	9.4	805	5	BQ745652	UI-M-EW0-
858	171.5	9.5	567	5	BP370399	BP370399	931	169	9.4	886	6	CD172256	AGENCOURT
859	171.5	9.5	568	6	CD674218	fs08a04.Y	932	169	9.4	888	7	CK409633	AUF 1flvr
860	171.5	9.5	579	7	CN359288	170005999	933	169	9.4	1143	6	CD503634	CD503634
861	171.5	9.5	580	5	BZ210849	BP210849	934	169	9.4	1735	2	AW888221	MKRA5 Hum
862	171.5	9.5	582	5	BP194652	BP194652	935	169	9.4	3553	3	AK081793	AK081793
863	171.5	9.5	583	7	CN359006	BP359006	936	168.5	9.3	528	6	CB719651	AMGNNUC:N
864	171.5	9.5	583	7	CN359285	170005326	937	168.5	9.3	539	1	AL918370	AL918370
865	171.5	9.5	587	5	BQ270237	ik08a10.Y	938	168.5	9.3	543	1	AU207958	AU207958
866	171.5	9.5	590	5	BP309421	BP309421	939	168.5	9.3	579	6	CB607385	AGENCOURT
867	171.5	9.5	603	5	BU789381	1040b04.Y	940	168.5	9.3	606	7	CV040428	4137944 B
868	171.5	9.5	603	5	BX316915	BX316915	941	168.5	9.3	671	7	CO389127	CO389127
869	171.5	9.5	668	6	CD296956	CD296956	942	168.5	9.3	673	6	CB248224	CB248224
870	171.5	9.5	685	7	CK544312	strwb0.01	943	168.5	9.3	2645	3	BC038036	Mus muscu
871	171.5	9.5	686	7	CO505010	GGE2EBI03	944	168.5	9.3	4199	3	AK030591	AK030591
872	171.5	9.5	726	6	CD636205	56030983J	945	168	9.3	535	2	AW786664	120025 MA
873	171.5	9.5	757	4	BG819912	602782004	946	168	9.3	571	4	BM272758	1999a06.Y
874	171.5	9.5	786	2	BE306404	BE306404	947	168	9.3	581	5	BP194328	BP194328
875	171.5	9.5	801	6	CD636213	601103309	948	168	9.3	639	6	CA328483	CA328483
876	171.5	9.5	806	6	CD636192	56031066J	949	168	9.3	762	7	CO245579	AGENCOURT
877	171.5	9.5	816	6	CD636238	56030942H	950	168	9.3	774	5	BU205766	603102289
878	171.5	9.5	1749	3	CR643698	Tetraodon	951	168	9.3	804	7	CR414090	CR414090
879	171	9.5	583	5	BP219778	BP219778	952	168	9.3	873	7	CF251316	esa023_e1
880	171	9.5	684	5	HU625289	UI-R-FGI-	953	168	9.3	921	5	BU520481	AGENCOURT
881	171	9.5	816	7	CF220776	AGENCOURT	954	167.5	9.3	573	1	AI685262	wa75e11.X
882	171	9.5	1386	3	CR608576	full1-leng	955	167.5	9.3	725	7	CK691938	2F101-P00
883	171	9.5	1653	3	BC024164	Homo sapi	956	167.5	9.3	736	7	CK367468	AGENCOURT
884	170.5	9.4	484	5	EX099260	EX099260	957	167.5	9.3	786	5	BU382983	603582371
885	170.5	9.4	526	7	CN677790	E0102B04-	958	167.5	9.3	798	7	CK481268	AGENCOURT

959	167.5	9.3	817	4	BG912522	602806620	1032	164	9.1	1164	3	AK008187	Mus muscu
960	167.5	9.3	831	5	BU491858	604131047	1033	164	9.1	1639	3	AK032833	Mus muscu
961	167.5	9.3	930	7	CK407450	AUF_ILfVr	1034	164	9.1	1701	3	AK013156	Mus muscu
962	167.5	9.3	981	5	BQ964910	AGENCOURT	1035	164	9.1	1930	3	AK003326	Mus muscu
963	167.5	9.3	1469	3	AK044527	Mus muscu	1036	164	9.1	2814	3	CR593108	full-leng
964	167	9.2	514	6	CB716703	AMGNNUC:N	1037	163.5	9.1	469	2	AW414520	48011 MAR
965	167	9.2	608	6	CD636186	56020455H	1038	163.5	9.1	584	6	CB586237	AMGNNUC:M
966	167	9.2	616	7	CN164688	995050 MA	1039	163.5	9.1	667	4	BI654678	603285596
967	167	9.2	696	1	A1542894	SD09407.5	1040	163.5	9.1	672	7	CN537405	UI-M-H50-
968	167	9.2	707	7	CK869511	AGENCOURT	1041	163.5	9.1	693	2	BB525933	BB525933
969	167	9.2	726	5	BU446195	603766375	1042	163.5	9.1	705	4	BI662853	603286287
970	167	9.2	912	7	CK870512	AGENCOURT	1043	163.5	9.1	711	7	CK951501	4091020 B
971	167	9.2	1289	3	CR729255	Tetraodon	1044	163.5	9.1	724	7	CF998350	AGENCOURT
972	167	9.2	3628	3	AK031696	Mus muscu	1045	163.5	9.1	750	7	CF965540	AGENCOURT
973	166.5	9.2	583	5	BP321297	BP321297	1046	163.5	9.1	791	7	CK867184	AGENCOURT
974	166.5	9.2	775	7	CF348727	AGENCOURT	1047	163.5	9.1	794	7	CF996588	AGENCOURT
975	166.5	9.2	779	1	AU125657	AU125657	1048	163.5	9.1	810	6	CA382308	662081 NC
976	166.5	9.2	812	6	CB723208	UI-M-GH0-	1049	163.5	9.1	855	4	BI554904	603236202
977	166.5	9.2	822	6	CA510738	UI-R-FJ0-	1050	163.5	9.1	889	7	CN501295	AGENCOURT
978	166.5	9.2	928	5	BQ891778	AGENCOURT	1051	163.5	9.1	910	7	CF266068	AGENCOURT
979	166	9.2	583	4	BG223754	IM00018F0	1052	163.5	9.1	923	7	CN322132	AGENCOURT
980	166	9.2	647	7	CK781448	UI-M-GV0-	1053	163.5	9.1	934	7	CK868656	AGENCOURT
981	166	9.2	656	7	CK659672	LP17591.5	1054	163.5	9.1	951	7	CK866211	AGENCOURT
982	166	9.2	680	7	CF899461	A0303E02-	1055	163.5	9.1	1776	3	AK010153	Mus muscu
983	166	9.2	740	4	BJ720179	BJ720179	1056	163.5	9.1	3248	3	AK004821	Mus muscu
984	166	9.2	796	6	CD653854	AGENCOURT	1057	163.5	9.1	3590	3	AK028479	Mus muscu
985	166	9.2	805	4	BG117787	602350472	1058	163	9.0	444	9	AY402969	Homo sapi
986	166	9.2	805	7	CF785901	AGENCOURT	1059	163	9.0	444	9	AY402970	Pan trogl
987	166	9.2	910	5	BX324896	BX324896	1060	163	9.0	444	9	AY402971	Mus muscu
988	165.5	9.2	420	6	CB798880	AMGNNUC:N	1061	163	9.0	548	7	CO323280	EK190105.
989	165.5	9.2	517	6	CD290273	StrPu538.	1062	163	9.0	557	7	CK541739	rswhb0.00
990	165.5	9.2	589	1	AA606149	fai6d03.8	1063	163	9.0	569	4	BM090970	ig18e09.X
991	165.5	9.2	634	6	CD803622	UI-M-GV0-	1064	163	9.0	635	1	AL878745	AL878745
992	165.5	9.2	659	6	CD802719	UI-M-GV0-	1065	163	9.0	645	5	BX276614	BX276614
993	165.5	9.2	699	6	CD802719	UI-M-GV0-	1066	163	9.0	658	5	BX260070	BX260070
994	165.5	9.2	793	7	CK635666	CK635666	1067	163	9.0	661	1	AL872179	AL872179
995	165.5	9.2	797	7	CK870310	AGENCOURT	1068	163	9.0	730	5	BU709173	UI-M-EV0-
996	165.5	9.2	798	7	CK870327	AGENCOURT	1069	163	9.0	744	4	BJ780707	BJ780707
997	165.5	9.2	886	5	BUS28897	AGENCOURT	1070	163	9.0	790	1	AU006391	AU006391
998	165.5	9.2	939	5	BQ646105	BQ646105	1071	163	9.0	803	7	CK311931	SB02010A2
999	165.5	9.2	1037	5	BX396408	BX396408	1072	163	9.0	904	4	BG760809	602717170
1000	165.5	9.2	1138	7	CK030399	AGENCOURT	1073	163	9.0	935	4	BG923654	602823392
1001	165	9.1	618	4	BI065024	pgfin.pk0	1074	163	9.0	1181	3	CR722859	Tetraodon
1002	165	9.1	624	1	AL968116	AL968116	1075	163	9.0	1694	3	AK040711	Mus muscu
1003	165	9.1	641	1	AL892168	AL892168	1076	162.5	9.0	562	1	AV614571	AV614571
1004	165	9.1	645	1	AL846277	AL846277	1077	162.5	9.0	580	4	BG710895	pglin.pk0
1005	165	9.1	693	7	CK781175	UI-M-GV0-	1078	162.5	9.0	590	7	CK824237	ig18e09.Y
1006	165	9.1	700	5	BX331242	BX331242	1079	162.5	9.0	601	1	AL703664	DKF2p686A
1007	165	9.1	748	6	CD079492	MA3-9999U	1080	162.5	9.0	685	7	CN537909	UI-M-H50-
1008	165	9.1	775	7	CN532584	UI-M-H00-	1081	162.5	9.0	699	7	CF536456	UI-H-D10-
1009	165	9.1	780	7	CF539770	UI-M-GV0-	1082	162.5	9.0	708	6	CA439206	UI-H-D10-
1010	165	9.1	786	7	CF216645	AGENCOURT	1083	162.5	9.0	728	5	EX499682	DKF2p779H
1011	165	9.1	898	7	CF223675	AGENCOURT	1084	162.5	9.0	755	7	CK018234	AGENCOURT
1012	165	9.1	912	7	CN093676	EC2BBABC	1085	162.5	9.0	763	4	BG921356	602824217
1013	165	9.1	1137	6	CD507144	CDAB3-C06	1086	162.5	9.0	763	4	BI080254	602876680
1014	164.5	9.1	559	5	BP370855	BP370855	1087	162.5	9.0	779	6	CD636252	56049016H
1015	164.5	9.1	561	7	CK618594	mk14a07.Y	1088	162.5	9.0	814	7	CO810649	AGENCOURT
1016	164.5	9.1	604	5	BU102167	PRODIGI.GID	1089	162.5	9.0	856	5	BU130635	603118991
1017	164.5	9.1	683	4	BI393255	pgpin.pk0	1090	162.5	9.0	860	6	CB193630	AGENCOURT
1018	164.5	9.1	743	6	CD494572	CD411-E10	1091	162.5	9.0	925	4	BI872091	603396391
1019	164.5	9.1	836	8	BH044916	RPCT-24-3	1092	162.5	9.0	930	7	CK409630	AUF_ILfVr
1020	164.5	9.1	839	7	CO922821	AGENCOURT	1093	162.5	9.0	933	5	BU856183	AGENCOURT
1021	164.5	9.1	859	4	BA413783	602987688	1094	162.5	9.0	3905	3	AK083069	Mus muscu
1022	164	9.1	387	7	CO298825	EK173933.	1095	162	9.0	455	4	BG358967	BOVMS1-00
1023	164	9.1	599	8	AZ585520	IM0390E18	1096	162	9.0	571	7	CK707773	ZF201-P00
1024	164	9.1	627	7	CN9833254	51876.126	1097	162	9.0	625	5	BP277969	BP277969
1025	164	9.1	644	6	CD372018	UI-R-G00-	1098	162	9.0	660	7	CF532017	UI-M-FY0-
1026	164	9.1	651	6	CD806831	UI-M-GV0-	1099	162	9.0	699	7	CF366889	841594 MA
1027	164	9.1	720	6	CBS20196	UI-M-G10-	1100	162	9.0	870	4	BI197164	602756667
1028	164	9.1	767	4	BG970299	602838903	1101	162	9.0	891	6	CB194073	AGENCOURT
1029	164	9.1	883	8	BZ222298	CH230-324	1102	162	9.0	962	6	CD080179	MA3-9999U
1030	164	9.1	924	5	BQ933843	AGENCOURT	1103	162	9.0	1056	5	BM925845	AGENCOURT
1031	164	9.1	964	5	BQ715124	AGENCOURT	1104	161.5	8.9	581	5	BP346467	BP346467

1105	161.5	8.9	583	5	BP347694	BP347694	1178	159.5	8.8	641	7	CK693848	CK693848
1106	161.5	8.9	622	2	BE864980	UI-M-BHI-	1179	159.5	8.8	699	4	BM728584	BM728584
1107	161.5	8.9	679	7	CF900715	A0319A05-	1180	159.5	8.8	717	5	BQ206762	UI-E-EJO-
1108	161.5	8.9	694	7	CK792923	AGENCOURT	1181	159.5	8.8	801	7	CF182513	UI-M-EYO-
1109	161.5	8.9	708	5	CK881610	EX881610	1182	159.5	8.8	806	4	BI762516	603048638
1110	161.5	8.9	723	4	BG974950	602844949	1183	159.5	8.8	808	4	BI833165	603090890
1111	161.5	8.9	731	7	CN528054	UI-M-HQO-	1184	159.5	8.8	832	2	BE563419	601335464
1112	161.5	8.9	733	4	BG545860	602573145	1185	159.5	8.8	850	1	AUI33135	AUI33135
1113	161.5	8.9	819	7	CK865025	AGENCOURT	1186	159.5	8.8	882	5	CK728325	AGENCOURT
1114	161.5	8.9	820	6	CD620694	56100873H	1187	159.5	8.8	938	7	CK866851	AGENCOURT
1115	161.5	8.9	855	6	CB588927	AGENCOURT	1188	159.5	8.8	940	5	BX369835	BX369835
1116	161.5	8.9	874	7	CO733078	SILTO2C04	1189	159.5	8.8	941	5	BU912943	AGENCOURT
1117	161.5	8.9	878	5	BQ887533	AGENCOURT	1190	159.5	8.8	947	5	BQ644258	AGENCOURT
1118	161.5	8.9	910	5	BQ650842	AGENCOURT	1191	159.5	8.8	2748	3	AK036352	Mus muscu
1119	161.5	8.9	979	4	BG420574	602448438	1192	159	8.8	259	2	BB607028	BB607028
1120	161	8.9	489	2	BF705825	268933 NA	1193	159	8.8	451	1	AL119880	AL119880
1121	161	8.9	556	7	CR452315	CR452315	1194	159	8.8	557	6	CA563258	K0311H02-
1122	161	8.9	581	4	BJ070444	BJ070444	1195	159	8.8	599	4	BJ058708	BJ058708
1123	161	8.9	670	7	CN538094	UI-M-HSO-	1196	159	8.8	692	6	CB526667	UI-M-FYO-
1124	161	8.9	757	7	CN366089	170005313	1197	159	8.8	719	6	CB724268	UI-M-FYO-
1125	161	8.9	714	7	CN366080	170004243	1198	159	8.8	259	2	BB607028	BB607028
1126	161	8.9	717	5	BU321343	603854520	1199	159	8.8	838	7	CR564541	CR564541
1127	161	8.9	730	7	CN366076	170005331	1200	159	8.8	934	5	BU903988	BU903988
1128	161	8.9	732	7	CN304969	170005325	1201	159	8.8	1013	7	CR801753	ILLUMIGEN
1129	161	8.9	738	4	BG864104	602797704	1202	159	8.8	1677	3	AK030635	Mus muscu
1130	161	8.9	757	7	CN304990	170004240	1203	159	8.8	3687	3	AK076215	Mus muscu
1131	161	8.9	766	5	BX869908	BX869908	1204	158.5	8.8	569	5	BP377634	BP377634
1132	161	8.9	770	5	BO444091	UI-M-EXO-	1205	158.5	8.8	574	2	BP540423	602050188
1133	161	8.9	879	6	CD557080	AGENCOURT	1206	158.5	8.8	582	5	BP208357	BP208357
1134	161	8.9	887	7	CK408075	AUF_lflvrt	1207	158.5	8.8	583	5	BP357634	BP357634
1135	161	8.9	901	7	CN319156	AGENCOURT	1208	158.5	8.8	586	5	BP254888	BP254888
1136	161	8.9	902	7	CR442151	CR442151	1209	158.5	8.8	600	5	BU918743	BU918743
1137	161	8.9	905	5	BU182251	AGENCOURT	1210	158.5	8.8	652	1	AL846235	AL846235
1138	161	8.9	908	5	BX386931	BX386931	1211	158.5	8.8	760	6	CA319537	UI-M-FWO-
1139	161	8.9	922	5	BO894075	AGENCOURT	1212	158.5	8.8	828	7	CV077258	AGENCOURT
1140	161	8.9	939	4	BM451147	AGENCOURT	1213	158.5	8.8	853	5	BQ719866	AGENCOURT
1141	161	8.9	1673	3	CR617412	full-leng	1214	158.5	8.8	906	5	BU916159	AGENCOURT
1142	161	8.9	3533	3	BC057284	Homo sapi	1215	158.5	8.8	964	9	CNS05CLJ	Tetradodon
1143	160.5	8.9	460	1	AA155245	mm4Qd12.r	1216	158.5	8.8	1057	5	BX398530	BX398530
1144	160.5	8.9	486	7	CR746947	CR746947	1217	158.5	8.8	1154	6	CD503211	CDAG1-A08
1145	160.5	8.9	530	2	BE226313	ia19a09.y	1218	158.5	8.8	1296	7	CF110468	Shultzoni
1146	160.5	8.9	582	5	BP361289	BP361289	1219	158.5	8.8	1580	9	AY411535	Pan trogl
1147	160.5	8.9	595	2	AV617433	AV617433	1220	158.5	8.8	3751	9	AY404031	Homo sapi
1148	160.5	8.9	602	7	CF727943	UI-M-HBO-	1221	158	8.7	382	6	CB809130	AGMNNUC.C
1149	160.5	8.9	606	5	BP505184	BP505184	1222	158	8.7	448	6	BY568324	BY568324
1150	160.5	8.9	711	4	BG115636	602316760	1223	158	8.7	450	2	BF731087	maB8La06.
1151	160.5	8.9	715	7	CN426680	170005321	1224	158	8.7	453	6	BY565338	BY565338
1152	160.5	8.9	782	7	CK026234	AGENCOURT	1225	158	8.7	539	7	CM679883	E0127F05-
1153	160.5	8.9	798	6	CD856120	AGENCOURT	1226	158	8.7	582	5	BP251115	BP251115
1154	160.5	8.9	800	5	BU319927	603487913	1227	158	8.7	595	2	BE291062	BE291062
1155	160.5	8.9	884	4	BI771277	603054624	1228	158	8.7	614	1	AI809639	AI809639
1156	160.5	8.9	889	7	CF266344	AGENCOURT	1229	158	8.7	670	4	BG085642	H3115G08-
1157	160.5	8.9	966	7	CF9505094	AGENCOURT	1230	158	8.7	671	1	AL859372	AL859372
1158	160.5	8.9	3146	3	AK084850	Mus muscu	1231	158	8.7	716	5	BU281132	603600750
1159	160	8.9	456	7	CF796349	892593 NC	1232	158	8.7	716	6	CA376321	CA376321
1160	160	8.9	630	6	CA376096	654336 NA	1233	158	8.7	717	7	CF724990	CF724990
1161	160	8.9	721	6	CA749345	UI-M-FYO-	1234	158	8.7	790	7	CK677667	2F101-P00
1162	160	8.9	727	6	CA749345	UI-M-FYO-	1235	158	8.7	790	5	BU306680	BU306680
1163	160	8.9	740	7	CF532374	UI-M-FYO-	1236	158	8.7	822	7	CO870384	CO870384
1164	160	8.9	819	5	BX424510	BX424510	1237	158	8.7	827	4	BI463685	BI463685
1165	160	8.9	820	7	CO395177	AGENCOURT	1238	158	8.7	899	7	CK866029	CK866029
1166	160	8.9	824	5	BQ444246	UI-M-EXO-	1239	158	8.7	914	5	BQ898909	BQ898909
1167	160	8.9	824	7	CK470323	AGENCOURT	1240	158	8.7	936	5	BX853896	BX853896
1168	160	8.9	865	1	AI134784	GH12331.5	1241	157.5	8.7	582	5	BP250662	BP250662
1169	160	8.9	1092	7	CK642662	ILLUMIGEN	1242	157.5	8.7	600	5	BU922970	7042-78 M
1170	160	8.9	3811	3	AK031246	Mus muscu	1243	157.5	8.7	617	5	BQ359313	BQ359313
1171	159.5	8.8	383	1	AA401292	4027892.1	1244	157.5	8.7	636	5	BU101548	BU101548
1172	159.5	8.8	493	6	CD739385	2063395	1245	157.5	8.7	650	4	BM049915	BM049915
1173	159.5	8.8	538	2	BP022068	uy46808.y	1246	157.5	8.7	664	4	BI373259	603624395
1174	159.5	8.8	582	5	BP315255	BP315255	1247	157.5	8.7	666	2	BE392233	BE392233
1175	159.5	8.8	600	5	BU101549	PRODIGID	1248	157.5	8.7	721	5	BQ769295	UI-M-FIO-
1176	159.5	8.8	615	4	BI067145	Pgfin.pk0	1249	157.5	8.7	755	7	CK868145	CK868145
1177	159.5	8.8	629	1	AL657340	AL657340	1250	157.5	8.7	762	7	CK397238	CK397238

1251	157.5	8.7	776	7	CF737877	UI-M-HD0-	CF737877	UI-M-HD0-	1324	156	8.6	477	7	CN359280	170005319
1252	157.5	8.7	796	5	BX923146	BX923146	BX923146	BX923146	1325	156	8.6	596	1	AL599774	DKP20313M
1253	157.5	8.7	810	6	CR868629	AGENCOURT	CR868629	AGENCOURT	1326	156	8.6	628	4	BJ685150	BJ685150
1254	157.5	8.7	860	6	CD627471	56067512J	CD627471	56067512J	1327	156	8.6	653	4	CK003476	AGENCOURT
1255	157.5	8.7	901	5	BQ881261	AGENCOURT	BQ881261	AGENCOURT	1328	156	8.6	691	1	AV384111	AV384111
1256	157.5	8.7	904	5	BQ685640	AGENCOURT	BQ685640	AGENCOURT	1329	156	8.6	729	4	BM621283	170006874
1257	157.5	8.7	939	5	BX452370	BX452370	BX452370	BX452370	1330	156	8.6	740	7	CN531505	UI-M-HQ0-
1258	157.5	8.7	952	5	BU514323	AGENCOURT	BU514323	AGENCOURT	1331	156	8.6	760	7	CN531514	UI-M-HQ0-
1259	157.5	8.7	953	7	CR865103	AGENCOURT	CR865103	AGENCOURT	1332	156	8.6	767	2	AW175139	f137f09.Y
1260	157.5	8.7	958	2	BF795536	602259467	BF795536	602259467	1333	156	8.6	775	6	CD080814	MA3-9999U
1261	157.5	8.7	987	5	BX375028	BX375028	BX375028	BX375028	1334	156	8.6	780	5	EX444240	EX444240
1262	157.5	8.7	1008	5	BX424991	BX424991	BX424991	BX424991	1335	156	8.6	784	6	CA350777	621665 NC
1263	157.5	8.7	1046	4	BM552640	AGENCOURT	BM552640	AGENCOURT	1336	156	8.6	795	7	CO248560	AGENCOURT
1264	157.5	8.7	1072	7	CN642560	ILLUMIGEN	CN642560	ILLUMIGEN	1337	156	8.6	810	7	CO799885	AGENCOURT
1265	157.5	8.7	1488	3	CR608619	full-leng	CR608619	full-leng	1338	156	8.6	1096	7	CN642525	ILLUMIGEN
1266	157.5	8.7	1594	3	CR617107	full-leng	CR617107	full-leng	1339	156	8.6	2036	3	AK089498	Mus muscu
1267	157.5	8.7	1742	9	AY413879	Mus muscu	AY413879	Mus muscu	1340	156	8.6	2850	3	AK047868	Mus muscu
1268	157.5	8.7	2090	3	AK003152	Mus muscu	AK003152	Mus muscu	1341	156	8.6	3312	3	AK004947	Mus muscu
1269	157.5	8.7	2209	3	AK017447	Mus muscu	AK017447	Mus muscu	1342	156	8.6	3449	3	AK041299	Mus muscu
1270	157.5	8.7	2735	3	AK029024	Mus muscu	AK029024	Mus muscu	1343	156	8.6	3559	9	AY404032	Pan trogl
1271	157.5	8.7	3652	3	AK030851	Mus muscu	AK030851	Mus muscu	1344	156	8.6	3687	3	AK079247	Mus muscu
1272	157.5	8.7	4118	3	AK031391	Mus muscu	AK031391	Mus muscu	1345	155.5	8.6	409	2	BE226893	us74a09.Y
1273	157	8.7	578	5	BP368062	BP368062	BP368062	BP368062	1346	155.5	8.6	581	5	BP193219	BP193219
1274	157	8.7	608	5	BX917921	BX917921	BX917921	BX917921	1347	155.5	8.6	581	5	BP195771	BP195771
1275	157	8.7	612	4	BM795050	K-BST0076	BM795050	K-BST0076	1348	155.5	8.6	605	7	CF368297	852930 MA
1276	157	8.7	641	2	BB664453	BB664453	BB664453	BB664453	1349	155.5	8.6	617	5	BM305475	BM305475
1277	157	8.7	690	6	CD636219	56031467J	CD636219	56031467J	1350	155.5	8.6	638	6	CD629100	56059934H
1278	157	8.7	695	7	CK949734	4074697 B	CK949734	4074697 B	1351	155.5	8.6	649	1	AL864304	AL864304
1279	157	8.7	722	6	CD805128	UI-M-GW0-	CD805128	UI-M-GW0-	1352	155.5	8.6	702	9	CNS02PTU	Tetraodon
1280	157	8.7	727	7	CK961924	4076329 B	CK961924	4076329 B	1353	155.5	8.6	718	6	CD636336	56048995J
1281	157	8.7	737	4	B1915307	603184382	B1915307	603184382	1354	155.5	8.6	727	4	BM290618	BM290618
1282	157	8.7	757	6	CR519019	UI-M-GH0-	CR519019	UI-M-GH0-	1355	155.5	8.6	769	7	CN505057	AGENCOURT
1283	157	8.7	781	6	CD346886	UI-M-FY0-	CD346886	UI-M-FY0-	1356	155.5	8.6	786	7	CN302526	170006001
1284	157	8.7	805	1	AU131165	AU131165	AU131165	AU131165	1357	155.5	8.6	796	5	AX923150	AX923150
1285	157	8.7	826	6	CB165550	BEQ603160	CB165550	BEQ603160	1358	155.5	8.6	796	5	AX926278	AX926278
1286	157	8.7	848	7	CN020324	AGENCOURT	CN020324	AGENCOURT	1359	155.5	8.6	797	6	CD642524	AGENCOURT
1287	157	8.7	850	5	BX739790	BX739790	BX739790	BX739790	1360	155.5	8.6	850	5	BP264898	BP264898
1288	157	8.7	876	7	CK948326	4073246 B	CK948326	4073246 B	1361	155.5	8.6	861	6	CO557070	AGENCOURT
1289	157	8.7	886	5	BQ945091	AGENCOURT	BQ945091	AGENCOURT	1362	155.5	8.6	861	6	CD636209	56031050J
1290	157	8.7	896	5	BX379273	AGENCOURT	BX379273	AGENCOURT	1363	155.5	8.6	880	5	BU542115	AGENCOURT
1291	157	8.7	910	5	BU192138	AGENCOURT	BU192138	AGENCOURT	1364	155.5	8.6	909	7	CN642097	ILLUMIGEN
1292	157	8.7	930	7	CN315936	AGENCOURT	CN315936	AGENCOURT	1365	155.5	8.6	1039	5	BQ057979	ILLUMIGEN
1293	157	8.7	933	9	AY417086	Mus muscu	AY417086	Mus muscu	1366	155.5	8.6	1091	7	CK232190	ILLUMIGEN
1294	157	8.7	1020	4	BM548873	AGENCOURT	BM548873	AGENCOURT	1367	155.5	8.6	1376	3	CR635265	Tetraodon
1295	157	8.7	1034	1	AL553289	AL553289	AL553289	AL553289	1368	155.5	8.6	4017	3	AK028983	Mus muscu
1296	157	8.7	1071	5	BU503048	AGENCOURT	BU503048	AGENCOURT	1369	155.5	8.6	5635	9	AY412619	Mus muscu
1297	157	8.7	1127	1	AL549623	AL549623	AL549623	AL549623	1370	155	8.6	427	7	CO436236	ddPCR2_17
1298	157	8.7	1514	3	CR617300	full-leng	CR617300	full-leng	1371	155	8.6	545	4	BM440456	BM440456
1299	157	8.7	1867	3	AK087272	Mus muscu	AK087272	Mus muscu	1372	155	8.6	571	4	BJ124803	BJ124803
1300	157	8.7	1892	3	CR622259	full-leng	CR622259	full-leng	1373	155	8.6	602	6	CA317092	UI-M-FW0-
1301	157	8.7	2791	3	BC013698	Homo sapi	BC013698	Homo sapi	1374	155	8.6	617	6	CD636187	56020455J
1302	156.5	8.7	568	1	A1629069	fc09b12.Y	A1629069	fc09b12.Y	1375	155	8.6	669	5	BU696122	LL21n1269
1303	156.5	8.7	618	4	B1065290	pgfin.pk0	B1065290	pgfin.pk0	1376	155	8.6	694	6	CD349249	UI-M-FY0-
1304	156.5	8.7	627	4	BU112590	BJ112590	BU112590	BJ112590	1377	155	8.6	705	7	CR753907	CR753907
1305	156.5	8.7	630	1	A1295266	LP08849.5	A1295266	LP08849.5	1378	155	8.6	710	7	CN053418	Salamande
1306	156.5	8.7	630	5	BQ390372	NISC mc12	BQ390372	NISC mc12	1379	155	8.6	726	7	CN302510	170005318
1307	156.5	8.7	684	6	CA354756	628528 NC	CA354756	628528 NC	1380	155	8.6	739	7	CN302524	170004710
1308	156.5	8.7	725	4	B1736575	603361039	B1736575	603361039	1381	155	8.6	755	7	CN302501	170005322
1309	156.5	8.7	740	5	BU058190	UI-M-F00-	BU058190	UI-M-F00-	1382	155	8.6	778	7	CK634628	UI-M-HN0-
1310	156.5	8.7	751	5	BP673676	BP673676	BP673676	BP673676	1383	155	8.6	781	5	BU383797	603581533
1311	156.5	8.7	768	7	CN172200	AGENCOURT	CN172200	AGENCOURT	1384	155	8.6	792	4	BI772811	603054461
1312	156.5	8.7	776	5	BO442214	UI-M-EX0-	BO442214	UI-M-EX0-	1385	155	8.6	793	7	CF288820	AGENCOURT
1313	156.5	8.7	858	5	BU470108	603365843	BU470108	603365843	1386	155	8.6	833	1	AA941031	LD23480.5
1314	156.5	8.7	914	7	CF594392	AGENCOURT	CF594392	AGENCOURT	1387	155	8.6	836	4	BI824985	603033468
1315	156.5	8.7	928	5	BQ733716	AGENCOURT	BQ733716	AGENCOURT	1388	155	8.6	891	6	CD384890	AGENCOURT
1316	156.5	8.7	937	7	CO248697	AGENCOURT	CO248697	AGENCOURT	1389	155	8.6	907	5	BQ928239	AGENCOURT
1317	156.5	8.7	1004	5	BU134013	603121573	BU134013	603121573	1390	155	8.6	913	2	BE912082	601663261
1318	156.5	8.7	1014	6	CB206098	ILLUMIGEN	CB206098	ILLUMIGEN	1391	155	8.6	922	5	BU518914	AGENCOURT
1319	156.5	8.7	1028	7	CN642108	CV182470	CN642108	CV182470	1392	155	8.6	933	9	AY417084	Homo sapi
1320	156.5	8.7	1319	7	CV182470	tal87902.	CV182470	tal87902.	1393	155	8.6	941	5	BQ928243	AGENCOURT
1321	156.5	8.7	3465	9	AY418996	Pan trogl	AY418996	Pan trogl	1394	155	8.6	993	1	AL560725	AL560725
1322	156.5	8.7	3689	3	AK004723	Mus muscu	AK004723	Mus muscu	1395	155	8.6	1047	7	CK230378	ILLUMIGEN
1323	156.5	8.7	3865	3	AK087355	Mus muscu	AK087355	Mus muscu	1396	155	8.6	1971	3	AK076123	Mus muscu

1397	155	8.6	1392	3	AK034125	Mus muscu	AK034125	Mus muscu	1470	152.5	8.4	430	5	BU947992	BU947992	io56ell.y
1398	155	8.6	3133	3	AK085723	Mus muscu	AK085723	Mus muscu	1471	152.5	8.4	548	5	EX271825	EX271825	EX271825
1399	154.5	8.6	247	7	CR474371	CR474371	CR474371	CR474371	1472	152.5	8.4	594	5	BW221728	BW221728	BW221728
1400	154.5	8.6	450	1	AA168307	me54b12.r	AA168307	me54b12.r	1473	152.5	8.4	668	4	BI394312	BI394312	BI394312
1401	154.5	8.6	498	6	CB070225	ie27f12.y	CB070225	ie27f12.y	1474	152.5	8.4	709	5	BU116030	BU116030	BU116030
1402	154.5	8.6	506	7	CO328919	EX291651.y	CO328919	EX291651.y	1475	152.5	8.4	710	9	AG286398	AG286398	Mus muscu
1403	154.5	8.6	598	1	AL856990	AL856990	AL856990	AL856990	1476	152.5	8.4	723	6	CB526860	CB526860	UI-M-FY0-
1404	154.5	8.6	648	8	AZ379719	IM0135K02	AZ379719	IM0135K02	1477	152.5	8.4	745	4	BI080347	BI080347	EX2816784
1405	154.5	8.6	670	5	BX622375	BX622375	BX622375	BX622375	1478	152.5	8.4	768	5	EX918182	EX918182	EX918182
1406	154.5	8.6	677	5	BU204691	604159805	BU204691	604159805	1479	152.5	8.4	769	5	EX856025	EX856025	EX856025
1407	154.5	8.6	702	7	CF533968	UI-M-GHO-	CF533968	UI-M-GHO-	1480	152.5	8.4	822	6	CB245137	CB245137	UI-M-FY0-
1408	154.5	8.6	689	6	CD620688	56087531H	CD620688	56087531H	1481	152.5	8.4	833	7	CN837756	CN837756	AGENCOURT
1409	154.5	8.6	715	4	BJ487033	BJ487033	BJ487033	BJ487033	1482	152.5	8.4	867	6	CA7888252	CA7888252	AGENCOURT
1410	154.5	8.6	732	4	BM292745	EST575287	BM292745	EST575287	1483	152.5	8.4	912	6	CD515059	CD515059	AGENCOURT
1411	154.5	8.6	778	5	BQ745865	UI-M-EXO-	BQ745865	UI-M-EXO-	1484	152.5	8.4	950	1	AL523470	AL523470	AL523470
1412	154.5	8.6	783	6	CD636195	56030944J	CD636195	56030944J	1485	152.5	8.4	1004	4	CN642068	CN642068	ILLUMIGEN
1413	154.5	8.6	808	4	BI523511	603175329	BI523511	603175329	1486	152.5	8.4	1028	9	CNS0070A	AL067489	Drosophila
1414	154.5	8.6	811	7	CF539481	UI-M-GHO-	CF539481	UI-M-GHO-	1487	152.5	8.4	2338	3	AK032604	AK032604	Mus muscu
1415	154.5	8.6	820	5	BF729243	EX729243	BF729243	EX729243	1488	152.5	8.4	4050	3	AK049704	AK049704	Mus muscu
1416	154.5	8.6	1002	4	BM472841	AGENCOURT	BM472841	AGENCOURT	1489	152.5	8.4	4655	9	AY412618	AY412618	Pan trogl
1417	154.5	8.6	1029	7	CN642582	ILLUMIGEN	CN642582	ILLUMIGEN	1490	152.5	8.4	530	7	CK580486	CK580486	IST W15.2
1418	154.5	8.6	1311	5	BP938160	BP938160	BP938160	BP938160	1491	152.5	8.4	602	5	BU741589	BU741589	UI-E-EOI-
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ALIGNMENTS

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LOCUS	Mus musculus adult male corpora quadrigemina cDNA, RIKEN			
DEFINITION	full-length enriched library, clone:B230328N06 product:NEUROTRIN			
ACCESSION	AK045973.1	GI:26337738		
VERSION	AK045973.1	GI:26337738		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wakiyama, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			

MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
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 ORIGIN
 Alignment Scores:
 Pred. No.:

Score: 1780.00 Matches: 337
 Percent Similarity: 99.42% Conservative: 5
 Best Local Similarity: 97.97% Mismatches: 2
 Query Match: 98.56% Indels: 0
 DB: 3 Gaps: 0
 US-10-017-084A-523 (1-344) x AK045973 (1-1808)
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 Db 204 ATGAAACCAATCCAGGCGAAATAATGCAATTTCTATCTCGTGGCAATCTTTCACGGGGCTG 263
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 Db 264 GCGGCTCTGTGCTCTTCCAGAGGAGTCCGGTGGTAGCGGAGATGCCACCTTTCCCAA 323
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 Db 324 GCTATGGACAACTGACGGTCCAGCGGGGAGAGCGCCACCTCAGGTGCACAAATTGAC 383
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 Db 384 AACCGAGTCACCCGGGTGGCTGGCTAAACCGCAGTACCATCTCTATGCTGGAAATGAC 443
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 444 AAGTGGTGGCTAGATCTCTGTGTCTCTCTGAGTAACACCCAGACCCAGTACAGCATT 503
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db      1164  AATGGACATCAAGGAGGAGGCTGCTTGGCTCTCCCTCTTCTGGTCTTACACCTG 1223
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RESULT 2
LOCUS   AK046377
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230377K17 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK046377
VERSION   1
KEYWORDS  HTG; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS  Carninci, P. and Hayashizaki, Y.
TITLE    High-efficiency full-length cDNA cloning
JOURNAL  Meth. Enzymol. 303, 19-44 (1999)
MEDLINE  99279253
PUBMED   10349636
REFERENCE
AUTHORS  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE    Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL  Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE  20499374
PUBMED   11042159
REFERENCE
AUTHORS  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL  Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE  20530913
PUBMED   11076861
REFERENCE
AUTHORS  The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE    Functional annotation of a full-length mouse cDNA collection
JOURNAL  Nature 409, 685-690 (2001)
PUBMED   11076861
REFERENCE
AUTHORS  The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE    Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL  Nature 420, 563-573 (2002)
PUBMED   12401000
REFERENCE
AUTHORS  Adachi, J., Aikawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, P., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE    Direct Submission
JOURNAL  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

COMMENT

FEATURES

source

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CDS

ORIGIN

Alignment Scores:

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Percent Similarity: 99.42% Conservative: 5
Best Local Similarity: 97.97% Mismatches: 2
Query Match: 98.56% Indels: 0
DB: 3 Gaps: 0

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US-10-017-084A-523 (1-344) x AK046377 (1-1808)

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Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 804 TGCAGCGCTCCAAACAGCTGGCGGCACCACTGGGTACGAAGAGTGAAGGTCAACGTGAAC 863
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Qy 1044 ACCTTTTCAAGCTCTCGAATGACATGACTATGGAACCTACATGATGTGGCTCCACAAAG 1103
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1104 CTGGGTACACCAACGCCAGCATCATGCTATTTGGTCCCGGTGCTGTCAAGTGAAGTCAAC 1163
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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LOCUS
DEFINITION Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406347.1 GI:39762321
VERSION
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM
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REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
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REFERENCE 2 (bases 1 to 874)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Score: 1506.00 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 93.39% Indels: 2
DB: 9 Gaps: 1
US-10-017-084A-523 (1-344) x AY406347 (1-874)
Qy 57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACATATTGACAAACCCGGTCAACCCGGTGGCTTAAACCCGAGCACCATCTCTAT 61
Qy 77 AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
Db 62 GCTGGGAGTACAAAGTGGTGCCTCGCATCTCGCGTGGTCTTCTTGAGCAACACCCAAACG 121
Qy 97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
Db 122 CAGTACAGATCGAGATCCAGACGTGGATGTATGACGAGGGCCCTTACACCTGCTCG 181
Qy 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
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Qy 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
Db 242 AAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 301
Qy 157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
Db 302 TGCATAGCAACTGGTAGACAGACCTACGGTTACTTGGAGACACATCTCTCCCAACCC 361
Qy 176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
Db 362 GCAGCGGTTGGCTTTGTGAGTGAAGACAAATACCTTGGAAATTCAGGGCATCACCGGGAG 421
Qy 195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
Db 422 CAGTCAGGGGACTACGAGTGCAGTCCCTCCAAATGACGTGGCGCGCCGCTGGTACGGAGA 481
Qy 215 VallysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValPro 234
Db 482 GTAAGGTCAACCGTGAACTATCCACCATACATTTTCAGNAGCAAGGGTACAGGTGTCCC 541
Qy 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
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Qy 255 TrpTyrLysAspAspLysArgLeuIleGluLysLysGlyValLysValGluAsnArg 274
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QY 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
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QY 315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
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Db 782 GCCGTGAGGAGTGCAGCAACGGCAGCTCGAGGAGGCGGCTGCTGGCTGCTGCT 841

QY 335 LeuLeuValLeuHisLeuLeuLysPhe 344
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Db 842 CTTCTGGTCTGCACCTGCTCTCAAAATTT 871

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LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406349
VERSION AY406349.1 GI:39762323
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL gene trios
PUBMED Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 874)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
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Alignment Scores:
Pred. No.: 5,29e-164 Length: 874
Score: 1488.00 Matches: 282
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Best Local Similarity: 97.24% Mismatches: 1
Query Match: 82.39% Indels: 2
DB: 9 Gaps: 1

US-10-017-084A-523 (1-344) x AY406349 (1-874)

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Db 2 TGCACAAATTGACACCGAGTACCCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGAT 61

QY 77 AlaGlyAsnAspLysTyrCysLeuAspProArgValValLeuLeuSerAsnThrClnThr 96
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QY 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
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QY 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
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QY 215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
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QY 315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
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Db 782 CTTCTGAGTGGTCAACATGGGACATCAAGGAGGCGGAGTGGATTTGGCTCTCTCTCT 841

QY 335 LeuLeuValLeuHisLeuLeuLysPhe 344
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Db 842 CTTCTGGTCTTACACCTGCTCTCTCAAAATTT 871

RESULT 5
AY406348 773 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406348
VERSION AY406348.1 GI:39762322
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 773)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL gene trios
Science 302 (5652), 1960-1963 (2003)

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 2 (bases 1 to 773)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 73.31% Indels: 2
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 Db 62 GCTGGGATGACAACTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACG 121
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QY 275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
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 QY 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
 Db 722 TGGGTGGCTCCAAACAAGTGGCCACACCAATGCCAGCATCATGCTATTT 772
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 DEFINITION
 CO635648
 ACCESSION
 CO635648.1 GI:50538871
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
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 Gallus gallus
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1450)
 REFERENCE
 AUTHORS
 Fitzsimmons, C.J., Savolainen, P., Amini, B., Hjalms, G., Lundeberg, J.,
 and Andersson, L.
 TITLE
 Detection of sequence polymorphisms in red junglefowl and White
 Leghorn ESTs
 JOURNAL
 Unpublished (2004)
 COMMENT
 Contact: Carolyn Fitzsimmons
 Leif Andersson IMBIM/Dept. Animal Breeding and Genetics
 Uppsala University/Swedish University of Agricultural Sciences
 Box 597, SE-751 24 Uppsala, SWEDEN
 Tel: 00 46 (0)18 471 4593
 Fax: 00 46 (0)18 471 4833
 Email: Carolyn.Fitzsimmons@bmc.uu.se
 This EST is a consensus sequence obtained from a Phrap assembly of
 4 cDNA libraries. The consensus sequence is submitted because SNP
 data in the publication 'Detection of sequence polymorphisms in red
 junglefowl and White Leghorn ESTs', is reported with reference to
 positions in the Phrap consensus sequence.
 Seq primer: (5'-end) M13 reverse.
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 the Superscript Plasmid System (Invitrogen)."
 ORIGIN
 Alignment Scores:
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 Score: 1321.00 Matches: 255
 Percent Similarity: 87.58% Conservative: 27
 Best Local Similarity: 79.19% Mismatches: 34
 Query Match: 73.15% Indels: 6
 Gaps: 2
 DB:
 US-10-017-084A-523 (1-344) x CO635648 (1-1450)
 QY 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
 Db 308 CAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAGCTATGACCACTGACT 367
 QY 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
 Db 368 GTGGCGCAAGGGGAGAGTGCACCGTCAAGGTGCTCCGTTGGACACCCGCTCACCCGCTG 427
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Db 305 GTGTACGATGAGGCGCCCTATTACCTGCTCGGTACAGACAGACCAACCCCTAAGACCTCC 364

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Qy 147 IleAenGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166

Db 425 ATTAATGAAGGGAACACATCAGCTCTACCTTGCATAGCCACAGGTAGACCGAGCCTACA 484

Qy 167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeu 186

Db 485 GTAACTCGAGACATATTTCTCCCAAGCGCGTTGGCTTTGTGAGTGAGGATGAGTACCTG 544

Qy 187 GluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAsp 206

Db 545 GAGATCCAGGCGCATCACTCGGGAACAGTCAGCGCAGTACGAGTGCGAGCGCTCCCAACGAC 604

Qy 207 ValAlaAlaProValValArgArgValLysValThrValAenTyrProTyrTrpIleSer 226

Db 605 GTGGCGGCACAGTGGTACGAAGAGTGAAGGTACCGTGAATATFCCACCATATCTCA 664

Qy 227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246

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RESULT 8

LOCUS BUI155617 856 bp mRNA linear EST 03-SEP-2002

DEFINITION AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839

VERSION BUI155617 5', mRNA sequence.

KEYWORDS BUI155617.1 GI:22669149

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 856)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLA013527 row: m column: 16
High quality sequence stop: 593.

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ORIGIN

Alignment Scores:

Pred. No.: 4.8e-130 Length: 856

Score: 1199.50 Matches: 243

Percent Similarity: 92.99% Conservative: 9

Best Local Similarity: 89.67% Mismatches: 13

Query Match: 66.42% Indels: 7

DB: Gaps: 3

US-10-017-084A-523 (1-344) x BUI155617 (1-856)

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Db 48 AGTCCCTCGTGGTGTCTCTCAGGCTGTGTTCCTTG---TACCC-ACAGGAGTGCCTC 103

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Db 464 AACAAATATTAGCCTCACCTGCATAGCACTGGTAGACAGACCTACGGTTACTTGGAGA 523

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Db 524 CACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGCAATACTTTGGAAATTCAGGGC 583

Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210

Db 584 ATCACCGGGAGCAGTACGCGGCTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCC 643

Qy 211 ValValArgArgValLysValThrValAenTyrProTyrIleSerGluAlaLysGly 230

Db 644 GTGTGTAGGAGGTAAAGGTCAACGTGAATTCACCATACATTTTCAGAGCCAGGGT 703

Qy 231 ThrGlyVal-ProValGlyGlnLysGlyThrLeuGln-CysGluAlaSerAlaValPro 250

Db 704 ACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAAACCTCAGCAGTCCCCT 763

Qy 250 erAlaGlu-PheGlnTrpTyrLysAspAsp---LysArgLeuIleGluGlyLysGly 268

Db 764 CAGCAGAAATTCAGTGTGTACAGGATGAACCAAGAGATGATTTTGAAGGGGAAAAAGGG 823

Qy 269 Val---LysValGluAsnArgProPhe 276

Db 824 GTGGAAGGGGGAACCAAGACCTTTC 850

RESULT 9

LOCUS BE798585

DEFINITION 601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',

ACCESSION BE798585

VERSION BE798585.1 GI:10219783

KEYWORDS EST.

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       NIH-MGC http://mgs.nci.nih.gov/
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue procurement: DCTD/DRP
            cDNA library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCW779 row: d column: 04
            High quality sequence stop: 849.

FEATURES    Location/Qualifiers
            source
            1..1039
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3935955"
            /tissue_type="small cell carcinoma"
            /cell_line="MGC3"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 7"
            /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Alignment Scores:
Pred. No.:      4,33e-126      Length:      1039
Score:          1167.00      Matches:     243
Percent Similarity: 80.71%      Conservative: 8
Best Local Similarity: 78.14%      Mismatches: 24
Query Match:      64.62%      Indels:      37
DB:              2          Gaps:        7

US-10-017-084A-523 (1-344) x BE798585 (1-1039)

QY 56 ArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeu 75
Db 66 AGGTGCACCTATTGACAAACCGGTCGCCCGGTGGCTGGCTAAACCGCAGCACCATCCTC 125
QY 76 TyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGln 95
Db 126 TATGCTGGGAATGACAAAGTGGCTGGATCTCGGTGCTCTTCTAGCAACACCCAA 185
QY 96 ThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCys 115
Db 186 AGCAGTACAGCATCGAGATCCAGAACGTCGATGATGATGACAGGGCCCTTACACCTGC 245
QY 116 SerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSer 135
Db 246 TCGGTGCAGACAGACAAACCAACGACCTTAGGGTCCACCTCATTTGTGCAAGTATCT 305
QY 136 ProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeu 155
Db 306 CCCAAATTTGTAGAGATTCTTCAGATATCTCATTAATGAAGGGGAACAATATTAGCCTC 365
QY 156 ThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys 175
Db 366 ACTGTCATAGCAACTGGTAGACAGAGCTAGGTTACTTGGAGACACATCTCTCCCAA 425
QY 176 AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGln 195
```

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Db 426 GCGGTGGCTTTGTGAGTGACGACGAATATTGGAAATTCAGGATCATCCCGGGAGCAG 485
QY 196 SerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgVal 215
Db 486 TCGGGGACTACAGTGGAGTCCCTCCCAATGACGTGGCCGCCCGCTGGTAGGAGATG 545
QY 216 LysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProVal 235
Db 546 AAGGTCCACCGTGAACCTATCCACCATACATTTTCAAGAGCCCAAGGTACAGGTGTCCCGGTG 605
QY 236 GlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrp 255
Db 606 GGACAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGG 665
QY 256 TyrLysAspAspLysArgLeuIleGluGly---LysLysGlyValLysValGluAsnArg 274
Db 666 TACAAGGATGACAAAGACTGATTGAGGACACAGACAGGGGTGAACAGTTGGAAACAGA 725
QY 275 ProPheLeuSerLysLeuIlePhe-----PheAsnValSer---GluHisAspTyr-Gl 291
Db 726 CTTTTTCTCTCTCAAAAGTCATTCTCTTCTTCAATGTCTCTGANCATGGACTATGGG 785
QY 291 YAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAla----- 306
Db 786 GAATACACTTTCGGGGGCTCCCA--AAAGCTGGGCACACCAATGCCAGATCATGCTATTG 843
QY 307 -----ArgAlaGly---CysValTrp 331
Db 961 AGCAAGTAGAGCGCGGTGGTGGCTCTGG 991

RESULT 10
CN362539 748 bp mRNA linear EST 16-MAY-2004
LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN362539
ACCESSION CN362539.1 GI:47362473
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 748)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TITLE Transcriptional characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 748 Std Error: 0.00.
FEATURES Location/Qualifiers
            1..748
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="embryonic stem cells, embryoid bodies
            derived from H1, H7 and H9 cells"
            /clone_lib="GRN_EB"
```


/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Alignment Scores:

Pred. No.: 1.77e-120 Length: 748
Score: 1117.50 Matches: 218
Percent Similarity: 96.09% Conservativity: 3
Best Local Similarity: 94.78% Mismatches: 8
Query Match: 61.88% Indels: 2
DB: 7 Gaps: 1

US-10-017-084A-523 (1-344) x CN362539 (1-748)

Qy 11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
Db 63 AGTGCTCGTGTGCTGCTCTCAGGCTGCTGCTTCCTTG---TACCC-ACAGGAGTGCCC 118
Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
Db 119 GTGGCAGCGAGATGCCACCTTCCCAAGCTATGGACAACGTGACGTCGCGCAGGG 178
Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaAlaTrpLeuAsn 70
Db 179 GAGAGCGCCACCTCAGGTGCACTATTGACAACCGGTGTCACCGGTGGCTGGCTTAAC 238
Qy 71 ArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
Db 239 CGCAGCACCATCTCTATGCTGGGAATGACAAGTGTGCTGGATCTCGCGTGTCTT 298
Qy 91 LeuSerAsnThrGlnThrGlnTySerIleGluIleGlnAsnValAspValTyAspGlu 110
Db 299 CTGAGCAACCCCAACGACGTACAGCATCGAGATCCAGAACGTTGATGTATGACGAG 358
Qy 111 GlyProTyThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
Db 359 GGCCCTTACACTGCTCGGTGCAGACACACCCCAAGACCTCTAGGGTCCACCTC 418
Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
Db 419 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGG 478
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
Db 479 AACCAATATTAGCCTCACCCTGCATAGCAACTGGTAGACAGACGCTTACTTGGAGA 538
Qy 171 HistIleSerProLysAlaValGlyPheValSerGluAspGluTyLeuGluIleGlnGly 190
Db 539 CACATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 598
Qy 191 IleThrArgGluGlnSerGlyAspTyTrpGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 599 ATCACCGGGAGCAGTACAGGGAGCTACGAGTGCAGTGCTCCATGATGCTGGCGCGGCC 658
Qy 211 ValValArgArgValLysValThrValAsnTyProProTyTrpIleSerGluAlaLysGly 230
Db 659 GTGGTACGGAGATAAAGGTCAACCGTCACTATCCACCATATCCACCATATTTCAAGAGCGG 718
Qy 231 ThrGlyValProValGlyGlnLysGlyThr 240
Db 719 ACAGGTGTCCCGTGGGACAAAGGGGACA 748

RESULT 11

CD327172
LOCUS CD327172 890 bp mRNA linear EST 28-MAY-2003
DEFINITION AGENCOURT 14148239 NICHHD_XGC_Eye1 Xenopus laevis cDNA clone
IMAGE:6949575 5', mRNA sequence.
ACCESSION CD327172
VERSION CD327172.1 GI:31091503
KEYWORDS EST.
Xenopus laevis (African clawed frog)

ORGANISM

Xenopus laevis

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

1 (bases 1 to 890)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM14565 row: k column: 14

High quality sequence stop: 757.

Location/Qualifiers

1..890

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6949575"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHHD_XGC_Eye1"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.3 kb. Constructed by Life

Technologies. Note: This is a Xenopus Gene Collection

(XGC) library."

ORIGIN

Alignment Scores: 1.02e-119 Length: 890
Pred. No.: 1112.00 Matches: 209
Score: 88.93% Conservativity: 32
Percent Similarity: 77.12% Mismatches: 28
Best Local Similarity: 61.57% Indels: 2
Query Match: 6 Gaps: 0
DB: 0

US-10-017-084A-523 (1-344) x CD327172 (1-890)

Qy 4 IleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeu 23
Db 69 CTGCAGGCNAGGATGCTGCACCTCGGTTCTTGGGTATCTTCAGTGGGCTGGCTGTTCTT 128
Qy 24 CysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAsp 43
Db 129 TGCCTCTCTGCAAGGAGTGCCTGCGCAGCGGGATGCGCGCTTCCCTTAAAGCCATGGAC 188
Qy 44 AsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgVal 63
Db 189 AACGTGACGGTTCACCAAGGGGACAGCCCATCTTCAGTGCACAGTAGACACAGAGTG 248
Qy 64 ThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCys 83
Db 249 ACACGAGTGGCTGGCTAAATCGTAGTACCATCTTGTACACTGGCAATGACAAAGTGGTCG 308
Qy 84 LeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIleGluIleGln 103
Db 309 ATAGACCCCGCTGGTGTCTTCGCCCAACAACAAGAGTCAGTACAGCATTTGAGATCCAA 368
Qy 104 AsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAspAsnHisPro 123
Db 369 AATGTGGACATTTATGATGAGGAGCCCTTACACCTGCTCTGTGCAGACAGACATCACCCC 428
Qy 124 LysThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSer 143


```

Db 429 AAAAACTCTCGTGTACATCTCAATGTGCAAGTTCCTCCCTCGAATGTTGATATTTCTTCA 488
Qy 144 AsplleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgPro 163
Db 489 AATATTGCTGTTAATGAAGCAGTAAATGTCAGCTGATTTGATTCGAACCGGAGACCT 548
Qy 164 GluProThrValThrTrpArgHisIleSerProLysAlaValAlaGlyPheValSerGluAsp 183
Db 549 GAACCCGTAGTGAACCTGGAGATACTTGTCCCTAAAGCAGCGGGTTTTGTAAAGTGAAGAT 608
Qy 184 GluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGluCysSerAla 203
Db 609 GAGTACCTGGAAATCAGGAATCACTAGGAGCAGTCTGGAATATATGAATGCAAGTGG 668
Qy 204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
Db 669 TCCATGATGTCGCGCACCAGATGTCGAGAGGGTTAAATTAACAGTTAATTAACCA 728
Qy 224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
Db 729 TACATTCGGAGCAGAACATCGGGCTCCCTTGGCCATCGAGGTATTTTGCAGTGT 788
Qy 244 GluAlaSerAlaValProSerAla-GluPheGlnTrpTyrLysAspAspLysArgLeuI1 263
Db 789 GAAGCCTCTGCTACCTGCGACCGGACTTCTTCTGTCACAGGAAGAACAAAGGCTGAG 848
Qy 263 eGluGlyLysLys-GlyValLysValGlu 272
Db 849 TGATTCAGGAGGGGGTCAAGTAGAG 877

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RESULT 12
CF737474
LOCUS
DEFINITION
  UI-M-HD0-cks-o-09-0-UI-r1 NIH BMAP_HD0 Mus musculus cDNA clone
  IMAGE:30614264 5', mRNA sequence.
ACCESSION
  CF737474
VERSION
  CF737474.1 GI:37633810
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: c9apbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefi.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pYX-5.

```

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FEATURES
  source
    1..759
      Location/Qualifiers
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="CS7BL/6"
        /db_xref="taxon:10090"
        /clone="IMAGE:30614264"
        /tissue_type="whole eye"
        /dev_stage="embryo 12.5,13.5,14.5 dpc"
        /lab_host="DH10B (T1 phage resistant)"
        /clone_lib="NIH BMAP_HD0"
        /note="Organ: Eye; Vector: pYX- Asc; Site 1: EcoR I;
        Site 2: Not I; The library was constructed according
        Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
        1996. Denatured RNA was size fractionated on a 1% agarose

```

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

```

Alignment Scores:
Pred. No.: 9,25e-118 Length: 759
Score: 1094.50 Matches: 216
Percent Similarity: 92.83% Conservative: 4
Best Local Similarity: 91.14% Mismatches: 14
Query Match: 60.60% Indels: 4
Db: 7 Gaps: 1

US-10-017-084A-523 (1-344) x CF737474 (1-759)

Qy 12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe-----GlnGly 28
Db 45 CTGCCCTGGAAGTGCCTCGTGTCTCTCTCAGGCTGCTATTCCTGTACCCACAGGA 104
Qy 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
Db 105 GTGCGGTGCGTAGCGGAGATGCCACCTTCCCAAGCTATGGACACGTCAGCGTCAGG 164
Qy 49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
Db 165 CAGGGGAGAGCGCCACCTCAGGTGCACATTTGACACCGAGTCACCGGGTGGCGCTGG 224
Qy 69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
Db 225 CTAACCCGAGTACCCTCTCTATGGAATGACAAAGTGTGTGCTAGATCTCTGTGTG 284
Qy 89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
Db 285 GTCTCTCTGAGTAACACCCACAGCCAGTACAGCATTGAGATCCAGATGTGTGTAC 344
Qy 109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
Db 345 GATGAGGCGCCCTATACCTGCTCGGTACAGACAGACCAACCCCTTAAGACCTCCAGGTC 404
Qy 129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
Db 405 CACCTCATTTGACAGATATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCCATTAT 464
Qy 149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
Db 465 GAAGGAACACATCAGCTCCTCATTGTCATGCCACAGTAGACCGGAGCCTACAGTAACC 524
Qy 169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
Db 525 TCGAGACATATTTCTCCCAAGCGCTTGGCTTTGTGAGTGAAGTACGATGAGTGCAGATC 584
Qy 189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
Db 585 CAGGGCATCATCGGGAACAGTCAGGAGTACGAGTACGAGCGCTCCAACACGCTGGGG 644
Qy 209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
Db 645 GCACCATGTTGACGAGAGTGAAGGTCAACCGTGNACTATCCACCATACATCTCAAGAGCT 704
Qy 229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAla 245
Db 705 AAGGCGACAGGTGTCCCGTGGGCAAGAGGACT-CTGCGAGTGTGAAGCT 754

```

RESULT 13
AL533026
LOCUS

1027 bp mRNA linear EST 24-MAR-2004

DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CSODN005YD20 5-PRIME, mRNA sequence.
 AL533026
 VERSION AL533026.3 GI:45707932
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1027)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:31070858.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6387.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CSODN005YD20&f=6387.f.
 FEATURES
 source
 1..1027
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODN005YD20"
 /tissue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 ORIGIN
 Alignment Scores:
 Pred. No.: 8 59e-114 Length: 1027
 Score: 1062.50 Matches: 211
 Percent Similarity: 84.19% Conservative: 2
 Best Local Similarity: 83.40% Mismatches: 0
 Query Match: 58.83% Indels: 40
 DB: 1 Gaps: 1
 US-10-017-084A-523 (1-344) x AL533026 (1-1027)
 Qy 132 ValGlnValSerProLysIleValGluLeuSerGluSerAspIleSerIleAsnGluGlyAsn 151
 : : : : :
 Db 98 ATTAAGATGATCTCCCAAAATTGTAGAGATTCTTCAGATATCTCCATTAATGAAGGAAC 157
 Qy 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
 Db 158 AATATTAGCCCTCACCTGTCATGCACTGGTAGACCAGAGCCCTACGGTTACTTTGGAGACAC 217
 Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
 Db 218 ATCTCTCCAAAGCGGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATC 277
 Qy 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
 Db 278 ACCCGGAGCAGCTCAGGGGACTACAGTGCAGTGCCTCCCAATGAGTGGCGCGCCCGTG 337
 Qy 212 ValArgArgValIleValThrValAsnTyrProTyrIleSerGluAlaIleGlyThr 231
 Db 338 GTACCGAGAGTAAGGTACCGGTGAACATATCCACCATTATTCAGAAGCCAAGGGTACA 397
 Qy 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251

Db 398 GGTGTCCTGGGGGCAAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 457
 Qy 252 GluPheGlnTrpTyrLysAspAsp-Lys----- 260
 Db 458 GAATTTCCAGTGTGTACAAGGATGACAAAAGAGCTGAAATCTCATTTCACAGTTTGGTTATGA 517
 Qy 260 ----- 260
 Db 518 TGGGAAAGCTTCCTCCCATGCTGGAGCAATGGTGTCAAACGGCCAGTGGGATCAATCA 577
 Qy 261 -----ArgLeuIleGluGlyLysLysGlyValGlyValGly 272
 Db 578 GCCTGACTTGTCTGCAGAAATCTCTCCGACTGATTGAAGGAAAGAGGGTGAAAGTGA 637
 Qy 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
 Db 638 AAACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAA 697
 Qy 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG 312
 Db 698 CTACACTTGGTGGCTTCCAAAGCTGGGCCACCAATGCCAGCATCATGCTATTGG 757
 Qy 312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLe 332
 Db 758 TCCAGGCGCGCTCAGCGAGGTGAGCAACGGCACGCTCGAGGAGGCGAGCTGCGTCTGGCT 817
 Qy 332 uLeuProLeuValLeuHisLeuLeuLysPhe 344
 Db 818 GCTGCTCTTCTGTGTGTGACCTGCTTCTCAAAATTT 854
 RESULT 14
 CR602526 2512 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CSODN005YD20 of Adult brain of Homo sapiens
 DEFINITION (human).
 ACCESSION CR602526
 VERSION CR602526.1 GI:50483333
 KEYWORDS HTC; CNSLT_cDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2512)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 2512)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 Location/Qualifiers
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 /clone="CSODN005YD20"
 /tissue_type="Adult brain"
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 /db_xref="taxon:9606"
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 /plasmid="pCMVSPORT_6"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.34e-113 Length: 2512

Score: 1062.50 Matches: 211
Percent Similarity: 84.19% Conservative: 2
Best Local Similarity: 83.40% Mismatches: 0
Query Match: 58.83% Indels: 40
DB: 3 Gaps: 1

US-10-017-084A-523 (1-344) x CR602526 (1-2512)

QY 132 ValGlnValSerProlylsileValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db 97 ATTAAAGTATCTCCCAAAATTTAGAGATTCTTCAGATATCTCCATTAATGAGGGAAC 156

QY 152 AnlIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
Db 157 AATATTAGCTCCTACCTGCGATAGCACTGTGTAGACAGAGCTACGCTTACTTGGAGACAC 216

QY 172 IleSerProLYAlaValGlyPheValSerGluAspGluThrLeuGluIleGlnGlyIle 191
Db 217 ATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGCAATATCTTGGAAATTCAGGSCATC 276

QY 192 ThrArgGluInSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
Db 277 ACCAGGAGCAGTCAGGGGACTACGAGTCAGTGCCTCCATGACGTGGCGCGCCGCG 336

QY 212 ValArgArgValIysValThrValAsnTyrProProTyrIleSerGluAlaIysGlyThr 231
Db 337 GTACGAGAGTAAGTCAACCGTCACTATCCACCATATCCAGAGCCCAAGGGGTACA 396

QY 232 GlyValProValGlyGlnIysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
Db 397 GGTGTCCCGCGGGACMAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 456

QY 252 GluPheGlnTrpTyrIysAspLys 260
Db 457 GAATTCACGCTGTACAAAGATGACAAAGAGCTGAATCTCATTCACAGCTTTGGTTATGA 516

QY 260 260

Db 517 TGGGAAAGCTTCTCCCTCCATGTGGCAGTAATGGTGTCAAACGCGCAGTGGGATCAATCA 576

QY 261 261

Db 577 GCCTGACTGCTCGCAGAAATCTCCGACTGATTAAGGAAAGAGGGGTGAAGGTGA 636

QY 272 uAnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
Db 637 AAACAGACCTTCTCTCAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGGA 696

QY 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG 312
Db 697 CTACACTTGGTGGGCTTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTGG 756

QY 312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrole 332
Db 757 TCAGGCGCGCTCAGGAGGTGAGCAACGCGACGTCGAGAGGGGAGGCTGCTGTCTGGCT 816

QY 332 uLeuProLeuValLeuHisLeuLeuLysPhe 344
Db 817 GCTGCTCTCTCTGCTTGTGACCTGCTCTCAAAATT 853

RESULT 15
BU368328
LOCUS 603789424F1 CSEQCHN72 Gallus gallus cDNA clone ChEST750p6 5', mRNA
DEFINITION sequence.
ACCESSION BU368328
VERSION BU368328.1 GI:25876329
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 740)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PubMed 12445392
COMMENT Contact: Simon Hubbard
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
Location/Qualifiers
1..740
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST750p6"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSRQCHN72"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Alignment Scores:
Pred. No.: 3,496-112 Length: 740
Score: 1047.00 Matches: 192
Percent Similarity: 91.85% Conservative: 22
Best Local Similarity: 82.40% Mismatches: 19
Query Match: 57.97% Indels: 0
DB: 5 Gaps: 0

US-10-017-084A-523 (1-344) x BU368328 (1-740)

QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 3 CAGATCCAGACGCTGACGTGATGAAGGGCCCTACCTGCTCGTGACAGAC 62

QY 121 AnHisProLYeThrSerArgValHisLeuIleValGlnValSerProLYsIleValGlu 140
Db 63 AATACCCCAAGACATCTCGGTGACCTCATTTGCAAGTGTGCCGAAATATTCCGAG 122

QY 141 IleSerSerAspIleSerIleAsnGluGlyAnAsnIleSerLeuThrCysIleAlaThr 160
Db 123 ATCTCTTCTGACATCTCCATCAATCAAGGTGGCAACGTCAGCTCAGCTGCATAGCACG 182

QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLYeAlaValGlyPheVal 180
Db 183 GCGAGGCCAGACCCCAATCACCTCGGAGACACATCTGCCCAAGCTGTGGGCTTCATC 242

QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 243 ACGGAGGACGAGTACTCTGAGATCACAGGCATCACAGGGAGCAGTCTGGGCGGAGTACGAG 302

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Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db |||||
Db 303 TGCAGTGGCTCCACGAGCTGGCCGGCTGTCTGTCAGCGAGTCAAAGTCACCGTCAAC 362
Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db |||||
Db 363 TACCCACCGTACATCTCGGATCGAAGAGCACCGGTGTGCCGTGGGGCAGAGGGCATC 422
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
Db |||||
Db 423 CTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTTCCAGTGGTACAAAGACGACAAG 482
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db |||||
Db 483 CGGCTGGCTGAAGACAGAAAGGCTGAAGTGGAAACAAAGCCCTTCTTCCGACTG 542
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db |||||
Db 543 ACTTTCTTCAAGTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCCTCCCAACCAG 602
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db |||||
Db 603 CTAGGAAACACCAAGCCAGCATGATCTTTATGGCCCCCGGTGCAGTGCACGATGGCAAC 662
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeu 333
Db |||||
Db 663 AGCGGTGGTGGCGCGGAGGAGCTGTGCCTGGCTGCTG 701
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